

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 611 West Sixth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90017  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
 SOFTWARE: WordPerfect (Version 5.1)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/192.943  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/936.422  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 197/241  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-192-943-14

Alignment Scores:  
 Pred. No.: 9.02e+03 Length: 14  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-192-943-14 (1-14)

QY 104 LeuSerLeuAIG 107  
 Db 12 CTGCTCTTGGCC 1  
 RESULT 272  
 US-09-647-344A-45/c  
 ; Sequence 45, Application US/09647344A  
 ; Patent No. 6586180  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruffner, Duane E.  
 ; APPLICANT: Pierce, Michael L.  
 ; APPLICANT: Chen, Zhidong  
 ; TITLE OF INVENTION: Directed Antisense Libraries  
 ; FILE REFERENCE: T6678.PCT.US  
 ; CURRENT APPLICATION NUMBER: US/09/647,344A  
 ; CURRENT FILING DATE: 2000-12-04  
 ; PRIOR APPLICATION NUMBER: PCT/US99/06742  
 ; PRIOR FILING DATE: 1999-03-28  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SEQ ID NO 45  
 ; LENGTH: 14  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: A sequence flanking a chloramphenicol (CAT) gene and containing a  
 US-09-647-344A-45

Alignment Scores:

Pred. No.: 9.02e+03 Length: 14  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-966-880A-8 (1-198) x US-09-647-344A-45 (1-14)  
 QY 171 ArgLeuSerAIG 174  
 Db 12 CGGCTCTGCGA 1  
 RESULT 273  
 US-09-401-063-1779/c  
 ; Sequence 1779, Application US/09401063  
 ; Patent No. 6623962  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Akhtar, Saghir  
 ; APPLICANT: Fell, Patricia  
 ; APPLICANT: McSwiggen, James  
 ; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT  
 ; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED  
 ; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH  
 ; TITLE OF INVENTION: FACTOR RECEPTORS  
 ; NUMBER OF SEQUENCES: 1877  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: EasySEQ for Windows 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/401,063  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/985,162  
 ; FILING DATE: 04 December 1997  
 ; APPLICATION NUMBER: 60/036,476  
 ; FILING DATE: 31 January 1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 230/107  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 1779:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-401-063-1779

Alignment Scores:  
 Pred. No.: 9.02e+03 Length: 14  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x US-09-401-063-1779 (1-14)

QY 130 HisargAlagly 133

DB 13 CACAGGCGAGG 2

RESULT 274

US-09-401-063-1821

; Sequence 1821, Application US/09401063

; Patent No. 6623962

; GENERAL INFORMATION:

; APPLICANT: Akhtar, Saghir

; APPLICANT: Fell, Patricia

; APPLICANT: McSwiggen, James

; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT

; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED

; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH

; TITLE OF INVENTION: FACTOR RECEPTORS

; NUMBER OF SEQUENCES: 1877

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/401,063

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/985,162

; FILING DATE: 04 December 1997

; APPLICATION NUMBER: 60/036,476

; FILING DATE: 31 January 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 230/107

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1821:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-401-063-1821

Alignment Scores:

Pred. No.:	9.02e+03	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-401-063-1821 (1-14)

QY 134 ValGinIleAla 137

DB 1 GUGCAGGCGCA 12

RESULT 275

US-09-874-601-17

; Sequence 17, Application US/09874601

; Patent No. 6632057

; GENERAL INFORMATION:

; APPLICANT: LEWIN, ALFRED S.

; APPLICANT: SHAW, LYNN C.

; APPLICANT: GRANT, MARIA B.

; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHO

; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES

; FILE REFERENCE: 4300.014100

; CURRENT APPLICATION NUMBER: US/09/874,601

; CURRENT FILING DATE: 2001-05-01

; PRIOR APPLICATION NUMBER: 09/063,667

; PRIOR FILING DATE: 1998-04-21

; PRIOR APPLICATION NUMBER: 60/046,147

; PRIOR FILING DATE: 1997-05-09

; PRIOR APPLICATION NUMBER: 60/044,492

; PRIOR FILING DATE: 1997-04-21

; NUMBER OF SEQ ID NOS: 182

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 17

; LENGTH: 14

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)..(1)

; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-874-601-17

Alignment Scores:

Pred. No.:	9.02e+03	Length:	14
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	4	Gaps:	0

US-09-966-880A-8 (1-198) x US-09-874-601-17 (1-14)

QY 83 SerTtpSerPro 86

DB 1 UUGUGUCCCU 12

RESULT 276

PCT-US94-04496-16/c

; Sequence 16, Application PC/TUS9404496

; GENERAL INFORMATION:

; APPLICANT: Croce, Carlo

; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods

; TITLE OF INVENTION: for Detection and treatment of Acute Leukemias

; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &

; STREET: One Liberty Place, 46th floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/04496

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: DeLuca Esq., Mark

REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: JUJ-1242  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: NO  
PCT-US94-04496-16

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x PCT-US94-04496-16 (1-14)

QY 46 PheGlyTyrLeu 49  
Db 13 TTTGGGTACCTT 2

RESULT 277  
5166057-8/c  
Patent No. 5166057  
APPLICANT: FALISE, PETER; PARVIN, JEFFREY D.; KRYSTAL, MARK  
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS  
EXPRESSION-SYSTEMS  
NUMBER OF SEQUENCES: 43  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/527,237  
FILING DATE: 22-MAY-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 440,053  
FILING DATE: 21-NOV-1989  
APPLICATION NUMBER: 399,728  
FILING DATE: 28-AUG-1989  
SEQ ID NO: 8:  
LENGTH: 14  
5166057-8

Alignment Scores:  
Pred. No.: 9.02e+03 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x 5166057-8 (1-14)

QY 59 LeuLeuPheLeu 62  
Db 14 CTCCTGTTCTA 3

RESULT 278  
US-07-990-297-21/c  
Sequence 21, Application US/07990297  
Patent No. 5340728  
GENERAL INFORMATION:  
APPLICANT: GROSZ, RON  
TITLE OF INVENTION: IMPROVED METHOD FOR  
TITLE OF INVENTION: AMPLIFICATION OF TARGETED  
TITLE OF INVENTION: SEGMENTS OF NUCLEIC ACID USING  
TITLE OF INVENTION: NESTED POLYMERASE CHAIN REACTION  
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: U.S.A.  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/990,297  
FILING DATE: 19921209  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: GEIGER, KATHLEEN W  
REGISTRATION NUMBER: 35,880  
REFERENCE/DOCKET NUMBER: MD-0103  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-892-8112  
TELEFAX: 302-892-7949  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-990-297-21

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-990-297-21 (1-15)

QY 86 ProCysTyrAsp 89  
Db 15 CCTGTGTACGAC 4

RESULT 279  
US-07-962-569A-1  
Sequence 1, Application US/07962569A  
Patent No. 5391497  
GENERAL INFORMATION:  
APPLICANT: MENON, RAVI S.  
APPLICANT: JEFFERS, KATHLEEN F.  
APPLICANT: CHANG, YING-FON  
APPLICANT: HAM, RICHARD G.  
TITLE OF INVENTION: HUMAN K-CASEIN  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FREDERICK W. PEPPER, PH.D.  
STREET: 11545 W. BERNARDO COURT, STE. 302  
CITY: SAN DIEGO  
STATE: CA  
COUNTRY: USA  
ZIP: 92127

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/962,569A  
FILING DATE: 19921013  
CLASSIFICATION: 435

```
; ATTORNEY/AGENT INFORMATION:
; NAME: PEPPER PH.D., FREDERICK W.
; REGISTRATION NUMBER: 31,286
; REFERENCE/DOCKET NUMBER: 920224.01
; TELEPHONE: (619) 451-1120
; TELEFAX: (619) 451-9628
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
US-07-962-569A-1

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-07-962-569A-1 (1-15)
QY 83 SerTipSerPro 86
Db 4 TCCTGGAGCCG 15

RESULT 280
US-08-365-189-10/c
; Sequence 10, Application US/08365189
; Patent No. 5514576
; GENERAL INFORMATION:
; APPLICANT: Bower, Patricia A.
; TITLE OF INVENTION: Cloned Pullulanase
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,189
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/132,648
; FILING DATE: October 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryser, David G.
; REGISTRATION NUMBER: 36,407
; REFERENCE/DOCKET NUMBER: 66-005-9367-4
; TELEPHONE: (414) 277-5717
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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```
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..15
US-08-365-189-10

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-365-189-10 (1-15)
QY 41 SerPheserieu 44
Db 12 AGCTTCAGCCTC 1

RESULT 281
US-08-145-704-45
; Sequence 45, Application US/08145704
; Patent No. 5567604
; GENERAL INFORMATION:
; APPLICANT: Rando, Robert F.
; APPLICANT: Pennewald, Susan
; APPLICANT: Zendegeui, Joseph G.
; APPLICANT: Joshua O. Ojwang
; TITLE OF INVENTION: Anti-Viral Guanosine-Rich
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,704
; FILING DATE: 28-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/053,027
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5574-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5151
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-145-704-45

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
```



```

DB:                                     1          Gaps: 0
US-09-966-880A-8 (1-198) x US-08-145-704-45 (1-15)
QY  33 VallysAICAG 36
    |||||
Db   1 GTAAACGACGG 12

RESULT 282
US-08-242-664-27/c
; Sequence 27, Application US/08242664
; Patent No. 5571937
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Kyoichi A.
; APPLICANT: Ren, Wu-yun
; APPLICANT: Well, Roger
; TITLE OF INVENTION: Complementary DNA and Toxins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; FILING DATE: May 12, 1994
; APPLICATION NUMBER: US/08/242,664
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-242-664-27

Alignment Scores:
Pred. No.: 9.65e+03          Length: 15
Score: 4.00                  Matches: 4
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02%          Indels: 0
DB: 1                          Gaps: 0

US-09-966-880A-8 (1-198) x US-08-242-664-27 (1-15)
QY  59 LeuLeupheLeu 62
    |||||
Db   13 TTGCTCTTCCTC 2

RESULT 283
US-08-311-760A-32
; Sequence 32, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy

```

```

; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,760A
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-311-760A-32

Alignment Scores:
Pred. No.: 9.65e+03          Length: 15
Score: 4.00                  Matches: 4
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02%          Indels: 0
DB: 1                          Gaps: 0

US-09-966-880A-8 (1-198) x US-08-311-760A-32 (1-15)
QY  180 LeuLeuProLeu 183
    |||||
Db   3 CUACUACCAUA 14

RESULT 284
US-08-311-760A-187
; Sequence 187, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

```

; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.760A
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 187:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-760A-187

```

```

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

```

```
US-09-966-880A-8 (1-198) x US-08-311-760A-187 (1-15)
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Qy 180 LeuLeuProLeu 183
Db 3 CUACUACCAUUA 14

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```

RESULT 285
US-08-182-968A-60
; Sequence 60, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA: 07/882,888
; APPLICATION NUMBER:
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-60

```

```

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

```

```
US-09-966-880A-8 (1-198) x US-08-182-968A-60 (1-15)
```

```

Qy 59 LeuLeuPheLeu 62
Db 3 UUGCUCUUCUC 14

```

```

RESULT 286
US-08-182-968A-175
; Sequence 175, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

```

INFORMATION FOR SEQ ID NO: 175:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-175

## Alignment Scores:

Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-175 (1-15)

QY 164 GlyLeuHisGlu 167

DB 3 GGCCUUCAGAA 14

## RESULT 287

US-08-182-968A-176  
Sequence 176, Application US/08182968A  
Patent No. 5610054

## GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
INHIBITING HEPATITIS C  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 176:

## SEQUENCE CHARACTERISTICS:

LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-182-968A-176

## Alignment Scores:

Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-176 (1-15)

QY 164 GlyLeuHisGlu 167

DB 2 GGCCUUCAGAA 13

## RESULT 288

US-08-182-968A-224/c  
Sequence 224, Application US/08182968A  
Patent No. 5610054

## GENERAL INFORMATION:

APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
INHIBITING HEPATITIS C  
TITLE OF INVENTION: INHIBITING HEPATITIS C  
NUMBER OF SEQUENCES: 497  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/182,968A  
FILING DATE: 13-JANUARY-1994

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/882,888  
FILING DATE: 14-MAY-1992

## ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 205/277  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 224:

## SEQUENCE CHARACTERISTICS:

LENGTH: 15

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-182-968A-224

## Alignment Scores:

Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-224 (1-15)

QY 72 ProGlyArgCys 75

DB 15 CCCGGAAGATGC 4

## RESULT 289

US-08-182-968A-225/c  
Sequence 225, Application US/08182968A  
Patent No. 5610054

GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/182,968A  
; FILING DATE: 13-JANUARY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: 14-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 205/277  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 225:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-182-968A-225

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-225 (1-15)

Qy 72 ProGlyArgCys 75  
Db 13 CCGGAGATGC 2

RESULT 290  
US-08-182-968A-226/c  
; Sequence 226, Application US/08182968A  
; Patent No. 5610054  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.

ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/182,968A  
; FILING DATE: 13-JANUARY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: 14-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 205/277  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 226:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-182-968A-226

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-226 (1-15)

Qy 72 ProGlyArgCys 75  
Db 12 CCGGAGATGC 1

RESULT 291  
US-08-182-968A-227  
; Sequence 227, Application US/08182968A  
; Patent No. 5610054  
; GENERAL INFORMATION:  
; APPLICANT: Draper, Kenneth G.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: INHIBITING HEPATITIS C  
; TITLE OF INVENTION: VIRUS REPLICATION  
; NUMBER OF SEQUENCES: 497  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/182,968A  
; FILING DATE: 13-JANUARY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/882,888  
; FILING DATE: 14-MAY-1992

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 227:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-227

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-227 (1-15)

QY 125 GlyLeuATGAG 128
Db 4 GGGUUGCGAGG 15

RESULT 292
US-08-182-968A-299/c
; Sequence 299, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 299:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
US-08-182-968A-299

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-299 (1-15)

QY 123 ProGluGlyLeu 126
Db 12 CCGAAGGCCTC 1

RESULT 293
US-08-182-968A-347
; Sequence 347, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-347

Alignment Scores:
Pred. No.: 9.65e+03 Length: 15
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-182-968A-347 (1-15)

```



STREET: 633 West Fifth Street  
STREET: Suite 4700  
City: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-319-492B-117

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-58 (1-15)

QY 103 AsnLeuSerLeu 106  
Db 1 AACUUGUCCUA 12

RESULT 297  
US-08-319-492B-117  
Sequence 117, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OF IL-5  
NUMBER OF SEQUENCES: 751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-319-492B-58

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-58 (1-15)

QY 103 AsnLeuSerLeu 106  
Db 1 AACUUGUCCUA 12

RESULT 297  
US-08-319-492B-117  
Sequence 117, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OF IL-5  
NUMBER OF SEQUENCES: 751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-319-492B-58

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-58 (1-15)

QY 103 AsnLeuSerLeu 106  
Db 1 AACUUGUCCUA 12

RESULT 297  
US-08-319-492B-117  
Sequence 117, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OF IL-5  
NUMBER OF SEQUENCES: 751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-319-492B-58

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-58 (1-15)

QY 103 AsnLeuSerLeu 106  
Db 1 AACUUGUCCUA 12

RESULT 297  
US-08-319-492B-117  
Sequence 117, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OF IL-5  
NUMBER OF SEQUENCES: 751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/319,492B  
FILING DATE: October 7, 1994

PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-319-492B-58

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-58 (1-15)

QY 103 AsnLeuSerLeu 106  
Db 1 AACUUGUCCUA 12

RESULT 297  
US-08-319-492B-117  
Sequence 117, Application US/08319492B  
Patent No. 5616488  
GENERAL INFORMATION:  
APPLICANT: Sullivan, Sean M.  
APPLICANT: Draper, Kenneth G.  
APPLICANT: McSwiggen, James  
APPLICANT: Stinchcomb, Dan T.  
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES  
TITLE OF INVENTION: OF IL-5  
NUMBER

```
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/319,492B
/ FILING DATE: October 7, 1994
/ PRIOR APPLICATION DATA: including application
/ PRIOR APPLICATION DATA: described below:
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/276
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 118:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-319-492B-118
/
/ Alignment Scores:
/ Pred. No.: 9.65e-03 Length: 15
/ Score: 4.00 Matches: 4
/ Percent Similarity: 100.00% Conservative: 0
/ Best Local Similarity: 100.00% Mismatches: 0
/ Query Match: 2.02% Indels: 0
/ DB: 1 Gaps: 0
/
/ US-09-966-880A-8 (1-198) x US-08-319-492B-118 (1-15)
/
/ QY 64 TyrlleSerAsp 67
/ Db 2 UAUUUUUCAGAU 13
/
/ RESULT 299
/ US-08-319-492B-119
/ Sequence 119, Application US/08319492B
/ Patent No. 5616488
/ GENERAL INFORMATION:
/ APPLICANT: Sullivan, Sean M.
/ APPLICANT: Draper, Kenneth G.
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
/ TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF IL-5
/ NUMBER OF SEQUENCES: 751
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ STATE: Los Angeles
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/319,492B
/ FILING DATE: October 7, 1994
/ PRIOR APPLICATION DATA: including application
/ PRIOR APPLICATION DATA: described below:
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
```

Two

```
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 209/276
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 119:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-319-492B-119
/
/ Alignment Scores:
/ Pred. No.: 9.65e-03 Length: 15
/ Score: 4.00 Matches: 4
/ Percent Similarity: 100.00% Conservative: 0
/ Best Local Similarity: 100.00% Mismatches: 0
/ Query Match: 2.02% Indels: 0
/ DB: 1 Gaps: 0
/
/ US-09-966-880A-8 (1-198) x US-08-319-492B-119 (1-15)
/
/ QY 64 TyrlleSerAsp 67
/ Db 1 UAUUUUUCAGAU 12
/
/ RESULT 300
/ US-08-319-492B-173
/ Sequence 173, Application US/08319492B
/ Patent No. 5616488
/ GENERAL INFORMATION:
/ APPLICANT: Sullivan, Sean M.
/ APPLICANT: Draper, Kenneth G.
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
/ TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF IL-5
/ NUMBER OF SEQUENCES: 751
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Suite 4700
/ STATE: Los Angeles
/ COUNTRY: U.S.A.
/ ZIP: 90071
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/319,492B
/ FILING DATE: October 7, 1994
/ PRIOR APPLICATION DATA: including application
/ PRIOR APPLICATION DATA: described below:
/ APPLICATION NUMBER: 08/008,895
/ FILING DATE: January 19, 1993
/ APPLICATION NUMBER: 07/989,849
/ FILING DATE: December 7, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard
```

Two



REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/276  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 173:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-319-492B-173

Alignment Scores:  
Pred. No.: 9.65e+03 Length: 15  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x US-08-319-492B-173 (1-15)

QY 30 CysTyrValVal 33  
DB 4 UGUUAUGUGUG 15

Search completed: March 5, 2004, 02:20:47  
Job time : 87 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 4, 2004, 23:31:58 ; Search time 397 Seconds  
(without alignments)  
2118.749 Million cell updates/sec

Title: US-09-966-880A-8

Perfect score: 198

Sequence: 1 MDSLLMNRKFLYQFNVRW.....ILLPLYEVDLRLDAFRTGL 198

Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1688237

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DBV=xlh  
-Q=/cgn2\_1/USPTO.spool/US09966880/runat\_04032004\_083152\_22377/app\_query.fasta\_1.391  
-DB=N Geneseq 29Jan04 -QFMT=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=300 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=20  
-USER=US09966880@cgn\_1\_1\_470@runat\_04032004\_083152\_22377 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Databases : N Geneseq 29Jan04:\*

1: Geneseqn19808:.\*  
2: Geneseqn19908:.\*  
3: Geneseqn20008:.\*  
4: Geneseqn2001as:.\*  
5: Geneseqn2001bs:.\*  
6: Geneseqn2002s:.\*  
7: Geneseqn2003as:.\*  
8: Geneseqn2003bs:.\*  
9: Geneseqn2003cs:.\*  
10: Geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	3.0	18	3 AAZ77408	Human bia
2	6	3.0	19	3 AAZ73262	Human bia
3	6	3.0	20	2 AAV09175	Phosphoro
4	6	3.0	20	2 AAX36050	PCR prime
5	6	3.0	20	3 AAZ74954	Human bia
6	6	3.0	20	3 AAZ73437	Chimeric
7	6	3.0	20	9 ACF36600	RXR-beta
8	5	2.5	15	2 AAX31672	Tag seque

C	9	5	2.5	15	4	AAF52623	Aaf52623 IGF-I oli
	10	5	2.5	15	4	AAF53096	Aaf53096 IGF-I oli
	11	5	2.5	15	6	ABK32626	Abk32626 Human pan
	12	5	2.5	15	7	ACD56498	Acg56498 HBV enzym
	13	5	2.5	15	9	ADD28710	Add28710 Escherich
C	14	5	2.5	15	9	ADD28861	Add28861 Escherich
	15	5	2.5	15	9	ADD28860	Add28860 Escherich
C	16	5	2.5	15	9	ADD28711	Add28711 Escherich
C	17	5	2.5	16	2	AAQ81257	Aaq81257 Ribozyme
C	18	5	2.5	16	6	ABL52895	Ab152895 Mutant cu
	19	5	2.5	17	2	RAAT53462	Rat ICAM
	20	5	2.5	17	2	RAAT53758	Rat ICAM
	21	5	2.5	17	2	RAAT53666	Rat ICAM
	22	5	2.5	17	2	RAAT53748	Rat ICAM
	23	5	2.5	17	2	RAAT53431	Rat ICAM
	24	5	2.5	17	2	RAAT74553	Mouse flt
	25	5	2.5	17	2	RAAT74554	Mouse flt
	26	5	2.5	17	2	RAAT71605	Human KDR
	27	5	2.5	17	2	RAAX6260	Human KDR
	28	5	2.5	17	2	RAAX71604	Human KDR
	29	5	2.5	17	2	RAAX71606	Human KDR
	30	5	2.5	17	2	RAAX69261	Human flt
C	31	5	2.5	17	2	RAAV94862	Mouse IL-
	32	5	2.5	17	2	RAAV94863	Mouse IL-
	33	5	2.5	17	2	RAA20716	Integrin
C	34	5	2.5	17	2	RAV91119	Human C-r
C	35	5	2.5	17	2	RAV93554	Human B-r
	36	5	2.5	17	2	RAV92402	Human A-R
C	37	5	2.5	17	2	RAA54363	NK-KB ant
C	38	5	2.5	17	3	AAA33807	Low adeno
	39	5	2.5	17	3	AAA36106	Human Gen
C	40	5	2.5	17	3	AAF19929	Human NF-
	41	5	2.5	17	3	AAA35939	Oestrogen
	42	5	2.5	17	3	AAA24771	Oestrogen
C	43	5	2.5	17	3	AAF04476	Hammerhea
C	44	5	2.5	17	4	ABK01373	Human NOG
C	45	5	2.5	17	4	ABK00382	Human NOG

#### ALIGNMENTS

#### RESULT 1

ID AAZ77408  
XX AAZ77408 standard; DNA; 18 BP.  
AC AAZ77408;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human biallelic marker downstream amplification primer SEQ ID NO:11764.  
XX  
KW Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9954500-A2.  
XX  
PD 28-OCT-1999.  
XX  
PF 21-APR-1999; 99WO-IB000822.  
XX  
PR 21-APR-1998; 98US-0082614P.  
PR 23-NOV-1998; 98US-0109732P.  
XX  
PA (GEST ) GENSET.  
XX  
PI Cohen D, Blumenfeld M, Chumakov I;  
XX  
DR WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.

XX Claim 9; Page 2738; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

XX SQ Sequence 18 BP; 3 A; 9 C; 0 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	914	Length:	18
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	3	Gaps:	0

US-09-966-880A-8 (1-198) x AAZ77408 (1-18)

QY 179 IleleuLeuProLeuTYR 184

DB 1 ATCTCTCCCACTTCA 18

RESULT 2

AAZ73262/c

ID AAZ73262 standard; DNA; 19 BP.

XX AC AAZ73262;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker upstream amplification primer SEQ ID NO:7618.

XX Human genome; biallelic marker; high density disequilibrium map;  
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
KW haplotyping; hybridisation; identification; characterisation;  
KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
KW diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST ) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium  
PT map of the human genome.

XX Claim 9; Page 1855; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present  
CC invention, which contain a polymorphic base at position 24 of their  
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
CC primers for the biallelic markers. The biallelic markers of the invention  
CC have a variety of uses: they can be used for high density mapping of the  
CC human genome, and in complex association studies and haplotyping studies  
CC which are useful in determining the genetic basis for disease states.  
CC Compositions and methods of the invention can also be useful for the  
CC identification of the targets for the development of pharmaceutical  
CC agents and diagnostic methods, as well as the characterisation of the  
CC differential efficacious responses to and side effects from  
CC pharmaceutical agents acting on a disease as well as other treatment.  
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
CC 3367, are not actually given a sequence in the Sequence Listing from the  
CC present invention

XX SQ Sequence 19 BP; 4 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	960	Length:	19
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	3	Gaps:	0

US-09-966-880A-8 (1-198) x AAZ73262 (1-19)

QY 167 GluAenSerValArgLeu 172

DB 19 GAAATAGTGTAAAGCTC 2

RESULT 3

AAV09175

ID AAV09175 standard; DNA; 20 BP.

XX AC AAV09175;

XX 09-JUN-1998 (first entry)

XX Phosphorothioate oligonucleotide sequence 8054 targeting IL1R mRNA.

XX Type I interleukin-1 receptor; IL1R; human; IL1 protein; hybridisation;  
KW inflammation; ss; 5' Cap region; phosphorothioate linkage.

XX Synthetic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT modified\_base 1..20

FT /\*tag= a

FT /note= "Phosphorothioate internucleotide linkage"

XX WO9744656-A1.

XX 27-NOV-1997.

XX 12-MAY-1997; 97WO-US007147.

XX 21-MAY-1996; 96US-00651692.

XX (ISIS-) ISIS PHARM INC.

XX Miraglia L, Bennett CF, Dean N, Geiger T;

XX WPI; 1998-018646/02.

XX 2'-substituted oligonucleotide(s) specific for interleukin-1 receptor  
PT type I - used to modulate expression and detect overexpression of the  
PT receptor.

XX Example 5; Page 19; 63pp; English.

PS This is a novel oligomer comprising 20 covalently linked nucleotides

CC which bind to the 5' Cap region of the interleukin-1 receptor (IL1R)

CC mRNA. Expression of IL1R, in cells and tissues can be modulated by

CC compositions comprising oligomers which are able to specifically

CC hybridise with target areas of its encoding sequence. The composition can

CC be used for treatment of disease in humans caused by excessive receptor

CC expression, e.g. inflammation. When labelled they can be used

CC diagnostically to determine overexpression of IL1R, also to determine

CC localisation and distribution of this expression for research, diagnostic

CC or therapeutic purposes

XX Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.01e+03	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x AAV09175 (1-20)

Qy 125 GlyLeuArgLeuHis 130

Db 2 GGGCTCGCGGCTCCAC 19

RESULT 4

AAZ96050

ID AAZ96050 standard; DNA; 20 BP.

XX AC AAZ96050;

XX 13-SEP-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia pneumoniae.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

XX sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;

XX neutralising epitope; PCR primer; ss.

XX Synthetic.

OS Chlamydothila pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.

XX 04-NOV-1998; 98US-0107078P.

XX (GEST ) GENSET.

XX Griffais R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

XX Page 1795; Disclosure; 1912pp; English.

XX AAX91991-X97517 represent PCR primers used to amplify open reading frames

CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae

CC (see AAX91990). C. pneumoniae causes respiratory disease such as

CC pneumonia and bronchitis and is thought to be a contributing factor in

CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema

CC nodosum or pharyngitis. The polypeptides encoded by the open reading

CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used

CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae

CC nucleotide sequences can also be used as immunogenic compositions,

CC especially where the vector directs the expression of a neutralising

CC epitope of C. pneumoniae

XX Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.01e+03	Length:	20
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.03%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x AAX96050 (1-20)

Qy 167 GluAsnSerValArgLeu 172

Db 1 GAGAACTCGGTGCGCTG 18

RESULT 5

AAZ74954

ID AAZ74954 standard; DNA; 20 BP.

XX AC AAZ74954;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:9310.

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotyping; hybridisation; identification; characterisation;

XX amplification; single nucleotide polymorphism; SNP; PCR primer;

XX diagnosis; ss.

XX Homo sapiens.

XX WO9954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST ) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

XX map of the human genome.

XX Claim 8; Page 2215; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention  
 SQ Sequence 20 BP; 6 A; 6 C; 2 G; 6 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.01e+03 Length: 20  
 Score: 6.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.03% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ74954 (1-20)

QY 40 ThrSerPheSerLeuAsp 45  
 DB 2 ACAAGTTTCTCATTAGAC 19

RESULT 6  
 ABST73437/C  
 ID ABS73437 standard; DNA; 20 BP.  
 XX AC ABS73437;  
 XX DT 03-DEC-2002 (first entry)  
 XX DE Chimeric phosphorotioate oligonucleotide #18.

XX Human; glioma-associated oncogene-2; antisense compound; infection;  
 KW inflammation; tumour formation; antiinflammatory; antitumour;  
 KW inhibitor of human glioma-associated oncogene-2 expression;  
 KW antisense gene therapy; phosphorothioate; ss.

XX Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.

XX US6440739-B1.

XX 27-AUG-2002.

XX 17-JUL-2001; 2001US-00907843.

XX 17-JUL-2001; 2001US-00907843.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Freier SM;

XX WPI; 2002-697096/75.

XX Novel antisense compound that hybridizes and inhibits nucleic acid  
 PT encoding human glioma-associated oncogene-2, useful for treatment of  
 PT diseases associated with human glioma-associated oncogene-2.

XX Claim 3; Col 45; 43pp; English.

XX The present invention relates to a new antisense compound targeted to  
 CC human glioma-associated oncogene-2. The invention is useful for  
 CC inhibiting the expression of human glioma-associated oncogene-2 in cells  
 CC or tissues. The invention is also useful for treatment of diseases  
 CC associated with human glioma-associated oncogene-2. The invention is  
 CC further useful for diagnostics, therapeutics, prophylaxis, as research  
 CC reagents and kits, for distinguishing functions of various members of a  
 CC biological pathway, and in antisense gene therapy. The invention is also  
 CC useful prophylactically, e.g., to prevent or delay infection,  
 CC inflammation or tumour formation. The present nucleic acid sequence  
 CC represents an oligonucleotide that was used in the methods of the  
 CC invention to inhibit human glioma-associated oncogene-2

SQ Sequence 20 BP; 2 A; 9 C; 7 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.01e+03 Length: 20  
 Score: 6.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 3.03% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABS73437 (1-20)

QY 122 GluProGluGlyLeuArg 127  
 DB 18 GAGCCTGAGGGCCTGGG 1

RESULT 7  
 ACF36600/C  
 ID ACF36600 standard; DNA; 20 BP.  
 XX AC ACF36600;  
 XX DT 18-DEC-2003 (first entry)

XX DE RXR-beta cDNA amplifying RT-PCR primer RXR-1.  
 XX KW KRAB; repressor fusion protein; Kruppel-associated box; KAP1; RXR-beta;  
 KW cloned cell production; drug screening; luciferase; RT-PCR; primer; ss.

XX Synthetic.

XX WO2003072788-A1.

XX 04-SEP-2003.

XX 20-FEB-2003; 2003WO-US005347.

XX 21-FEB-2002; 2002US-0358599P.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX Rauscher FJ, Ayyanathan K, Schultz DC;

XX WPI; 2003-712733/67.

XX Producing a cloned cell containing a stably silenced target gene, useful  
 PT in research and drug screening, comprises introducing a nucleic acid  
 PT molecule expressing a chimeric repressor fusion protein into a parent  
 PT cell.

XX Example 7; Page 54; 113pp; English.

XX The invention relates to producing a cloned cell containing a stably  
 CC silenced target gene. The method involves introducing a nucleic acid  
 CC molecule expressing a chimeric repressor fusion protein into a parent  
 CC cell. The repressor fusion protein comprises a first amino acid sequence  
 CC comprising a Kruppel-Associated Box (KRAB) domain or its variant that  
 CC binds to the protein KAP1 and has DNA-dependent repressor activity fused  
 CC to a second amino acid targeting sequence that binds to the target gene,  
 CC fused to a switch component, that, in the presence of a ligand or  
 CC inducer, permits the second amino acid sequence to bind to the target  
 CC gene, where the fusion protein is under the control of regulatory  
 CC sequences capable of directing its expression in the parent cell. The  
 CC methods are useful for producing cloned cells that are particularly  
 CC useful in research and drug screening, e.g., identifying a test molecule  
 CC that activates the expression of a stably silenced target gene, or  
 CC manipulating expression of target gene in a cell. Sequences ACF36600-01  
 CC representing primers used in a RT-PCR assay for detecting levels of RXR-beta  
 CC mRNA in NIH3T3 cells

SQ Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.01e+03 Length: 20  
 Score: 6.00 Matches: 6  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.03% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ACF36600 (1-20)

QY 127 AtcArgLeuHisArgAla 132  
DB 18 CGCAGATTGCACAGGCC 1

RESULT 8

AAAX31672  
ID AAAX31672 standard; DNA; 15 BP.  
XX  
AC AAAX31672;  
XX  
XX  
DT 21-MAY-1999 (first entry)  
XX  
DE Tag sequence of a transcript increased in pancreatic cancer.  
XX  
KW Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;  
KW diagnosis; prognosis; treatment; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9853319-A2.  
XX  
PD 26-NOV-1998.  
XX  
PF 20-MAY-1998; 98WO-US010277.  
XX  
PR 21-MAY-1997; 97US-0047352P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Vogelstein B, Kinzler KW;  
XX  
DR WPI; 1999-070161/06.  
XX  
PT Use of isolated gene transcripts - useful for developing products for the  
PT diagnosis, prognosis and treatment of cancers, particularly colon and  
PT pancreatic cancer.  
XX  
PS Claim 13; Page 68; 120pp; English.

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

QY 93 HisValAlaAspPhe 97  
DB: |||||

US-09-966-880A-8 (1-198) x AAAX31672 (1-15)

Db 1 CATGTTGCTGACTTT 15

RESULT 9

AAAF52623/c  
ID AAFA52623 standard; DNA; 15 BP.  
XX  
AC AAFA52623;  
XX  
DT 30-MAR-2001 (first entry)  
XX  
DE IGF-1 oligonucleotide #3583.  
XX

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;  
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
KW hyperneovascular condition; hyperplasia; kidney disease;  
KW neovascular condition of the retina; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200078341-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 21-JUN-2000; 2000WO-AU000693.  
XX  
PR 21-JUN-1999; 99US-0140345P.  
XX  
PA (MURD-) MURDOCH CHILDRENS RES INST.  
XX  
PI Wraight CJ, Werther GA, Edmondson SR;  
XX  
DR WPI; 2001-041421/05.  
XX

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
XX inhibits or reduces growth factor mediated cell proliferation and/or  
XX inflammation.  
XX  
PS Example 8; Page 84; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of  
XX skin disorders. The method comprises contacting the skin with an  
XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
XX inhibiting or reducing growth factor mediated cell proliferation,  
XX inflammation and/or other disorders. The present sequence is an  
XX oligonucleotide which can be used to design the antisense  
XX oligonucleotides of the present invention (see AAF45151 and AAF45153-  
XX F45161). The method is useful for ameliorating the effects of psoriasis,  
XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
XX hyperneovascular condition such as a neovascular condition of the retina,  
XX brain or skin, growth factor-mediated malignancies, other sclerotic  
XX disease, kidney disease, hyperproliferation of the inside of blood  
XX vessels or any other hyperplasia  
XX

XX Sequence 15 BP; 1 A; 7 C; 2 G; 5 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 7.25e+03 Length: 15  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAFA52623 (1-15)

QY 124 GluGlyLeuArgArg 128

Db 15 GAGGACTCAGGAGA 1  
 RESULT 10  
 AAF53096  
 ID AAF53096 standard; DNA; 15 BP.  
 XX  
 AC AAF53096;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE IGF-I oligonucleotide #4056.  
 XX  
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
 KW cytostatic; dermatological; cardiant; viricide; ophthalmological; keloid;  
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pteryriasis;  
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;  
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
 KW hyperneovascular condition; hyperplasia; kidney disease;  
 KW neovascular condition of the retina; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078341-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 PF 21-JUN-2000; 2000WO-AU000693.  
 XX  
 PR 21-JUN-1999; 99US-0140345P.  
 XX  
 PA (MURD-) MURDOCH CHILDRENS RES INST.  
 XX  
 PI Wright CJ, Werther GA, Edmondson SR;  
 XX  
 DR WPI; 2001-041421/05.  
 XX  
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
 PT inhibits or reduces growth factor mediated cell proliferation and/or  
 PT inflammation.  
 XX  
 PS Example 8; Page 87; 201pp; English.  
 XX  
 CC The present invention relates to a method for ameliorating the effects of  
 CC skin disorders. The method comprises contacting the skin with an  
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
 CC inhibiting or reducing growth factor mediated cell proliferation,  
 CC inflammation and/or other disorders. The present sequence is an  
 CC oligonucleotide which can be used to design the antisense  
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
 CC F45161). The method is useful for ameliorating the effects of psoriasis,  
 CC ichthyosis, pteryriasis, ruba, pilaris, serborrhea, keloids, keratosis,  
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
 CC hyperneovascular condition such as a neovascular condition of the retina,  
 CC brain or skin, growth factor-mediated malignancies, other sclerotic  
 CC disease, kidney disease, hyperproliferation of the inside of blood  
 CC vessels or any other hyperplasia  
 XX  
 SQ Sequence 15 BP; 3 A; 6 C; 4 G; 2 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.25e+03 Length: 15  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAF53096 (1-15)

QY 174 ArgGlnLeuArgArg 178  
 Db 1 CGCCAGCTTCGACGA 15  
 RESULT 11  
 ABK32626  
 ID ABK32626 standard; DNA; 15 BP.  
 XX  
 AC ABK32626;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Human pancreatic cancer SAGE tag #178.  
 XX  
 KW Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;  
 KW serial analysis of gene expression; diagnostic; prognostic; probe;  
 KW cancer marker; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6333152-B1.  
 XX  
 PD 25-DEC-2001.  
 XX  
 PF 20-MAY-1998; 98US-00081646.  
 XX  
 PR 20-MAY-1998; 98US-00081646.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW, Zhang L, Zhou W;  
 XX  
 DR WPI; 2002-153821/20.  
 XX  
 PT New human nucleic acid containing specific SAGE tags, useful as  
 PT diagnostic markers for cancer, also derived probes.  
 XX  
 PS Disclosure; Col 82; 161pp; English.  
 XX  
 CC The invention relates to an isolated, purified human nucleic acid (I)  
 CC that has the same sequence as a mRNA found in humans and is a SAGE  
 CC (serial analysis of gene expression) tag comprising a single stranded  
 CC probe containing at least 10 consecutive nucleotides. SAGE tags, are  
 CC diagnostic and prognostic markers of cancer, especially of the colon and  
 CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer  
 CC SAGE tags of the invention  
 XX  
 SQ Sequence 15 BP; 2 A; 3 C; 3 G; 7 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.25e+03 Length: 15  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-966-880A-8 (1-198) x ABK32626 (1-15)  
 QY 93 HisValAlaAspPhe 97  
 Db 1 CATGTTGCTGACTTT 15  
 RESULT 12  
 ACD56498  
 ID ACD56498 standard; RNA; 15 BP.  
 XX  
 AC ACD56498;  
 XX  
 DT 24-SEP-2003 (first entry)  
 XX  
 DE HBV enzymatic nucleic acid substrate sequence #179.  
 XX



KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNase; inozyme; zinzyme;  
 KW ambrzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW viricide; antiinflammatory; substrate; ss.  
 XX  
 OS Hepatitis B virus.  
 XX  
 FN WO200281494-A1.  
 XX  
 PD 17-OCT-2002.  
 XX  
 PF 26-MAR-2002; 2002WO-US009187.  
 XX  
 PR 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (SLAY/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX  
 PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX  
 DR WPI; 2003-229207/22.  
 XX  
 PT Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX  
 PS Example 1; Page 221; 387pp; English.  
 XX  
 CC The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, ambrzymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HBV, and compounds  
 CC that modulate the expression and/or replication of HCV. The compounds and  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC enzymatic nucleic acid sequences disclosed in the present invention  
 XX  
 SQ Sequence 15 BP; 2 A; 6 C; 1 G; 0 T; 6 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.25e+03 Length: 15  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0

Qy 172 LeuSerArgGlnLeu 176  
 Db 1 CUUUUCGCCACUU 15  
 RESULT 13  
 ADD28710  
 ID ADD28710 standard; DNA; 15 BP.  
 XX  
 AC ADD28710;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Escherichia coli 0157:H7 VNTR amplicon sequence SEQ ID NO:325.  
 XX  
 KW molecular sub-typing system; Escherichia coli;  
 KW variable number tandem repeat; VNTR; genetic data;  
 KW epidemiological database; research; ds.  
 XX  
 OS Escherichia coli.  
 XX  
 FN WO2003050269-A2.  
 XX  
 PD 19-JUN-2003.  
 XX  
 PF 11-DEC-2002; 2002WO-US039914.  
 XX  
 PR 11-DEC-2001; 2001US-0339687P.  
 PA (UYAR-) UNIV ARIZONA.  
 PA (KEIM/) KEIM P.  
 PA (KEYS/) KEYS C.  
 XX  
 PI Keim P, Keys C;  
 XX  
 DR WPI; 2003-864934/80.  
 XX  
 PT Molecular sub-typing system for Escherichia coli, comprises observing and  
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA  
 PT sample.  
 XX  
 PS Claim 7; SEQ ID NO 325; 166pp; English.  
 XX  
 CC The present invention describes a molecular sub-typing system (S) for  
 CC Escherichia coli, which comprises observing and recording variable number  
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also  
 CC described: (1) VNTR loci (I) for sub-typing E. coli O157:H7; (2) primers  
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus  
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails  
 CC (III) for multiplex amplification of (I) comprising two or more primers  
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR  
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for  
 CC maintaining hybridisation and amplification condition in a PCR instrument  
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.  
 CC coli O157:H7 strains by multiplex, comprising (III), and amplifying in a  
 CC reagents for maintaining hybridisation and amplification condition in a  
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub  
 CC typing (M1) an E. coli strain, comprising: (a) obtaining one or more  
 CC primers for amplifying loci comprising VNTR, where the primers have an  
 CC observable indicator; (b) obtaining single-stranded sample DNA from the  
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA  
 CC and amplifying reagents under hybridising and amplifying conditions in a  
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)  
 CC separating the amplicons by size; (e) evaluating numbers and sizes of  
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of  
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for  
 CC producing discrete genetic data for an epidemiological database. (I) is  
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.  
 CC coli. The present sequence represents an E. coli VNTR loci related  
 CC amplicon sequence which is used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 15 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)  
 CC separating the amplicons by size; (e) evaluating numbers and sizes of  
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of  
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for  
 CC producing discrete genetic data for an epidemiological database. (1) is  
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.  
 CC coli. The present sequence represents an oligonucleotide which is used in  
 CC the exemplification of the present invention.  
 XX  
 SQ Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 U; 0 Other;  
 Alignment Scores: 7.25e+03 Length: 15  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 9  
 US-09-966-880A-8 (1-198) x ADD28861 (1-15)  
 QY 72 ProGlyArgCysTyr 76  
 Db 15 CCTGGACGGTGCTAC 1  
 RESULT 15  
 ADD28860  
 ID ADD28860 standard; DNA; 15 BP.  
 AC ADD28860;  
 XX  
 XX 15-JAN-2004 (first entry)  
 DT  
 XX Escherichia coli 0157:H7 VNTR related oligonucleotide SEQ ID NO:479.  
 DE molecular sub-typing system; Escherichia coli;  
 XX variable number tandem repeat; VNTR; genetic data;  
 KW epidemiological database; research; ss.  
 XX  
 XX Synthetic.  
 OS Escherichia coli.  
 XX  
 XX WO2003050269-A2.  
 PN 19-JUN-2003.  
 PD  
 XX  
 XX 11-DEC-2002; 2002WO-US039914.  
 PF  
 XX 11-DEC-2001; 2001US-0339687P.  
 PR (UYAR-) UNIV ARIZONA.  
 PA (KEIM/) KEIM P.  
 PA (KEYS/) KEYS C.  
 XX  
 XX Keim P, Keys C;  
 PI WPI; 2003-864934/80.  
 DR  
 XX Molecular sub-typing system for Escherichia coli, comprises observing and  
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA  
 PT sample.  
 XX Disclosure; SEQ ID NO 479; 166pp; English.  
 PS The present invention describes a molecular sub-typing system (S) for  
 XX Escherichia coli, which comprises observing and recording variable number  
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also  
 CC described: (1) VNTR loci (1) for sub-typing E. coli 0157:H7; (2) primers  
 CC (II) for amplifying (1); (3) amplicon comprising (II) and a locus  
 CC comprising a VNTR sequence from E. coli 0157:H7; (4) multiplex cocktails  
 CC (III) for multiplex amplification of (1) comprising two or more primers  
 CC of (II); (5) kits for molecular sub-typing of E. coli 0157:H7 by PCR  
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for

CC Alignment Scores: 7.25e+03 Length: 15  
 CC Pred. No.: 5.00 Matches: 5  
 CC Score: 100.00% Conservative: 0  
 CC Percent Similarity: 100.00% Mismatches: 0  
 CC Best Local Similarity: 100.00% Indels: 0  
 CC Query Match: 2.53% Gaps: 0  
 CC DB: 9  
 CC US-09-966-880A-8 (1-198) x ADD28710 (1-15)  
 QY 72 ProGlyArgCysTyr 76  
 Db 1 CCTGGACGGTGCTAC 15  
 RESULT 14  
 ADD28861/C  
 ID ADD28861 standard; DNA; 15 BP.  
 XX  
 AC ADD28861;  
 XX  
 XX 15-JAN-2004 (first entry)  
 DT  
 XX Escherichia coli 0157:H7 VNTR related oligonucleotide SEQ ID NO:480.  
 DE molecular sub-typing system; Escherichia coli;  
 KW variable number tandem repeat; VNTR; genetic data;  
 KW epidemiological database; research; ss.  
 XX  
 XX Synthetic.  
 OS Escherichia coli.  
 XX  
 XX WO2003050269-A2.  
 PN 19-JUN-2003.  
 PD  
 XX  
 XX 11-DEC-2002; 2002WO-US039914.  
 PF  
 XX 11-DEC-2001; 2001US-0339687P.  
 PR (UYAR-) UNIV ARIZONA.  
 PA (KEIM/) KEIM P.  
 PA (KEYS/) KEYS C.  
 XX  
 XX Keim P, Keys C;  
 PI WPI; 2003-864934/80.  
 DR  
 XX Molecular sub-typing system for Escherichia coli, comprises observing and  
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA  
 PT sample.  
 XX Disclosure; SEQ ID NO 480; 166pp; English.  
 PS The present invention describes a molecular sub-typing system (S) for  
 XX Escherichia coli, which comprises observing and recording variable number  
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also  
 CC described: (1) VNTR loci (1) for sub-typing E. coli 0157:H7; (2) primers  
 CC (II) for amplifying (1); (3) amplicon comprising (II) and a locus  
 CC comprising a VNTR sequence from E. coli 0157:H7; (4) multiplex cocktails  
 CC (III) for multiplex amplification of (1) comprising two or more primers  
 CC of (II); (5) kits for molecular sub-typing of E. coli 0157:H7 by PCR  
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for  
 CC maintaining hybridisation and amplification condition in a PCR instrument  
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.  
 CC coli 0157:H7 strains by multiplex, comprising (III), and amplifying  
 CC reagents for maintaining hybridisation and amplification condition in a  
 CC multiplex instrument with DNA from an E. coli 0157:H7 strain; and (7) sub  
 CC primers for amplifying loci comprising VNTR, where the primers have an  
 CC observable indicator; (b) obtaining single-stranded sample DNA from the  
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA  
 CC and amplifying reagents under hybridising and amplifying conditions in a

CC maintaining hybridisation and amplification condition in a PCR instrument  
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.  
 CC coli O157:H7 strains by multiplex, comprising (iii), and amplifying  
 CC reagents for maintaining hybridisation and amplification condition in a  
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub  
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more  
 CC primers for amplifying loci comprising VNTR, where the primers have an  
 CC observable indicator; (b) obtaining single-stranded sample DNA from the  
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA  
 CC and amplifying reagents under hybridising and amplifying conditions in a  
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)  
 CC separating the amplicons by size; (e) evaluating numbers and sizes of  
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of  
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for  
 CC producing discrete genetic data for an epidemiological database. (1) is  
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.  
 CC coli. The present sequence represents an oligonucleotide which is used in  
 CC the exemplification of the present invention.

SQ Sequence 15 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores: 15  
 Pred. No.: 7.25e+03 Length: 15  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD28860 (1-15)

QY 72 ProGlyArgCysTyr 76  
 Db 1 CCTGGACGGTGCTAC 15

RESULT 16

ADD28711/c  
 ID ADD28711 standard; DNA; 15 BP.

AC ADD28711;

XX 15-JAN-2004 (first entry)

DE Escherichia coli O157:H7 VNTR amplicon sequence SEQ ID NO:326.

XX molecular sub-typing system; Escherichia coli;  
 KW variable number tandem repeat; VNTR; genetic data;  
 KW epidemiological database; research; gene; ds.  
 XX Escherichia coli.

OS Escherichia coli.

XX W02003050269-A2.

XX 19-JUN-2003.

XX 11-DEC-2002; 2002WO-US039914.

XX 11-DEC-2001; 2001US-0339687P.

XX (UYAR-) UNIV ARIZONA.

PA (KEIM/) KEIM P.

PA (KEYS/) KEYS C.

XX Keim P, Keys C;

XX WPI; 2003-864934/80.

XX Molecular sub-typing system for Escherichia coli, comprises observing and  
 PT recording variable number tandem repeat arrays in an Escherichia coli DNA  
 PT sample.

XX Claim 7; SEQ ID NO 326; 166pp; English.

XX

CC The present invention describes a molecular sub-typing system (S) for  
 CC Escherichia coli, which comprises observing and recording variable number  
 CC tandem repeats (VNTR) repeat arrays in an E. coli DNA sample. Also  
 CC described: (1) VNTR loci (I) for sub-typing E. coli O157:H7; (2) primers  
 CC (II) for amplifying (I); (3) amplicon comprising (II) and a locus  
 CC comprising a VNTR sequence from E. coli O157:H7; (4) multiplex cocktails  
 CC (III) for multiplex amplification of (I) comprising two or more primers  
 CC of (II); (5) kits for molecular sub-typing of E. coli O157:H7 by PCR  
 CC comprising primers for VNTR loci in E. coli, and amplifying reagents for  
 CC maintaining hybridisation and amplification condition in a PCR instrument  
 CC with DNA from an E. coli strain; (6) kits for molecular sub-typing of E.  
 CC coli O157:H7 strains by multiplex, comprising (iii), and amplifying  
 CC reagents for maintaining hybridisation and amplification condition in a  
 CC multiplex instrument with DNA from an E. coli O157:H7 strain; and (7) sub  
 CC -typing (M1) an E. coli strain, comprising: (a) obtaining one or more  
 CC primers for amplifying loci comprising VNTR, where the primers have an  
 CC observable indicator; (b) obtaining single-stranded sample DNA from the  
 CC E. coli sample to be subtyped; (c) combining the primers, the sample DNA  
 CC and amplifying reagents under hybridising and amplifying conditions in a  
 CC PCR instrument to form amplicons comprising the primers and the VNTR; (d)  
 CC separating the amplicons by size; (e) evaluating numbers and sizes of  
 CC separated amplicons; and (f) comparing the evaluation to an evaluation of  
 CC amplicons obtained by PCR from a known E. coli strain. M1 is useful for  
 CC producing discrete genetic data for an epidemiological database. (1) is  
 CC useful as a research tool. (S) is useful for subtyping pathogenic E.  
 CC coli. The present sequence represents an E. coli VNTR loci related  
 CC amplicon sequence which is used in the exemplification of the present  
 CC invention.

SQ Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Alignment Scores: 15  
 Pred. No.: 7.25e+03 Length: 15  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD28711 (1-15)

QY 72 ProGlyArgCysTyr 76

Db 15 CCTGGACGGTGCTAC 1

RESULT 17

AAQ81257/c

ID AAQ81257 standard; mRNA; 16 BP.

XX AAQ81257;

XX 25-MAR-2003 (revised)

DT 07-SEP-1995 (first entry)

XX Ribozyyme target sequence in TGF-beta mRNA (bases 735-750).

XX Target site; ribozyme; hammerhead; hairpin; hepatitis delta virus;  
 KW group 1 intron; RNasep RNA motif; transforming growth factor-beta;  
 KW TGF-beta; fibrous; connective; tissue disease; TGF-alpha; inhibin;  
 KW epidermal growth factor; EGF; activin; amphiregulin; insulin;  
 KW bone morphogenic protein; fibroblast growth factor; relaxin; as.

XX Homo sapiens.

XX W09429452-A2.

XX 22-DEC-1994.

XX 02-JUN-1994; 94WO-US006331.

XX 09-JUN-1993; 93US-00074343.

XX (RIBO-) RIBOZYME PHARM INC.

XX Draper KG;  
 XX WPI; 1995-051612/07.  
 XX Enzymatic RNA molecule with, e.g. a hammerhead or hairpin motif - cleaves  
 PT mRNA associated with fibrous or connective tissue disease, and is useful  
 PT for treatment or prophylaxis of such diseases.  
 XX  
 XX Claim 3; Page 4; 63pp; English.  
 XX  
 CC The sequences (AA081238-1304) represent the target sites where a ribozyme  
 CC (hammerhead, hairpin, hepatitis delta virus, group 1 intron or RNaseP RNA  
 CC motif) cleaves the mRNA of the transforming growth factor-beta (TGF-beta)  
 CC gene. This sequence corresponds to bases 735-750 of the TGF-beta mRNA.  
 CC The ribozymes can also target the mRNAs of genes associated with the  
 CC development or maintenance of fibrous or connective tissue disease in  
 CC order to prevent or treat these diseases. Such genes include TGF-alpha or  
 CC beta, epidermal growth factor, inhibitors, activins, amphiregulin, bone  
 CC morphogenic proteins, fibroblast growth factors a and b, insulin growth  
 CC factor 1 or 2, insulin or relaxin. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 SQ Sequence 16 BP; 1 A; 8 C; 1 G; 0 T; 6 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.69e+03 Length: 16  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AA081257 (1-16)  
 QY 21 AlalysGlyArgArg 25  
 Db 15 GCARAAAGGTAGGAGG 1  
 RESULT 18  
 ABL52895/c  
 ID ABL52895 standard; DNA; 16 BP.  
 AC ABL52895;  
 XX  
 XX 25-JUN-2002 (first entry)  
 DT  
 DE Mutant cutinase PCR primer Dop2-R.  
 XX  
 XX Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; PCR; primer; ss.  
 KW  
 OS Synthetic.  
 XX  
 XX WO200192502-A1.  
 PN  
 XX  
 XX 06-DEC-2001.  
 PD  
 XX  
 XX 22-MAY-2001; 2001WO-DK000350.  
 PF  
 XX  
 XX 02-JUN-2000; 2000DK-00000861.  
 PR  
 XX 23-OCT-2000; 2000DK-00001577.  
 PR  
 XX 24-NOV-2000; 2000DK-00001772.  
 PR  
 XX 19-JAN-2001; 2001DK-00000100.  
 PR  
 XX (NOVO) NOVOZYMES AS.  
 PA  
 XX  
 XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;  
 FI  
 XX WPI; 2002-216714/27.  
 DR  
 XX  
 XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic  
 PT oligomers of poly(ethylene terephthalate) comprises a substitution of  
 PT amino acid residues corresponding to positions of Humicola insolens

PT cutinase.  
 XX  
 XX Example 1; Page 37; 41pp; English.  
 XX  
 CC The present invention relates to wild-type mature cutinase from Humicola  
 CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant  
 CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic  
 CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases  
 CC have improved thermostability, and are used for enzymatic hydrolysis of  
 CC cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing  
 CC of yarn or fabric from poly(ethylene terephthalate) fibers. The present  
 CC sequence is a PCR primer, which was used during the construction of the  
 CC cutinase mutants  
 XX  
 SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 7.69e+03 Length: 16  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-966-880A-8 (1-198) x ABL52895 (1-16)  
 QY 70 LeuAspProGlyArg 74  
 Db 16 CTGGATCCAGGGCGT 2  
 RESULT 19  
 AAT53462  
 ID AAT53462 standard; RNA; 17 BP.  
 AC AAT53462;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT  
 DT 27-MAR-1997 (first entry)  
 XX  
 DE Rat ICAM hammerhead ribozyme target sequence (nt. position 668).  
 XX  
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 KW ss.  
 XX  
 XX Rattus rattus.  
 OS  
 XX WO9523225-A2.  
 PN  
 XX  
 XX 31-AUG-1995.  
 PD  
 XX  
 XX 23-FEB-1995; 95WO-IB000156.  
 PF  
 XX  
 XX 23-FEB-1994; 94US-00201109.  
 PR  
 XX 29-MAR-1994; 94US-00218934.  
 PR  
 XX 04-APR-1994; 94US-0022795.  
 PR  
 XX 07-APR-1994; 94US-00224483.  
 PR  
 XX 15-APR-1994; 94US-00227958.  
 PR  
 XX 15-APR-1994; 94US-00228041.  
 PR  
 XX 18-MAY-1994; 94US-00245736.  
 PR  
 XX 06-JUL-1994; 94US-00271280.  
 PR  
 XX 15-AUG-1994; 94US-00291932.  
 PR  
 XX 16-AUG-1994; 94US-00291433.  
 PR  
 XX 17-AUG-1994; 94US-00292620.  
 PR  
 XX 19-AUG-1994; 94US-00293520.

PR 02-SEP-1994; 94US-00300000.  
 PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 23-SEP-1994; 94US-00311749.  
 PR 28-SEP-1994; 94US-00314397.  
 PR 03-OCT-1994; 94US-00316771.  
 PR 07-OCT-1994; 94US-00319492.  
 PR 11-OCT-1994; 94US-00321993.  
 PR 04-NOV-1994; 94US-00334847.  
 PR 10-NOV-1994; 94US-00337608.  
 PR 28-NOV-1994; 94US-00345516.  
 PR 16-DEC-1994; 94US-00357577.  
 PR 23-DEC-1994; 94US-00363233.  
 PR 30-JAN-1995; 95US-00380734.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LM;  
 PI Grimm S, Karpeisky A, Kistich K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 XX  
 DR WPI; 1995-351090/45.  
 XX  
 XX Ribozymes having modified bases and methods for producing them - for use  
 PT in inhibiting disease related genes.  
 PT  
 PS Claim 2; Page 201; 407pp; English.  
 PS  
 XX The present sequence represents a preferred target sequence for an  
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
 CC nucleotide base position indicated in the DE line. Regions of the mRNA  
 CC that do not form secondary folding structures and that contain potential  
 CC hammerhead and hairpin ribozyme cleavage sites were identified by  
 CC computer analysis. Ribozymes directed against these mRNA sequences were  
 CC designed and synthesised with modifications that improve their nuclease  
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 CC inhibit ICAM-1 expression, making them useful for reducing transplant  
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)  
 XX  
 SQ Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT53462 (1-17)

QY 58 GluLeuLeuPheLeu 62  
 Db 1 GAACUGCUCUCCUC 15  
 RESULT 20  
 AAT53758  
 ID AAT53758 standard; RNA; 17 BP.  
 XX  
 AC AAT53758;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 03-APR-1997 (first entry)  
 XX  
 DE Rat ICAM hammerhead ribozyme target sequence (nt. position 2909).  
 XX  
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;

KW translocation; chronic myelogenous leukaemia; CML; cancer;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 ss.

XX Rattus rattus.  
 OS  
 XX WO9523225-A2.  
 FN  
 XX 31-AUG-1995.  
 PD  
 XX 23-FEB-1995; 95WO-IB000156.  
 PF  
 XX 23-FEB-1994; 94US-00201109.  
 PR 29-MAR-1994; 94US-00218934.  
 PR 04-APR-1994; 94US-00222795.  
 PR 07-APR-1994; 94US-00224483.  
 PR 15-APR-1994; 94US-00227958.  
 PR 15-APR-1994; 94US-00228041.  
 PR 18-MAY-1994; 94US-00245736.  
 PR 06-JUL-1994; 94US-00271280.  
 PR 15-AUG-1994; 94US-00291932.  
 PR 16-AUG-1994; 94US-00291433.  
 PR 17-AUG-1994; 94US-00292620.  
 PR 19-AUG-1994; 94US-00293520.  
 PR 02-SEP-1994; 94US-00300000.  
 PR 08-SEP-1994; 94US-00303039.  
 PR 23-SEP-1994; 94US-00311486.  
 PR 23-SEP-1994; 94US-00311749.  
 PR 28-SEP-1994; 94US-00314397.  
 PR 03-OCT-1994; 94US-00316771.  
 PR 07-OCT-1994; 94US-00319492.  
 PR 11-OCT-1994; 94US-00321993.  
 PR 04-NOV-1994; 94US-00334847.  
 PR 10-NOV-1994; 94US-00337608.  
 PR 28-NOV-1994; 94US-00345516.  
 PR 16-DEC-1994; 94US-00357577.  
 PR 23-DEC-1994; 94US-00363233.  
 PR 30-JAN-1995; 95US-00380734.  
 PR  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LM;  
 PI Grimm S, Karpeisky A, Kistich K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Usman N, Wincott FE, Woolf T;  
 XX  
 DR WPI; 1995-351090/45.

Ribozymes having modified bases and methods for producing them - for use  
 in inhibiting disease related genes.

Claim 2; Page 204; 407pp; English.

The present sequence represents a preferred target sequence for an  
 enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
 nucleotide base position indicated in the DE line. Regions of the mRNA  
 that do not form secondary folding structures and that contain potential  
 hammerhead and hairpin ribozyme cleavage sites were identified by  
 computer analysis. Ribozymes directed against these mRNA sequences were  
 designed and synthesised with modifications that improve their nuclease  
 resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 inhibit ICAM-1 expression, making them useful for reducing transplant  
 rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)

SQ Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT53758 (1-17)

QY 58 GluteLeuPheLeu 62  
 DB 1 GAACUGCUCUCCUC 15

RESULT 21

ID AAT53666  
 ID AAT53666 standard; RNA; 17 BP.

AC AAT53666;

DT 25-MAR-2003 (revised)

DT 27-MAR-1997 (first entry)

XX Rat ICAM hammerhead ribozyme target sequence (nt. position 2376).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 XX ss.

OS Rattus rattus.

XX WO9523225-A2.

PN 31-AUG-1995.

PD 23-FEB-1995;

XX 95WO-IB000156.

XX 23-FEB-1994;

XX 94US-00201109.

XX 29-MAR-1994;

XX 94US-00218934.

XX 04-APR-1994;

XX 94US-00222795.

XX 07-APR-1994;

XX 94US-00224483.

XX 15-APR-1994;

XX 94US-00227958.

XX 18-MAY-1994;

XX 94US-00245736.

XX 06-JUL-1994;

XX 94US-00271280.

XX 15-AUG-1994;

XX 94US-00291932.

XX 16-AUG-1994;

XX 94US-00291433.

XX 17-AUG-1994;

XX 94US-00292620.

PI Stinchcomb DT, Chowira B, Dizenzo A, Draper KG, Dudyec IW;  
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;  
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;  
 PI Tracz D, Ueman N, Wincott FE, Woolf T;  
 XX WPI; 1995-351090/45.

XX Ribozymes having modified bases and methods for producing them - for use  
 in inhibiting disease related genes.

XX Claim 2; Page 203; 407pp; English.

XX The present sequence represents a preferred target sequence for an  
 enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the  
 nucleotide base position indicated in the DE line. Regions of the mRNA  
 that do not form secondary folding structures and that contain potential  
 hammerhead and hairpin ribozyme cleavage sites were identified by  
 computer analysis. Ribozymes directed against these mRNA sequences were  
 designed and synthesised with modifications that improve their nuclease  
 resistance. The ribozymes cleave the ICAM-1 target sequences and thereby  
 inhibit ICAM-1 expression, making them useful for reducing transplant  
 rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)

SQ Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT53666 (1-17)

QY 58 GluteLeuPheLeu 62

DB 1 GAACUGCUCUCCUC 15

RESULT 22

AAT53748

ID AAT53748 standard; RNA; 17 BP.

XX AAT53748;

DT 25-MAR-2003 (revised)

DT 03-APR-1997 (first entry)

XX Rat ICAM hammerhead ribozyme target sequence (nt. position 2904).

XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;  
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;  
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;  
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;  
 KW Philadelphia chromosome; inflammation; autoimmune disease;  
 KW atherosclerosis; myocardial infarction; stroke; restenosis;  
 KW transplant rejection; rheumatoid arthritis; psoriasis;  
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;  
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;  
 XX ss.

XX Rattus rattus.

XX WO9523225-A2.

XX 31-AUG-1995.

XX 23-FEB-1995;

XX 95WO-IB000156.

XX 23-FEB-1994;

XX 94US-00201109.

(RIBO-) RIBOZYME PHARM INC.

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PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 18-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00311749.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 204; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were
XX designed and synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
XX inhibit ICAM-1 expression, making them useful for reducing transplant
XX rejection and alleviating symptoms in patients with rheumatoid arthritis,
XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.13e+03 Length: 17
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAT53748 (1-17)
XX
XX QY 58 GluLeuLeuPheLeu 62
XX
XX Db 1 GAACUGCUCUCCUC 15
XX
XX RESULT 23
XX AAT53431
XX ID AAT53431 standard; RNA; 17 BP.
XX

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AC AAT53431;
XX
XX 25-MAR-2003 (revised)
XX 27-MAR-1997 (first entry)
XX
XX Rat ICAM hammerhead ribozyme target sequence (nt. position 26).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumour necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX ss.
XX
XX Rattus rattus.
XX
XX W09523225-A2.
XX
XX 31-AUG-1995.
XX
XX 23-FEB-1995; 95WO-IB000156.
XX
XX 23-FEB-1994; 94US-00201109.
XX 29-MAR-1994; 94US-00218934.
XX 04-APR-1994; 94US-00222795.
XX 07-APR-1994; 94US-00224483.
XX 15-APR-1994; 94US-00227958.
XX 15-APR-1994; 94US-00228041.
XX 18-MAY-1994; 94US-00245736.
XX 06-JUL-1994; 94US-00271280.
XX 15-AUG-1994; 94US-00291932.
XX 16-AUG-1994; 94US-00291433.
XX 17-AUG-1994; 94US-00292620.
XX 19-AUG-1994; 94US-00293520.
XX 02-SEP-1994; 94US-00300000.
XX 08-SEP-1994; 94US-00303039.
XX 23-SEP-1994; 94US-00311486.
XX 23-SEP-1994; 94US-00311749.
XX 28-SEP-1994; 94US-00311749.
XX 03-OCT-1994; 94US-00316771.
XX 07-OCT-1994; 94US-00319492.
XX 11-OCT-1994; 94US-00321993.
XX 04-NOV-1994; 94US-00334847.
XX 10-NOV-1994; 94US-00337608.
XX 28-NOV-1994; 94US-00345516.
XX 16-DEC-1994; 94US-00357577.
XX 23-DEC-1994; 94US-00363233.
XX 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
XX Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
XX Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozymes having modified bases and methods for producing them - for use
XX in inhibiting disease related genes.
XX
XX Claim 2; Page 201; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by

```

CC computer analysis. Ribozymes directed against these mRNA sequences were  
 CC designed and synthesised with modifications that improve their nuclease  
 CC resistance. The ribozymes cleave the ICAW-1 target sequences and thereby  
 CC inhibit ICAW-1 expression, making them useful for reducing transplant  
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,  
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to  
 CC correct PI field.)

SQ Sequence 17 BP; 2 A; 6 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT53431 (1-17)

QY 58 GluLeuLeuPheLeu 62  
 ID AAX74553 standard; RNA; 17 BP.  
 DB 1 GAACUCUCUCCUC 15

RESULT 24

AAX74553  
 ID AAX74553 standard; RNA; 17 BP.  
 AC AAX74553;

XX  
 XX 28-JUL-1999 (first entry)  
 DT  
 XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #81.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.

XX Mus sp.

XX WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR ) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 157; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples

CC of nucleic acid molecules from the present invention  
 XX Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX74553 (1-17)

QY 179 IleLeuLeuProLeu 183  
 ID AAX74554 standard; RNA; 17 BP.  
 DB 2 AUAUCUCUACCCUG 16

RESULT 25

AAX74554  
 ID AAX74554 standard; RNA; 17 BP.  
 AC AAX74554;

XX  
 XX 28-JUL-1999 (first entry)  
 DT  
 XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #82.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.

XX Mus sp.

XX WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR ) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA

XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,

XX rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 157; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention

XX Sequence 17 BP; 4 A; 6 C; 1 G; 0 T; 6 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17



Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX74554 (1-17)

QY 179 IleLeuLeuProLeu 183

Db 1 AUACUCUUAACCCUG 15

RESULT 26

AAX71605

ID AAX71605 standard; RNA; 17 BP.

XX

AC AAX71605;

XX

DT 28-JUL-1999 (first entry)

XX

DE Human KDR VEGF receptor hammerhead ribozyme substrate #617.

XX

KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.

XX

OS Homo sapiens.

XX

PN WO9715662-A2.

XX

PD 01-MAY-1997.

XX

PF 25-OCT-1996; 96WO-US017480.

XX

PR 26-OCT-1995; 95US-0005974P.

XX

PR 11-JAN-1996; 96US-00584040.

XX

(RIBO-) RIBOZYME PHARM INC.

PA

PA (CHIR ) CHIRON CORP.

XX

PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX

WPI; 1997-259017/23.

XX

CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
stability - useful for treating e.g. tumour angiogenesis, psoriasis,

PT

PT rheumatoid arthritis, etc., in a human patient.

XX

PS Claim 4; Page 115; 218pp; English.

XX

CC The present invention describes nucleic acid molecules which modulate the  
synthesis, expression and/or stability of a mRNA encoding 1 or more  
receptors of vascular endothelial growth factor (VEGF). A patient  
(preferably human) having a condition associated with the level of the  
fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
treated by administering the nucleic acid molecule or the expression  
vector to the patient. AAX67275 to AAX75752 represent specific examples  
of nucleic acid molecules from the present invention

XX

SQ Sequence 17 BP; 6 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX71605 (1-17)

QY 157 ArgThrPhelysAla 161

Db 2 AGAACUUUUAAGCU 16

RESULT 27

AAX69260

ID AAX69260 standard; RNA; 17 BP.

XX

AC AAX69260;

XX

DT 28-JUL-1999 (first entry)

XX

DE Human flt1 VEGF receptor hammerhead ribozyme substrate #555.

XX

KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;  
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;  
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
KW foetal liver kinase 1; ss.

XX

OS Homo sapiens.

XX

PN WO9715662-A2.

XX

PD 01-MAY-1997.

XX

PF 25-OCT-1996; 96WO-US017480.

XX

PR 26-OCT-1995; 95US-0005974P.

XX

PR 11-JAN-1996; 96US-00584040.

XX

(RIBO-) RIBOZYME PHARM INC.

PA

PA (CHIR ) CHIRON CORP.

XX

PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX

WPI; 1997-259017/23.

XX

CC Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
stability - useful for treating e.g. tumour angiogenesis, psoriasis,

PT

PT rheumatoid arthritis, etc., in a human patient.

XX

PS Claim 4; Page 63; 218pp; English.

XX

CC The present invention describes nucleic acid molecules which modulate the  
synthesis, expression and/or stability of a mRNA encoding 1 or more  
receptors of vascular endothelial growth factor (VEGF). A patient  
(preferably human) having a condition associated with the level of the  
fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
treated by administering the nucleic acid molecule or the expression  
vector to the patient. AAX67275 to AAX75752 represent specific examples  
of nucleic acid molecules from the present invention

XX

SQ Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX69260 (1-17)

QY 102 ProhLeuSerieu 106

Db 3 CCGAAUCUUAUCUUG 17

```

RESULT 28
AAAX71604
ID AAX71604 standard; RNA; 17 BP.
XX
AC AAX71604;
XX
DT 28-JUL-1999 (first entry)
DE Human KDR VEGF receptor hammerhead ribozyme substrate #616.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
(RIBO-) RIBOZYME PHARM INC.
(PA) (CHIR) CHIRON CORP.
XX
PA Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
PI WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 115; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 6 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e-03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX71604 (1-17)

QY 157 ArgThrPhelysala 161
DB 3 AGAACUUUUAAGCU 17

RESULT 29
AAAX71606
ID AAX71606 standard; RNA; 17 BP.
XX
AC AAX71606;
XX

```

```

DT 28-JUL-1999 (first entry)
XX
DE Human KDR VEGF receptor hammerhead ribozyme substrate #618.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
(RIBO-) RIBOZYME PHARM INC.
(PA) (CHIR) CHIRON CORP.
XX
PA Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
PI WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 115; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 7 A; 2 C; 3 G; 0 T; 5 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e-03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX71606 (1-17)

QY 157 ArgThrPhelysala 161
DB 1 AGAACUUUUAAGCU 15

RESULT 30
AAAX69261
ID AAX69261 standard; RNA; 17 BP.
XX
AC AAX69261;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #556.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;

```

KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;  
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;  
 KW foetal liver kinase 1; ss.  
 XX Homo sapiens.  
 XX  
 PN WO9715662-A2.  
 XX  
 PD 01-MAY-1997.  
 XX  
 XX 25-OCT-1996; 96WO-US017480.  
 XX  
 XX 26-OCT-1995; 95US-0005974P.  
 PR  
 PR 11-JAN-1996; 96US-00584040.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (CHIR ) CHIRON CORP.  
 XX  
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;  
 XX WPI; 1997-259017/23.  
 DR  
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA  
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,  
 PT rheumatoid arthritis, etc., in a human patient.  
 XX  
 PS Claim 4; Page 63; 218pp; English.  
 XX  
 CC The present invention describes nucleic acid molecules which modulate the  
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more  
 CC receptors of vascular endothelial growth factor (VEGF). A patient  
 CC (preferably human) having a condition associated with the level of the  
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing  
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour  
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be  
 CC treated by administering the nucleic acid molecule or the expression  
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples  
 CC of nucleic acid molecules from the present invention  
 XX  
 SQ Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAX69261 (1-17)  
 QY 102 ProAsnLeuSerLeu 106  
 Db 1 CCGAUCUAUCUUG 15  
 RESULT 31  
 AAV94862/c  
 ID AAV94862 standard; RNA; 17 BP.  
 XX  
 XX AAV94862;  
 AC  
 XX 24-FEB-1999 (first entry)  
 DE Mouse IL-2 receptor g-chain substrate position 42.  
 XX  
 XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;  
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;  
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;  
 KW graft rejection; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9824913-A2.  
 XX  
 PD 11-JUN-1998.  
 XX  
 XX 02-DEC-1997; 97WO-US021748.  
 PF  
 PR 03-DEC-1996; 96US-00758306.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX Stinchcomb DT, Mcswiggen JA;  
 PI WPI; 1998-333332/29.  
 DR

XX 11-JUN-1998.  
 PD  
 XX 02-DEC-1997; 97WO-US021748.  
 PF  
 XX 03-DEC-1996; 96US-00758306.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX Stinchcomb DT, Mcswiggen JA;  
 PI WPI; 1998-333332/29.  
 DR  
 XX Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer,  
 PT autoimmune disease and allergies.  
 XX  
 XX Claim 4; Page 40; 61pp; English.  
 XX  
 CC The present sequence invention describes ribozymes targeted to modulate  
 CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.  
 CC AAV93889 to AAV94574 represent specifically claimed ribozymes, and  
 CC AAV94575 to AAV95260 represent specifically claimed substrate sequences  
 CC from the present invention. The ribozymes can be used for the treatment  
 CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy  
 CC and other inflammatory conditions. The ribozymes are also used to induce  
 CC tolerance in a recipient to alloantigen from a donor  
 XX  
 SQ Sequence 17 BP; 2 A; 6 C; 1 G; 0 T; 8 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAV94862 (1-17)  
 QY 124 GluGlyLeuArgArg 128  
 Db 17 GAGGACTRAGAGG 3  
 RESULT 32  
 AAV94863/c  
 ID AAV94863 standard; RNA; 17 BP.  
 XX  
 XX AAV94863;  
 AC  
 XX 24-FEB-1999 (first entry)  
 DE Mouse IL-2 receptor g-chain substrate position 43.  
 XX  
 XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;  
 KW hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;  
 KW autoimmune disease; psoriasis; allergy; inflammatory disease;  
 KW graft rejection; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9824913-A2.  
 XX  
 PD 11-JUN-1998.  
 XX  
 XX 02-DEC-1997; 97WO-US021748.  
 PF  
 PR 03-DEC-1996; 96US-00758306.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX Stinchcomb DT, Mcswiggen JA;  
 PI WPI; 1998-333332/29.  
 DR

XX Ribozymes targetted to interleukin 2 - useful for treating e.g. cancer,  
PT autoimmune disease and allergies.  
XX  
XX Claim 4; Page 40; 6lpp; English.  
XX  
XX The present sequence invention describes ribozymes targetted to modulate  
CC the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.  
CC AA193889 to AA194574 represent specifically claimed ribozymes, and  
CC AA194575 to AA195260 represent specifically claimed substrate sequences  
CC from the present invention. The ribozymes can be used for the treatment  
CC of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy  
CC and other inflammatory conditions. The ribozymes are also used to induce  
CC tolerance in a recipient to alloantigen from a donor  
XX  
XX Sequence 17 BP; 2 A; 6 C; 1 G; 0 T; 8 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0  
US-09-966-880A-8 (1-198) x AA194563 (1-17)  
Qy 124 GluclyLeuArg 128  
Db 16 GAAGGACTAAGAGG 2  
RESULT 33  
AA1920716  
ID AA1920716 standard; RNA; 17 BP.  
XX  
XX AA1920716;  
XX  
XX 19-JUN-2000 (first entry)  
XX  
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:3942.  
XX  
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;  
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;  
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
KW age related macular degeneration; inflammation; neovascular glaucoma;  
KW myopic degeneration; psoriasis; verruca vulgaris; angiobroma;  
KW tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;  
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9950403-A2.  
XX  
XX 07-OCT-1999.  
XX  
XX 24-MAR-1999; 99WO-US006507.  
XX  
XX 27-MAR-1998; 98US-0079678P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;  
XX WPI; 1999-591315/50.  
XX  
XX Novel ribozymes for modulating the synthesis, expression and/or stability  
PT of an mRNA encoding an angiogenic factors.  
XX  
XX Claim 55; Page 163; 305pp; English.  
XX  
XX The present invention describes enzymatic nucleic acid molecules with RNA

CC cleaving activity, which specifically cleave RNA encoded by an aryl  
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to  
CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,  
CC and AA17168 to AA17560 and AA17623 to AA17684 represent their  
CC corresponding target sequences; AA17685 to AA18385 and AA19087 to  
CC AA19154 represent ribozyme sequences for Tie-2, and AA18386 to AA19086  
CC and AA19155 to AA19222 represent their corresponding target sequences;  
CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme  
CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and  
CC AA21596 to AA21688 represent their corresponding target sequences;  
CC AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequences  
CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to  
CC AA23422 represent their corresponding target sequences. The ribozymes of  
CC the invention are used for modulating the synthesis, expression and/or  
CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
CC especially used to treat cancer, diabetic retinopathy, age related  
CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
CC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber  
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,  
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
CC integrin subunit alpha-6, or integrin subunit beta-3  
XX  
XX Sequence 17 BP; 6 A; 1 C; 4 G; 0 T; 6 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0  
US-09-966-880A-8 (1-198) x AA1920716 (1-17)  
Qy 177 ArgArgileLeuLeu 181  
Db 1 AGAAGGAUUGUCU 15  
RESULT 34  
AA191119/c  
ID AA191119 standard; RNA; 17 BP.  
XX  
XX AA191119;  
XX  
XX 18-FEB-1999 (first entry)  
XX  
XX Human C-raf target site nucleotide position 1251.  
XX  
XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
KW screening; identification; synthesis; deprotection; purification; cancer;  
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
KW restenosis; rheumatoid arthritis; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO9850530-A2.  
XX  
XX 12-NOV-1998.  
XX  
XX 05-MAY-1998; 98WO-US009249.  
XX  
XX 09-MAY-1997; 97US-0046059P.  
XX  
XX 09-JUN-1997; 97US-0049002P.  
XX  
XX 03-JUL-1997; 97US-0051718P.  
XX  
XX 22-AUG-1997; 97US-0056808P.  
XX  
XX 02-OCT-1997; 97US-0061321P.  
XX  
XX 02-OCT-1997; 97US-0061324P.  
XX  
XX 05-NOV-1997; 97US-0064868P.  
XX  
XX 19-DEC-1997; 97US-0068212P.

XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
XX PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
XX PI Thompson J, Workman CT, Beaudry A, Svedler D;  
XX WPI; 1999-009494/01.  
XX DR Identifying new catalytic nucleic acid that modulates selected processes  
XX PT - especially ribozymes that cleave Raf RNA for treating cancer,  
XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
XX PT used as antiviral agents and synthons.  
XX PS Claim 177; Page 149; 259pp; English.  
XX CC A method has been developed for the identification of a nucleic acid  
XX CC capable of modulating a process in a biological system. The method  
XX CC comprises: (a) introducing into the system a random library of nucleic  
XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
XX CC in systems where modulation has occurred and/or determining the sequence  
XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
XX CC endonuclease activity and catalytic activity, from the present invention,  
XX CC are used to modulate gene expression in plant and mammalian cells and to  
XX CC cleave target nucleic acid, particularly for treating systemic diseases  
XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
XX CC ascites and infection. They may also be used to detect genetic drift and  
XX CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs  
XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
XX CC generally any condition associated with the level of c-rat. Introduction  
XX CC of sugar/phosphate modifications increases stability against nuclease and  
XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
XX CC method, specifically for modulating the expression of a Raf gene  
XX SQ Sequence 17 BP; 5 A; 3 C; 4 G; 0 T; 5 U; 0 Other;  
XX Alignment Scores:  
XX Pred. No.: 8.13e+03 Length: 17  
XX Score: 5.00 Matches: 5  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 2.53% Indels: 0  
XX DB: 2 Gaps: 0  
XX US-09-966-880A-8 (1-198) x AAV91119 (1-17)  
XX QY 107 ArgillePheThra 111  
XX Db 17 AGGATCTTACTGCA 3  
XX RESULT 35  
XX AAV93554/c  
XX ID AAV93554 standard; RNA; 17 BP.  
XX AC AAV93554;  
XX CC  
XX DT 18-FEB-1999 (first entry)  
XX DE Human B-raf substrate nucleotide position 1662.  
XX KW Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;  
XX KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;  
XX KW screening; identification; synthesis; deprotection; purification; cancer;  
XX KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;  
XX KW restenosis; rheumatoid arthritis; ss.  
XX OS Homo sapiens.  
XX XX  
XX PN WO9850530-A2.  
XX XX  
XX PD 12-NOV-1998.

XX PF 05-MAY-1998; 98WO-US009249.  
XX PR 09-MAY-1997; 97US-0046059P.  
XX PR 09-JUN-1997; 97US-0049002P.  
XX PR 03-JUL-1997; 97US-0051718P.  
XX PR 22-AUG-1997; 97US-0056808P.  
XX PR 02-OCT-1997; 97US-0061321P.  
XX PR 02-OCT-1997; 97US-0061324P.  
XX PR 05-NOV-1997; 97US-0064866P.  
XX PR 19-DEC-1997; 97US-0068212P.  
XX PA (RIBO-) RIBOZYME PHARM INC.  
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;  
XX PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;  
XX PI Thompson J, Workman CT, Beaudry A, Svedler D;  
XX WPI; 1999-009494/01.  
XX DR Identifying new catalytic nucleic acid that modulates selected processes  
XX PT - especially ribozymes that cleave Raf RNA for treating cancer,  
XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates  
XX PT used as antiviral agents and synthons.  
XX PS Claim 177; Page 170; 259pp; English.  
XX CC A method has been developed for the identification of a nucleic acid  
XX CC capable of modulating a process in a biological system. The method  
XX CC comprises: (a) introducing into the system a random library of nucleic  
XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising  
XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC  
XX CC in systems where modulation has occurred and/or determining the sequence  
XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with  
XX CC endonuclease activity and catalytic activity, from the present invention,  
XX CC are used to modulate gene expression in plant and mammalian cells and to  
XX CC cleave target nucleic acid, particularly for treating systemic diseases  
XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic  
XX CC ascites and infection. They may also be used to detect genetic drift and  
XX CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs  
XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are  
XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or  
XX CC generally any condition associated with the level of c-rat. Introduction  
XX CC of sugar/phosphate modifications increases stability against nuclease and  
XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the  
XX CC method, specifically for modulating the expression of a Raf gene  
XX SQ Sequence 17 BP; 2 A; 4 C; 6 G; 0 T; 5 U; 0 Other;  
XX Alignment Scores:  
XX Pred. No.: 8.13e+03 Length: 17  
XX Score: 5.00 Matches: 5  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 2.53% Indels: 0  
XX DB: 2 Gaps: 0  
XX US-09-966-880A-8 (1-198) x AAV93554 (1-17)  
XX QY 82 ThrSerTrpSerPro 86  
XX Db 17 ACAAGCTGGAGCCCT 3  
XX RESULT 36  
XX AAV92402  
XX ID AAV92402 standard; RNA; 17 BP.  
XX AC AAV92402;  
XX CC  
XX DT 18-FEB-1999 (first entry)  
XX DE Human A-Raf substrate position 327.  
XX XX

Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.

OS Homo sapiens.

XX WO9850530-A2.

XX 12-NOV-1998.

XX 05-MAY-1998; 98WO-US009249.

XX 09-MAY-1997; 97US-0046059P.

XX 09-JUN-1997; 97US-0049002P.

XX 23-JUL-1997; 97US-0051718P.

XX 22-AUG-1997; 97US-0056808P.

XX 02-OCT-1997; 97US-0061321P.

XX 02-OCT-1997; 97US-0061324P.

XX 05-NOV-1997; 97US-0064866P.

XX 19-DEC-1997; 97US-0068212P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;

XX Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;

XX Thompson J, Workman CT, Beaudry A, Sweedler D;

XX WPI; 1999-009494/01.

XX Identifying new catalytic nucleic acid that modulates selected processes

XX - especially ribozymes that cleave Raf RNA for treating cancer,

XX restenosis, and also new ribozymes and modified nucleoside triphosphates

XX used as antiviral agents and synthons.

XX Claim 177; Page 157; 259pp; English.

XX A method has been developed for the identification of a nucleic acid

XX capable of modulating a process in a biological system. The method

XX comprises: (a) introducing into the system a random library of nucleic

XX acid catalysts (NAC) having a substrate binding domain (SBD), comprising

XX a random sequence, and a catalytic domain (CD); and (b) identifying NAC

RESULT 37  
AA54363/C  
ID AAX54363 standard; DNA; 17 BP.

XX AAX54363;

XX 05-JUL-1999 (first entry)

XX NK-kB antisense oligonucleotide fragment.

XX Antisense oligonucleotide; multiple target; antisense treatment;  
KW impaired respiration; inflammation; lung disease;  
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
KW acute asthma; allergy; asthma; impeded respiration;  
KW respiratory distress syndrome; pain; cystic fibrosis;  
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
KW prostate cancer; ss.

XX Synthetic.

XX WO9913886-A1.

XX 25-MAR-1999.

XX 17-SEP-1998; 98WO-US019419.

XX 17-SEP-1997; 97US-0059160P.

XX 09-JUN-1998; 98US-00093972.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 1999-229400/19.

XX New antisense oligonucleotides used in treatment of, e.g. pulmonary

XX vasoconstriction.

XX Disclosure; Page 63; 120pp; English.

XX The specification describes antisense oligonucleotides (AAX52869-X55271) directed against at least 2 mRNAs selected from target genes, coding and non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX5272-74. These multiple target oligonucleotides (specifically AAX5180-271) can be used for the antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer

XX Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0

QY 171 ArgLeuSerArgGln 175  
DB 2 CGACUCUCUAGACAA 16

US-09-966-880A-8 (1-198) x AAV92402 (1-17)

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps:

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAx54363 (1-17)

Qy 36 ArgAspSerAlaThr 40

Db 15 CCGGACAGCGCCACC 1

RESULT 38

AAA33807/c

ID AAA33807 standard; DNA; 17 BP.

XX AC AAA33807;

XX 28-JUL-2000 (first entry)

XX Low adenosine antisense oligonucleotide SEQ ID NO:1496.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;

KW phosphothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;

KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;

KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;

KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;

KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

PN 24-FEB-2000.

PD 03-AUG-1999; 99WO-US017712.

PF 03-AUG-1998; 98US-0095212P.

PR (UYEC-) UNIV EAST CAROLINA.

PA Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary

PT vasoconstriction, inflammation, allergies, asthma, hypertension, or

PT bronchitis, emphysema, respiratory distress syndrome, ischemia or

PT cancers.

XX Claim 18; Page 451; 1343pp; English.

XX The present invention describes a new composition comprising an antisense

CC oligonucleotide (ON) with low adenosine (up to 15%), which targets

CC nucleic acids involved in bronchoconstriction, allergies, and/or

CC inflammation. The ON can have antiinflammatory, antiallergic,

CC antiasthmatic, cytostatic and analgesic activities. The compositions are

CC useful for the treatment of diseases associated with inflammation,

CC impaired airways, including lung disease and diseases whose secondary

CC effects afflict the lungs of a subject. They can be used for treating

CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,

CC impeded respiration, respiratory distress syndrome, pain, cystic

CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive

CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,

CC carcinomas, and cancers which may metastasise to the lungs, including

CC breast and prostate cancer. The reduction of the adenosine content of the

CC ONs reduces side effects. The A-containing ONs break down with the

CC release of deoxyadenosine which activates adenosine receptors causing

CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the

CC nucleotide sequences given in the sequence listing from the present

CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185

CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ

CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to

CC AAA33992) are specifically claimed ONs from the present invention. N.B.

CC Sequences given in the disclosure of the present invention do not match

CC up with their corresponding SEQ ID NO: sequences given in the sequence

CC listing

XX Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA33807 (1-17)

Qy 36 ArgAspSerAlaThr 40

Db 15 CCGGACAGCGCCACC 1

RESULT 39

AAA36106

ID AAA36106 standard; DNA; 17 BP.

XX AC AAA36106;

XX 26-JUL-2000 (first entry)

XX Human genomic SNP allele specific oligonucleotide SEQ ID NO:163.

XX Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;

KW allele specific oligonucleotide; ASO; reduced complexity genome; RCG;

KW genomic classification; identification; DNA fingerprinting;

KW tumour characterisation; hybridisation; ss.

XX Homo sapiens.

OS WO200018960-A2.

PN 06-APR-2000.

PD 24-SEP-1999; 99WO-US022283.

PF 25-SEP-1998; 98US-0101757P.

PR (MASI ) MASSACHUSETTS INST TECHNOLOGY.

PA Landers JB, Jordan B, Housman DE, Charest A;

PI WPI; 2000-293181/25.

XX Detection of single nucleotide polymorphisms in genomes by preparation

PT and analysis of reduced complexity genomes, useful for genotyping,

PT fingerprinting and determining allele frequency of SNPs.

XX Disclosure; Page 58; 111pp; English.

XX A method has been developed for detecting the presence or absence of a

CC single nucleotide polymorphism (SNP) allele in a genomic sample. The

CC method comprises preparing a reduced complexity genome (RCG) from the

CC genomic sample and analysing the RCG for the presence or absence of a SNP

CC allele. The method can be used to characterise a tumour, to generate a

CC genomic pattern for an individual genome or to generate a genomic

CC classification code for a genome. The method can be used to assess

CC whether a subject is at risk for developing a disease or to identify a

CC set of SNP alleles associated with a disease. The method can also be used

CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences

CC used in the exemplification of the present invention. AAA35948 to

CC AAA36632 represent nucleotide sequences containing SNPs

XX Sequence 17 BP; 3 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA36106 (1-17)

Qy 169 SerValArgLeuser 173

Db 3 AGCGTCCGGTTAAGT 17

RESULT 40

AAAF19929/c

ID AAAF19929 standard; DNA; 17 BP.

XX AAF19929;

DT 14-MAR-2001 (first entry)

XX Human NF-kB polynucleotide fragment #1496.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
KW human; airway disorder; bronchoconstriction; lung inflammation;  
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
KW immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;  
KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;  
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
KW cancer; ss.

XX Homo sapiens.

OS W0200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

XX Nyce JW;

XX WPI; 2000-679539/66.

XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.

XX Claim 14; Page 257; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The

CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention

SQ Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAF19929 (1-17)

Qy 36 ArgAspSerAlaThr 40

Db 15 CCGGACAGCCACC 1

RESULT 41

AAA25939

ID AAA25939 standard; DNA; 17 BP.

XX AAA25939;

XX 19-JUL-2000 (first entry)

DT Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:2437.

DE Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;

KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;

KW gene expression modification; cancer; phosphorothioate; endonuclease;

KW anticancer; breast cancer; endometrium cancer; ss.

XX Homo sapiens.

XX WO9954459-A2.

XX 28-OCT-1999.

XX 19-APR-1999; 99WO-US008547.

XX 20-APR-1998; 98US-0082404P.

XX 23-JUN-1998; 98US-00103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;

PI Matulic-Adamic J;

XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target sequences,  
PT used to treat cancer.

XX Claim 77; Page 95; 149pp; English.

XX The present invention describes nucleic acids (A) that interact stably  
CC with a target sequence and contain at least one phosphorothioate  
CC link, having endonuclease activity. (A), and more generally any catalytic  
CC nucleic acid (A), that modulates expression of the oestrogen receptor  
CC gene, are used to treat cancer (particularly of breast or endometrium),



CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype.  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 3 A; 2 C; 4 G; 8 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAA25939 (1-17)  
 QY 57 ValGlueLeuPhe 61  
 Db 1 GTAGAGCTCTGTGT 15  
 RESULT 42  
 AAA24771  
 ID AAA24771 standard; DNA; 17 BP.  
 XX  
 AC AAA24771;  
 XX  
 DT 19-JUL-2000 (first entry)  
 XX  
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1269.  
 XX  
 KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;  
 KW gene expression modification; cancer; phosphorothioate; endonuclease;  
 KW anticancer; breast cancer; endometrium cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO9954459-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 19-APR-1999; 99WO-US008547.  
 XX  
 PR 20-APR-1998; 98US-0082404P.  
 PR 23-JUN-1998; 98US-00103636.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;  
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeberli P;  
 PI Matulic-Adamic J;  
 XX  
 DR WPI; 2000-013248/01.  
 XX  
 PT New nucleic acids that interact, and optionally cleave, target sequences,  
 PT used to treat cancer.  
 XX  
 PS Claim 77; Page 57; 148pp; English.  
 XX  
 CC The present invention describes nucleic acids (A) that interact stably  
 CC with a target sequence and contain at least one phosphoro(dithioate

CC link, having endonuclease activity. (A), and more generally any catalytic  
 CC nucleic acid (A') that modulates expression of the oestrogen receptor  
 CC gene, are used to treat cancer (particularly of breast or endometrium),  
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or  
 CC for other conditions associated with levels of oestrogen receptor.  
 CC Because of the high selectivity for targeted RNA, (A) can also be used to  
 CC correlate inhibition of gene expression with alterations in phenotype,  
 CC particularly for identification of therapeutic targets, and as research  
 CC reagents (for RNA, in the same way that restriction endonucleases are  
 CC used with DNA). The combination of modifications in (A) improves  
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to  
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and  
 CC AAA24748 to AAA25992 represent their corresponding target sequences.  
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme  
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target  
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and  
 CC antisense oligonucleotides used in the exemplification of the present  
 CC invention  
 XX  
 SQ Sequence 17 BP; 2 A; 8 C; 5 G; 2 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAA24771 (1-17)  
 QY 127 ArgArgLeuHisArg 131  
 Db 1 CGCGGCTTCACCGG 15  
 RESULT 43  
 AAUF04476/C  
 ID AAUF04476 standard; DNA; 17 BP.  
 XX  
 AC AAUF04476;  
 XX  
 DT 16-FEB-2001 (first entry)  
 XX  
 DE Hammerhead ribozyme substrate #1992.  
 XX  
 KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;  
 KW interferon alpha; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2000061729-A2.  
 XX  
 PD 19-OCT-2000.  
 XX  
 PF 11-APR-2000; 2000WO-US009721.  
 XX  
 PR 12-APR-1999; 99US-0129390P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;  
 PI WPI; 2000-647423/62.  
 XX  
 DR Enzymatic and antisense nucleic acid inhibition of repressor genes,  
 PT useful for producing e.g. granulocyte colony stimulating factor protein,  
 PT interferon alpha and erythropoietin.  
 XX  
 PS Claim 4; Page 101; 164pp; English.  
 XX  
 CC The present invention relates to enzymatic and antisense nucleic acid  
 CC molecules that act as inhibitors of the expression of repressor genes  
 CC encoding the TR2 Orphan receptor, EAR3/COUP-1f-1, the GATA transcription

CC factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).  
 CC Inhibition of the repressors removes prevents inhibition (and  
 CC consequently increases expression of) genes involved in the production of  
 CC erythropoietin, granulocyte colony stimulating factor protein and  
 CC interferon alpha

XX Sequence 17 BP; 8 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e-03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAF04476 (1-17)

QY 11 PheLeuTyGlnPhe 15  
 DB 15 TTTCTCTATCAGTTC 1

RESULT 44

ABK01373/c

ID ABK01373 standard; RNA; 17 BP.

XX ABK01373;

AC ABK01373;

XX 12-MAR-2002 (first entry)

DT 12-MAR-2002 (first entry)

XX Human NOGO Inozyme #643.

DE Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

XX cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNazyme; inozyme; G-cleaver; amberszyme; zinczyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

PI WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

XX constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

PT central nervous system injury.

XX Claim 88; Page 88; 200pp; English.

XX

XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with an NNN motif) or  
 CC an amberszyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV immunodeficiency virus associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is an inozyme of the invention

SQ Sequence 17 BP; 6 A; 4 C; 2 G; 0 T; 5 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e-03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK01373 (1-17)

QY 194 ArgThrLeuGlyLeu 198

DB 17 AGAACITTTGGTTTA 3

RESULT 45

ABK00382/c

ID ABK00382 standard; RNA; 17 BP.

XX ABK00382;

XX 12-MAR-2002 (first entry)

DT 12-MAR-2002 (first entry)

XX Human NOGO Hammerhead Ribozyme #382.

DE Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

XX cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNazyme; inozyme; G-cleaver; amberszyme; zinczyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS

OS Synthetic.  
 XX WO200159103-A2.  
 XX 16-AUG-2001.  
 XX 09-FEB-2001; 2001WO-US004273.  
 XX 11-FEB-2000; 2000US-0181797P.  
 XX 28-FEB-2000; 2000US-0185516P.  
 XX 06-MAR-2000; 2000US-0187128P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX Blatt L, Mcswiggen J, Chowrira BM;  
 XX WPI; 2001-607195/69.  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene and antisense  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX Claim 88; Page 72; 200pp; English.  
 XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGR motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of the  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a hammerhead ribozyme of the invention  
 XX  
 SQ Sequence 17 BP; 7 A; 3 C; 4 G; 0 T; 3 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatve: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: Gaps: 0  
 US-09-966-880a-8 (1-198) x ABK00382 (1-17)  
 QY 169 SerValArgLeuSer 173

Db RESULT 46  
 ASK01374/c  
 ID ABK01374 standard; RNA; 17 BP.  
 XX  
 AC ABK01374;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human NOGO Inozyme #644.  
 XX  
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNzyme; inozyme; G-cleaver; amberyne; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200159103-A2.  
 XX 16-AUG-2001.  
 XX 09-FEB-2001; 2001WO-US004273.  
 XX 11-FEB-2000; 2000US-0181797P.  
 XX 28-FEB-2000; 2000US-0185516P.  
 XX 06-MAR-2000; 2000US-0187128P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX Blatt L, Mcswiggen J, Chowrira BM;  
 XX WPI; 2001-607195/69.  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene and neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX Claim 88; Page 88; 200pp; English.  
 XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberyne (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGR motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of the  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a hammerhead ribozyme of the invention  
 XX

CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is an inozyme of the invention

XX Sequence 17 BP; 6 A; 4 C; 1 G; 0 T; 6 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK01374 (1-17)

QY 194 ArgThrLeuGlyLeu 198

DB 16 AGAACTTGGGTTA 2

RESULT 47

ABK02555/c

ID ABK02555 standard; RNA; 17 BP.

AC ABK02555;

XX 12-MAR-2002 (first entry)

XX Human NOGO Amberzyme #227.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 08-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

XX

DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.

XX Claim 88; Page 135; 200pp; English.

PS The invention relates to a nucleic acid molecule which down regulates  
 XX expression of a CD20 gene and a nucleic acid molecule which down  
 XX regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCR motif), a G-cleaver (cleaving RNA with a NIN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably  $Mg^{2+}$ .  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably  $Mg^{2+}$ . Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is an amberzyme molecule of the invention

SQ Sequence 17 BP; 8 A; 4 C; 3 G; 0 T; 2 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK02555 (1-17)

QY 58 GluLeuLeuPheLeu 62

DB 15 GAGCTTCTGTTCTT 1

RESULT 48

ABK02240

ID ABK02240 standard; RNA; 17 BP.

XX AC ABK02240;

XX 12-MAR-2002 (first entry)

XX Human NOGO DNzyme #152.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.  
 OS Synthetic.  
 XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

PI Blatt L, Mcswiggen J, Chowrira BM;

XX WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.

XX Claim 88; Page 115; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NIGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an ambezyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytooma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NIGO-  
 CC targeting nucleic acid is used to cleave RNA of the NIGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NIGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NIGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NIGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NIGO expression. The present  
 CC sequence is a DNzyme molecule of the invention

XX Sequence 17 BP; 6 A; 2 C; 4 G; 0 T; 5 U; 0 Other;

Alignment Scores: 8.13e+03 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score:

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK02240 (1-17)

Qy 8 ArgArgGlyGlyPheLeu 12

Dd 1 AGGAGAAAUAUCCUU 15

RESULT 49

ABK01263/C

ID ABK01263 standard; RNA; 17 BP.

XX ABK01263;

XX 12-MAR-2002 (first entry)

DE Human NIGO Inozyme #533.

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neuroprotective; antiparkinsonian; ribozyme;  
 KW muscular; CD20; neurite growth inhibitor gene; NIGO; hammerhead ribozyme;  
 KW DNzyme; inozyme; G-cleaver; ambezyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytooma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.

OS Synthetic.

XX WO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-0185516P.

PR 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWRIRA B M.

PI Blatt L, Mcswiggen J, Chowrira BM;

XX WPI; 2001-607195/69.

Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 constructs, which down regulate expression of a CD20 gene or neurite  
 growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 central nervous system injury.

Claim 88; Page 86; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates  
 expression of a CD20 gene and a nucleic acid molecule which down  
 regulates expression of a neurite growth inhibitor gene (NIGO). The  
 nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 an ambezyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 the cell and treat a patient having a condition associated with the level  
 of CD20. The treatment may further comprise the use of one or more  
 therapies. In particular, the CD20 targeting nucleic acid may be used to  
 treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 lymphoma (MCL), immunocytooma (IMC), small B-cell lymphocytic lymphoma,  
 immune thrombocytopaenia, and inflammatory arthropathy. The NIGO-  
 targeting nucleic acid is used to cleave RNA of the NIGO gene in the  
 presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 nucleic acid may be contacted with a cell to reduce NIGO activity of the  
 cell and treat a patient having a condition associated with the level of  
 NIGO. The treatment may further comprise the use of one or more  
 therapies. In particular, the NIGO-targeting nucleic acid may be used to  
 treat central nervous system (CNS) injury and cerebrovascular accident  
 (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 disease, muscular dystrophy, and/or other neurodegenerative disease  
 states which respond to the modulation of NIGO expression. The present  
 sequence is a DNzyme molecule of the invention

CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is an inozyme of the invention

SQ Sequence 17 BP; 7 A; 3 C; 4 G; 0 T; 3 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK01263 (1-17)

Qy 169 SerValArgLeuSer 173

Db 15 TCAGTGAGACTTCT 1

RESULT 50

ABK01219/c  
 ID ABK01219 standard; RNA; 17 BP.

XX AC ABK01219;

DT 12-MAR-2002 (first entry)

XX DE Human NOGO Inozyme #489.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

XX W0200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWEIRA B M.  
 XX Blatt L, Mcswiggen J, Chowira BM;  
 PI WPI; 2001-607195/69.  
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 DR constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX Claim 88; Page 85; 200pp; English.  
 PS The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is an inozyme of the invention

SQ Sequence 17 BP; 8 A; 5 C; 3 G; 0 T; 1 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABK01219 (1-17)

Qy 58 GluLeuLeuPheLeu 62

Db 16 GAGCTTCGTCTTCT 2

RESULT 51

ABA80972/c

ID ABA80972 standard; DNA; 17 BP.

XX AC ABA80972;

DT 24-JAN-2002 (first entry)

DE LDLR mutation correcting oligonucleotide SEQ ID NO: 3818.

XX Human, gene therapy; adenosine deaminase deficiency; p53; beta-globin;

KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;

KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;

KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;

KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;

KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;

KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;

KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;

KW Alzheimer's disease; cystostatic; antiskilling; antianaemic; haemostatic;

KW antileptic; ss.

XX Homo sapiens.

XX WO200173002-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009761.

XX 27-MAR-2000; 2000US-0192176P.

XX 27-MAR-2000; 2000US-0192179P.

XX 01-JUN-2000; 2000US-0208538P.

XX 30-OCT-2000; 2000US-0244989P.

XX (UYDE ) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC;

XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for

XX treating cystic fibrosis, comprises at least one mismatch and chemical

XX modification.

XX Claim 7; Page 251; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can

XX be used for the targeted alteration of genomic sequences, where the

XX oligonucleotide has at least one mismatch compared with the genomic

XX sequence to be altered. In particular, these sequences are directed at

XX the following genes: adenosine deaminase, p53, beta-globin,

XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A

XX (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus

XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,

XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase

XX (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and

XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases

XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,

XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,

XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and

XX various syndromes. The present sequence is one of the gene correcting

XX oligonucleotides of the invention

SQ Sequence 17 BP; 6 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABA80972 (1-17)

QY 93 HisVallalaApphe 97

DB 15 CATGTTGCAGCTTT 1

RESULT 52

ABA80973

ID ABA80973 standard; DNA; 17 BP.

XX ABA80973;

XX 24-JAN-2002 (first entry)

XX LDLR mutation correcting oligonucleotide SEQ ID NO: 3819.

XX Human, gene therapy; adenosine deaminase deficiency; p53; beta-globin;

XX retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;

XX cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;

XX adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;

XX haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;

XX mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;

XX familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;

XX UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;

XX Alzheimer's disease; cystostatic; antiskilling; antianaemic; haemostatic;

XX antileptic; ss.

XX Homo sapiens.

XX WO200173002-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-US009761.

XX 27-MAR-2000; 2000US-0192176P.

XX 27-MAR-2000; 2000US-0192179P.

XX 01-JUN-2000; 2000US-0208538P.

XX 30-OCT-2000; 2000US-0244989P.

XX (UYDE ) UNIV DELAWARE.

XX Kmiec EB, Gamper HB, Rice MC;

XX WPI; 2001-639230/73.

XX Oligonucleotide for targeted alterations of genetic sequences and for

XX treating cystic fibrosis, comprises at least one mismatch and chemical

XX modification.

XX Claim 7; Page 251; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can

XX be used for the targeted alteration of genomic sequences, where the

XX oligonucleotide has at least one mismatch compared with the genomic

XX sequence to be altered. In particular, these sequences are directed at

XX the following genes: adenosine deaminase, p53, beta-globin,

XX retinoblastoma, BRCA1, BRCA2, CFTR, cyclin-dependent kinase inhibitor 2A

XX (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus

XX 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,

XX apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase

XX (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and

XX presenilin-2 (PSEN2). These can be used in the gene therapy of diseases

XX such as cancer, adenosine deaminase deficiency, cystic fibrosis,

XX haemophilia, hypercholesterolaemia, thalassaemia, sickle cell anaemia,

XX Alzheimer's disease, melanoma, adenomatous polyposis of the colon and

XX various syndromes. The present sequence is one of the gene correcting

XX oligonucleotides of the invention

SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABA80973 (1-17)

93 HisValalasphe 97  
| | | | | | | | | |  
3 CATGTTGCAGACTTT 17

RESULT 53  
ABA78569  
ABA78569 standard; DNA, 17 BP.  
ABA78569;  
24-JAN-2002 (first entry)  
CDKN2A mutation correcting oligonucleotide SEQ ID NO: 1415.

Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CTRR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOB; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1; Alzheimer's disease; cytostatic; antineoplastic; antianaemic; haemostatic; antileptic; ss.

Homo sapiens.  
WO200173002-A2.  
04-OCT-2001.  
27-MAR-2001; 2001WO-US009761.  
27-MAR-2000; 2000US-0192176P.  
27-MAR-2000; 2000US-0192179P.  
01-JUN-2000; 2000US-0208538P.  
30-OCT-2000; 2000US-0244989P.  
(UYDE ) UNIV DELAWARE.  
Kniec EB, Gamper HB, Rice MC;  
WPI; 2001-639230/73.  
Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical modification.  
Claim 7; Page 130; 294pp; English.  
The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblastoma, BRCA1, BRCA2, CTRR, cyclin-dependent kinase inhibitor 2A (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and presenilin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting oligonucleotides of the invention  
Sequence 17 BP; 1 A; 6 C; 9 G; 1 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8,13e+03 Length: 17  
Score: 5.00 Matches: 5  
D Score: 100.00% Conservative: 0  
D Score: 100.00% Conservative: 0



SQ Sequence 17 BP; 1 A; 9 C; 6 G; 1 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x ABA78570 (1-17)

QY 129 LeuHisArgAlaGly 133

Db 16 CTGCACCGGCGGG 2

RESULT 55

AAH43675

ID AAH43675 standard; DNA; 17 BP.

XX AC

XX AAH43675;

DT 21-JAN-2002 (first entry)

DE Primer RCPyrG5.

XX A. fumigatus; pyrG; mutant bank; mutation; inducible; haploid; PCR;  
KW diploid; phenotype; amplify; polymerase chain reaction; primer; ss.

XX Synthetic.

XX WO200177295-A1.

XX XX

XX 18-OCT-2001.

XX 11-APR-2001; 2001WO-GB001626.

XX 11-APR-2000; 2000GB-00008748.

XX (TWO-) P2G LTD.

XX Denning DW, Brookman JL, Rickers A, Birch M;

XX WPI; 2001-657169/75.

XX Mutant bank of diploid microorganisms for identifying genes which  
PT contribute to a chosen phenotype, has population of mutant cells in which  
PT at least one cell has a random mutation which disrupts the activity of a  
PT gene.

XX Example 1; Page 32; 64pp; English.

XX The sequences given in AAH43675-80 are primers which were used to isolate  
CC the mutated pyrG gene in plasmid pMB3 linearised with XbaI. The isolated  
CC sequence was used in the method of the invention in the production of a  
CC mutant bank of diploid microorganisms which comprises a population of  
CC mutant cells in which at least one cell has a mutation that disrupts the  
CC activity of a gene, and which is inducible into haploid form. The mutant  
CC bank is useful for identifying genes in a microorganism which contribute  
CC to a chosen phenotype. The method comprises exposing the diploid  
CC microorganisms, where the population collectively have a mutation in  
CC every gene within the genome, to an agent that induces the microorganisms  
CC into haploid form, separating and culturing the haploid microorganism as  
CC single clones, and selecting clones or colonies for which the chosen  
CC phenotype is altered relative to a wild type microorganism, and  
CC identifying the mutated gene in each of the selected clones. The complete  
CC diploid population may be cultured under suitable conditions. This is  
CC possible because the wild type copy of the gene will rescue any  
CC individual that may otherwise grow poorly, or even not be viable, should  
CC the mutant copy of the gene predominate. Thus, the diploid mutant bank  
CC may comprise a population of mutant, viable cells in which essentially  
CC the activity of every gene within the genome is disrupted rather than an  
CC incomplete population comprising non-lethal mutants

SQ Sequence 17 BP; 3 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH43675 (1-17)

QY 176 LeuArgArgileLeu 180

Db 3 TTGAGGCGAATTC 17

RESULT 56

ABN09591/c

ID ABN09591 standard; DNA; 17 BP.

XX AC

XX ABN09591;

DT 29-MAY-2002 (first entry)

XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9583.

DE Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;  
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000670.

XX 05-FEB-2001; 2001US-0266860P.

XX (ABOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.

XX Disclosure; SEQ ID NO 9583; 214pp; English.

XX The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1

CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP-1  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09591 (1-17)

Qy 41 SerPheSerLeuAsp 45  
 Db 15 AGCTTTTCCCTCGAC 1

RESULT 57

ABN09638  
 ID ABN09638 standard; DNA; 17 BP.

AC ABN09638;

DT 29-MAY-2002 (first entry)

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9630.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.

OS Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 05-FEB-2001; 2001US-0266860P.

(ABOM-) AEOMICA INC.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon MB;  
 XX WPI; 2002-179446/23.  
 DR  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.  
 XX  
 XX Disclosure; SEQ ID NO 9630; 214pp; English.  
 XX  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP-  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 3 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09638 (1-17)

Qy 124 GluGlyLeuArgArg 128

Db 3 GAAGGGCTCCGGAGG 17

RESULT 58

ABN09773

ID ABN09773 standard; DNA; 17 BP.

XX ABN09773;

XX 29-MAY-2002 (first entry)

XX Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9765.

XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.

XX WO200192524-A2.

XX 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.  
PR 30-JAN-2001; 2001WO-US000661.  
PR 30-JAN-2001; 2001WO-US000662.  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 05-FEB-2001; 2001WO-US000670.  
PR 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
XX WPI; 2002-179446/23.  
DR  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
XX Disclosure; SEQ ID NO 9765; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
Gaps: 0

US-09-966-880a-8 (1-198) x ABN09773 (1-17)

Qy 103 AsnLeuSerLeuArg 107  
|||||  
Db 3 AACCTTCGCTGAGG 17

RESULT 59  
ABN09639  
ID ABN09639 standard; DNA; 17 BP.  
XX  
AC ABN09639;  
XX  
DT 29-MAY-2002 (first entry)  
XX

Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9631.  
Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
skeletal muscle disorder; amplicon; screening; ss.  
OS Homo sapiens.  
XX  
PN WO200192524-A2.  
XX  
PD 06-DEC-2001.  
XX  
XX 25-MAY-2001; 2001WO-US016981.  
XX  
XX 26-MAY-2000; 2000US-0207456P.  
PR  
XX 21-SEP-2000; 2000US-0234687P.  
PR  
XX 27-SEP-2000; 2000US-0236359P.  
PR  
XX 04-OCT-2000; 2000GB-00024263.  
PR  
XX 30-JAN-2001; 2001WO-US000661.  
PR  
XX 30-JAN-2001; 2001WO-US000662.  
PR  
XX 30-JAN-2001; 2001WO-US000663.  
PR  
XX 30-JAN-2001; 2001WO-US000664.  
PR  
XX 30-JAN-2001; 2001WO-US000665.  
PR  
XX 30-JAN-2001; 2001WO-US000666.  
PR  
XX 30-JAN-2001; 2001WO-US000667.  
PR  
XX 30-JAN-2001; 2001WO-US000668.  
PR  
XX 30-JAN-2001; 2001WO-US000669.  
PR  
XX 05-FEB-2001; 2001US-0266860P.  
XX  
PA (AEOM-) AEOMICA INC.  
XX  
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
XX  
XX WPI; 2002-179446/23.  
DR  
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
PT or as specific biomolecule capture probes for surface-enhanced laser  
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.  
XX  
XX Disclosure; SEQ ID NO 9631; 214pp; English.  
XX  
CC The present invention describes a human genome-derived myosin-like  
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
CC nucleic acids can be used as probes to detect, characterise and quantify  
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-  
CC -1 proteins, as standards in assays used to determine the concentration  
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
CC capture probes for surface-enhanced laser desorption/ionisation, as  
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
CC production, and in vaccines or for replacement therapy. The  
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
CC disorder associated with the expression of hGDMPLP-1, in particular heart  
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
CC The present sequence represents an oligomer used in the screening of the  
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 17 BP; 4 A; 3 C; 9 G; 1 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09639 (1-17)

QY 124 GluglyLeuArgArg 128  
|||||

DB 2 GAAGGCTCCGGAGG 16

RESULT 60

ABN09774

ID ABN09774 standard; DNA; 17 BP.

AC ABN09774;

XX

DT 29-MAY-2002 (first entry)

XX

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9766.

XX

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WC200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234887P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.

XX

PA (ABOM-) AEOMICA INC.

XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX

DR WPI; 2002-179446/23.

XX

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX

XX Disclosure; SEQ ID NO 9766; 214pp; English.

XX

XX The present invention describes a human genome-derived myosin-like

CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1

CC nucleic acids can be used as probes to detect, characterise and quantify

CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMPLP-1

CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be

CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

CC -1 proteins, as standards in assays used to determine the concentration

CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule

CC capture probes for surface-enhanced laser desorption ionization, as

CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The

CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMPLP-1, in particular heart

CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the

CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequence

XX

SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABN09774 (1-17)

QY 103 AsnLeuSerLeuArg 107  
|||||

DB 2 AACCTCTCGCTGAGG 16

RESULT 61

ABN09590/c

ID ABN09590 standard; DNA; 17 BP.

XX

AC ABN09590;

XX

DT 29-MAY-2002 (first entry)

XX

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9582.

XX

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;

KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

KW skeletal muscle disorder; amplicon; screening; ss.

XX

OS Homo sapiens.

XX

PN WC200192524-A2.

XX

PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US016981.

XX

PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234887P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 05-FEB-2001; 2001US-0266860P.

XX

PA (ABOM-) AEOMICA INC.

XX

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX

DR WPI; 2002-179446/23.

XX

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

PT or as specific biomolecule capture probes for surface-enhanced laser

PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX

XX Disclosure; SEQ ID NO 9582; 214pp; English.

XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX Sequence 17 BP; 5 A; 2 C; 7 G; 3 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-966-880A-8 (1-198) x ABN09590 (1-17)  
 QY 41 SerPreSerLeuasp 45  
 Db 16 AGCTTTTCCTCGAC 2  
 RESULT 62  
 ABN09640  
 ID ABN09640 standard; DNA; 17 BP.  
 XX  
 AC ABN09640;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT  
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9632.  
 XX  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200192524-A2.  
 PN  
 PD 06-DEC-2001.  
 XX  
 XX 25-MAY-2001; 2001WO-US016981.  
 PF  
 XX  
 XX 26-MAY-2000; 2000US-0207456P.  
 PR  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR  
 PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 XX (AEOM-) AEOMICA INC.  
 PA  
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 FI WPI; 2002-179446/23.  
 XX  
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,  
 XX or as specific biomolecule capture probes for surface-enhanced laser  
 XX desorption/ionization, comprises human myosin-like protein hGDMPLP-1.  
 PT  
 PT Disclosure; SEQ ID NO 9632; 214pp; English.  
 ES  
 XX The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionisation, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX Sequence 17 BP; 5 A; 3 C; 8 G; 1 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-966-880A-8 (1-198) x ABN09640 (1-17)  
 QY 124 GluGlyLeuArgArg 128  
 Db 1 GAAGGGCTCGAGG 15  
 RESULT 63  
 ABN09775  
 ID ABN09775 standard; DNA; 17 BP.  
 XX  
 AC ABN09775;  
 XX  
 XX 29-MAY-2002 (first entry)  
 DT  
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9767.  
 XX  
 XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;  
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KW skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200192524-A2.  
 PN

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PF 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0266860P.

XX PA (AEOM-) AEOMICA INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption/ionization, comprises human myosin-like protein hGDMPLP-1.

XX PT Disclosure; SEQ ID NO 9767; 214pp; English.

XX PS The present invention describes a human genome-derived myosin-like protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-1 can be used in gene therapy and vaccine production. The hGDMPLP-1 nucleic acids can be used as probes to detect, characterize and quantify hGDMPLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMPLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMPLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMPLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption/ionisation, as therapeutic supplement in patients having specific deficiency in hGDMPLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a disorder associated with the expression of hGDMPLP-1, in particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMPLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence

XX SQ Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	8.13e-03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	6	Gaps:	0

XX US-09-966-880A-8 (1-198) x ABN09775 (1-17)

XX QY 103 AsnLeuSerLeuArg 107

XX Db 1 AACCTCTCGTGAGG 15

XX RESULT 64

ABN09589/c

ID ABN09589 standard; DNA; 17 BP.

XX AC ABN09589;

XX DT 29-MAY-2002 (first entry)

XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:9581.

XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0266860P.

XX PA (AEOM-) AEOMICA INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption/ionization, comprises human myosin-like protein hGDMPLP-1.

XX PT Disclosure; SEQ ID NO 9581; 214pp; English.

XX PS The present invention describes a human genome-derived myosin-like protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-1 can be used in gene therapy and vaccine production. The hGDMPLP-1 nucleic acids can be used as probes to detect, characterize and quantify hGDMPLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMPLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMPLP-1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMPLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption/ionisation, as therapeutic supplement in patients having specific deficiency in hGDMPLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a disorder associated with the expression of hGDMPLP-1, in particular heart and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMPLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence

XX SQ Sequence 17 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

oligonucleotides are particularly useful for creating plants with desired phenotypes, e.g. environmental or abiotic stress tolerance, improved nutritional value (e.g. altering amino acid content of plants or conferring amino acid over production), herbicide resistance (e.g. glyphosate resistance, imidazolinone and sulphonylurea herbicide resistance, porphyrin herbicide resistance or triazine resistance), disease resistance, modified oil production, modified starch production (e.g. increased starch or production of waxy starch), altered floral morphology (e.g. male-sterile plants) or modified fatty acid content (e.g. reduced palmitate, increased stearate or reduced linolenic acid). The oligonucleotides are also useful for producing albino mutants for the analysis of photosynthetic processes. This sequence represents a genome altering oligonucleotide of the invention

Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.13e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	6	Gaps:	0

US-09-966-880A-8 (1-198) x ABK25912 (1-17)

QY 171 ArgleuSerArgGln 175

DB 15 CGACTGAGTCGTCAG 1

RESULT 66

ABK25647/C

ID ABK25647 standard; DNA; 17 BP.

AC ABK25647;

XX 09-APR-2002 (first entry)

DT

DE Stress tolerance conferring genome altering oligonucleotide #115.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;

KW o-methyl modification; LNA modification; phosphorothioate linkage;

KW DNA repair; DNA alteration; improved nutritional tolerance; hygromycin-B;

KW abiotic stress tolerance; improved nutritional value; hygromycin-B; amino acid over production; herbicide resistance; glyphosate resistance; imidazolinone herbicide resistance; sulphonylurea herbicide resistance; porphyrin herbicide resistance; triazine resistance; disease resistance; modified oil production; modified starch production; waxy starch; altered floral morphology; male-sterile plant; albino mutant;

KW modified fatty acid content; reduced palmitate production; albino plant; increased stearate production; reduced linolenic acid production; photosynthetic process.

XX Arabidopsis thaliana.

OS Synthetic.

XX WO200192512-A2.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

PR 27-MAR-2001; 2001US-00818875.

(UYDE ) UNIV DELAWARE.

XX Kmiec EB, Gamber HB, Rice MC, Kim J;

PI WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful for

oligonucleotides are particularly useful for creating plants with desired phenotypes, e.g. environmental or abiotic stress tolerance, improved nutritional value (e.g. altering amino acid content of plants or conferring amino acid over production), herbicide resistance (e.g. glyphosate resistance, imidazolinone and sulphonylurea herbicide resistance, porphyrin herbicide resistance or triazine resistance), disease resistance, modified oil production, modified starch production (e.g. increased starch or production of waxy starch), altered floral morphology (e.g. male-sterile plants) or modified fatty acid content (e.g. reduced palmitate, increased stearate or reduced linolenic acid). The oligonucleotides are also useful for producing albino mutants for the analysis of photosynthetic processes. This sequence represents a genome altering oligonucleotide of the invention

Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	8.13e+03	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	6	Gaps:	0

US-09-966-880A-8 (1-198) x AEN09589 (1-17)

QY 41 SerPheSerLeuAsp 45

DB 17 AGCTTTTCCTCGAC 3

RESULT 65

ABK25912/C

ID ABK25912 standard; DNA; 17 BP.

XX

AC ABK25912;

XX 09-APR-2002 (first entry)

DT

DE Albino plant producing genome altering oligonucleotide #84.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;

KW o-methyl modification; LNA modification; phosphorothioate linkage;

KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;

KW abiotic stress tolerance; improved nutritional value; hygromycin-B; amino acid over production; herbicide resistance; glyphosate resistance; imidazolinone herbicide resistance; sulphonylurea herbicide resistance; porphyrin herbicide resistance; triazine resistance; disease resistance; modified oil production; modified starch production; waxy starch; altered floral morphology; male-sterile plant; albino mutant;

KW modified fatty acid content; reduced palmitate production; albino plant; increased stearate production; reduced linolenic acid production; photosynthetic process.

XX Triticum aestivum.

OS Synthetic.

XX WO200192512-A2.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

PR 27-MAR-2001; 2001US-00818875.

(UYDE ) UNIV DELAWARE.

XX Kmiec EB, Gamber HB, Rice MC, Kim J;

PI WPI; 2002-106307/14.

XX New oligonucleotides with modified nuclease-resistant termini, useful for

creating plants with desired phenotypes, e.g. stress tolerance, improved nutritional value, herbicide or disease resistance, or modified oil production.

Claim 7; Page 119; 220pp; English.

The invention relates to an oligonucleotide for targeted alteration of a genetic sequence, which comprises a single-stranded oligonucleotide having a DNA domain. The DNA domain has at least one mismatch with respect to the genetic sequence to be altered and further comprises chemical modifications of the oligonucleotide. The chemical modifications consist of o-methyl modification, an LNA modification, two or more phosphorothioate linkages on a terminus, or a combination of any two or more of these modifications. The oligonucleotides are useful for directing repair or alteration of plant genetic information. The

PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.

PS Claim 7; Page 103; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention

SQ Sequence 17 BP; 5 A; 5 C; 1 G; 6 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK25647 (1-17)

QY 32 ValVallysArgArg 36

DB 15 GTTGTCAAAAGGAGA 1

RESULT 67

ABK25648  
 ID ABK25648 standard; DNA; 17 BP.

XX

AC ABK25648;

XX 09-APR-2002 (first entry)

XX Stress tolerance conferring genome altering oligonucleotide #116.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KW o-methyl modification; LNA modification; phosphorothioate linkage;  
 KW DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KW abiotic stress tolerance; improved nutritional value; hygromycin-B;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW modified fatty acid content; reduced palmitate production; albino plant;  
 KW increased stearate production; reduced linolenic acid production;  
 KW photosynthetic process.

XX Arabidopsis thaliana.

OS Synthetic.

XX WO200192512-A2.

PN

XX

PD 06-DEC-2001.

XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244989P.

PR 27-MAR-2001; 2001US-00818875.

PA (UVDE ) UNIV DELAWARE.

XX

PI Kmlec EB, Gamper HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.

DR

XX New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.

PS Claim 7; Page 103; 220pp; English.

XX The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention

SQ Sequence 17 BP; 6 A; 1 C; 5 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK25648 (1-17)

QY 32 ValVallysArgArg 36

DB 3 GTTGTCAAAAGGAGA 17

RESULT 68

ABK25911

ID ABK25911 standard; DNA; 17 BP.

XX

AC ABK25911;

XX 09-APR-2002 (first entry)

XX

XX Albino plant producing genome altering oligonucleotide #83.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;

XX o-methyl modification; LNA modification; phosphorothioate linkage;

XX DNA repair; DNA alteration; environmental tolerance; hygromycin-B;

KW



KW abiotic stress tolerance; improved nutritional value; hygromycin; primer;  
 KW amino acid over production; herbicide resistance; glyphosate resistance;  
 KW imidazolinone herbicide resistance; herbicide resistance; sulphonylurea herbicide resistance;  
 KW porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KW modified oil production; modified starch production; waxy starch;  
 KW altered floral morphology; male-sterile plant; albino mutant;  
 KW modified fatty acid content; reduced palmitate production; albino plant;  
 KW increased stearate production; reduced linolenic acid production;  
 KW photosynthetic process.

XX Triticum aestivum.  
 OS Synthetic.  
 XX WO200192512-A2.

XX 06-DEC-2001.  
 XX 01-JUN-2001; 2001WO-US017672.

XX 01-JUN-2000; 2000US-0208538P.  
 XX 30-OCT-2000; 2000US-024989P.  
 XX 27-MAR-2001; 2001US-00818875.

XX (UYDE ) UNIV DELAWARE.  
 XX Kmiec EB, Gamper HB, Rice MC, Kim J;

XX WPI; 2002-106307/14.  
 XX New oligonucleotides with modified nuclease-resistant termini, useful for

PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.

XX Claim 7; Page 119; 220pp; English.  
 XX The invention relates to an oligonucleotide for targeted alteration of a

CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of O-methyl modification, an RNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linolenic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention

XX SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK25911 (1-17)  
 QY 171 ArgLeuSerArgGln 175  
 |||||

Db 3 CGACTGAGTCGTCAG 17

RESULT 69  
 AAL48300

ID AAL48300 standard; DNA; 17 BP.  
 AC AAL48300;

XX 03-OCT-2002 (first entry)  
 XX HPV ribozyme cleavage site #14.

XX Ribozyme; catalytic nucleic acid; infection; PCR; target site; ss.  
 XX Human papillomavirus.  
 XX WO200246449-A2.

XX 13-JUN-2002.  
 XX 07-DEC-2001; 2001WO-US046178.

XX 07-DEC-2000; 2000US-0251810P.  
 XX (UYPE-) UNIV PENNSYLVANIA STATE.

XX Clawson G, Pan W;  
 XX WPI; 2002-519672/55.

XX Identifying cleavage sites of a target RNA, by adding target RNA to  
 PT library of nucleic acids e.g. ribozyme, which comprise catalytic core  
 PT flanked by random nucleotides and isolating nucleic acid that cleave  
 PT target RNA.

XX Example 5; Page 52; 79pp; English.  
 XX The present invention relates to a method of identifying cleavage sites

CC in a target RNA which are accessible to a ribozyme comprising a catalytic  
 CC core flanked by random nucleotides. A target RNA is added to the library  
 CC of nucleic acids and nucleic acids that bind to and/or cleave the target  
 CC RNA are isolated. The method is useful for identifying ribozyme cleavage  
 CC sites in sequences and in real time PCR assays. The present sequence is a  
 CC ribozyme target site described in the exemplification of the invention  
 XX SQ Sequence 17 BP; 8 A; 3 C; 5 G; 0 T; 1 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AAL48300 (1-17)  
 QY 174 ArgGlnLeuArgArg 178  
 |||||

Db 3 AGACAGCUCAGAGA 17  
 RESULT 70  
 ABV79962

ID ABV79962 standard; DNA; 17 BP.  
 AC ABV79962;

XX 03-JAN-2003 (first entry)  
 XX Human HTPL scanning oligonucleotide SEQ ID 1208.

XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;

KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN BP1229046-A2.  
 XX  
 XX  
 PD 07-AUG-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 XX Zhan J;  
 XX WPI; 2002-676582/73.  
 DR  
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 XX Example 2; Page 222; 718pp; English.  
 XX  
 CC The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 SQ Sequence 17 BP; 5 A; 5 C; 3 G; 4 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-966-880A-8 (1-198) x ABV79962 (1-17)  
 QY 172 LeuSerArgGlnLeu 176  
 Db 1 CTTTCCAGACACTG 15  
 RESULT 71  
 ID ABV79960  
 ABV79960 standard; DNA; 17 BP.  
 XX  
 AC ABV79960;

XX 03-JAN-2003 (first entry)  
 XX Human HTPL scanning oligonucleotide SEQ ID 1206.  
 DE  
 XX  
 XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
 KW human testis expressed Patched like protein; testis; adrenal; liver;  
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN BP1229046-A2.  
 XX  
 PD 07-AUG-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 XX Zhan J;  
 XX WPI; 2002-676582/73.  
 DR  
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPL.  
 XX  
 XX Example 2; Page 221; 718pp; English.  
 XX  
 CC The present invention relates to human testis expressed Patched like  
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPL is  
 CC important in regulating male germ cell development, and the HTPL gene was  
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-966-880A-8 (1-198) x ABV79960 (1-17)  
 QY 172 LeuSerArgGlnLeu 176  
 |||||||  
 |||||||

Db 3 CTTCCAGACAACTG 17

RESULT 72

ABV79961

ID ABV79961 standard; DNA; 17 BP.

XX

AC ABV79961;

XX

DT 03-JAN-2003 (first entry)

XX

DE Human HTPL scanning oligonucleotide SEQ ID 1207.

XX

KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;

KW human testis expressed patched like protein; testis; adrenal; liver;

KW male germ cell development; bone marrow; brain; kidney; lung; placenta;

KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX

OS Homo sapiens.

XX

PN EP1229046-A2.

XX

PD 07-AUG-2002.

XX

PF 28-JAN-2002; 2002EP-00001167.

XX

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.

XX

PA (AEOM-) AEOMICA INC.

XX

PI Zhan J;

XX

DR WPI; 2002-676582/73.

XX

PT Novel isolated human testis expressed Patched like protein (HTPL), useful

PT for identifying agonist and antagonist and specific binding partners, and

PT for treating subjects having defects in HTPL.

XX

PS Example 2; Page 222; 718pp; English.

XX

CC The present invention relates to human testis expressed Patched like

CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL

CC has two isoforms, with a few single base pair differences between the

CC two. One of the single base pair changes introduces a premature stop

CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL

CC shares an overall structure organisation with the Patched protein. The

CC shared structural features strongly imply that HTPL plays a role similar

CC to that of Patched, and is a potential tumour suppressor. HTPL is

CC important in regulating male germ cell development, and the HTPL gene was

CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are

CC useful for diagnosing a disorder caused by mutation in HTPL, and in

CC therapy and manufacture of a medicament for treatment or prevention of

CC such disorder associated with decreased expression or activity of human

CC HTPL. Such disorders include disorders of testis, or adrenal, adult and

CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,

CC skeletal muscle or colon function. HTPL proteins and nucleic acids are

CC clinically useful diagnostic markers and potential therapeutic agents for

CC male infertility and cancer. The present oligonucleotide was used in an

CC example from the invention

XX

SQ Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABV79961 (1-17)

QY 172 LeuSerArgGlnLeu 176

Db 2 CTTCCAGACAACTG 16

RESULT 73

AAS99517/c

ID AAS99517 standard; DNA; 17 BP.

XX

AC AAS99517;

XX

DT 07-AUG-2003 (revised)

DT 12-MAR-2002 (first entry)

XX

DE Mycobacterium species identification additional probe #2.

XX

KW Drug resistance detection; mycobacterial species identification; probe;

KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;

KW primer.

XX

OS Mycobacterium fortuitum.

OS Mycobacterium flavescens.

XX

PN WO200192573-A1.

XX

PD 06-DEC-2001.

XX

PF 30-MAY-2001; 2001WO-KR000904.

XX

PR 30-MAY-2000; 2000KR-00029369.

XX

PA (BIOM-) BIOMEDLAB CO LTD.

XX

PI Kim H, Kim N, Yoon S, Kim J, Park M;

XX

DR WPI; 2002-075472/10.

XX

PT Kit for mycobacterial species identification and drug resistance

PT detection, has oligonucleotide chip with species identification probe, a

PT mycobacterial drug-resistance detection probe, and its contrast group

PT probe.

XX

PS Disclosure; Page 12; 74pp; English.

XX

CC The invention relates to a diagnostic kit for mycobacterial species

CC identification and drug resistance detection comprising an

CC oligonucleotide chip including a species identification probe, a

CC mycobacterial drug-resistance detection probe, a contrast group probe

CC corresponding to each drug resistance detection probe, and a marker for

CC detecting a hybridisation of the oligonucleotide chip and a specimen. The

CC identification probe is comprised of species-specific DNA sequences of

CC mycobacterial rpoB gene and the detection probe is comprised of one or

CC more modified codons of mycobacterial rpoB gene. The method involves

CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction

CC (PCR) and discriminating species by fluorescent intensity corresponding

CC to a particular species. The specimen is preferably uncultured sputum,

CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569

CC represent mycobacterium species identification probes and primers of the

CC invention. (Updated on 07-AUG-2003 to correct OS field.)

XX

SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AAS99517 (1-17)

Qy 174 ArgGlnLeuArgArg 178  
Db 17 CGACAGCTGCAGCT 3

RESULT 74

ABV90749  
ID ABV90749 standard; DNA; 17 BP.

XX AC ABV90749;

XX DT 23-DEC-2002 (first entry)

XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1462.

XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
XX KW gene therapy; transgenic; ss.

XX OS Homo sapiens.

XX PN EP1239051-A2.

XX PD 11-SEP-2002.

XX PF 28-JAN-2002; 2002EP-00001165.

XX PR 30-JAN-2001; 2001WO-US0000663.

XX PR 30-JAN-2001; 2001WO-US0000664.

XX PR 30-JAN-2001; 2001WO-US0000665.

XX PR 30-JAN-2001; 2001WO-US0000666.

XX PR 30-JAN-2001; 2001WO-US0000667.

XX PR 30-JAN-2001; 2001WO-US0000668.

XX PR 30-JAN-2001; 2001WO-US0000669.

XX PR 30-JAN-2001; 2001WO-US0000670.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 10-OCT-2001; 2001US-0328205P.

XX PA (AEOM-) AEOMICA INC.

XX PI Shannon M;

XX WPI; 2002-684061/74.

XX DR Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL  
XX PT -1, useful for treating disorders associated with decreased expression or  
XX PT activity of human POSHL1.  
XX PS Example 2; SEQ ID NO 1462; 60pp + Sequence Listing; English.  
XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
XX CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
XX CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),  
XX CC (SI) having 95% deviations, especially conservative substitutions or a  
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.  
XX CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
XX CC adaptor protein that interacts with Rho family small GTPases as well as  
XX CC downstream components of the signal transduction pathway. (I) is useful  
XX CC for identifying a specific binding partner. (I) and nucleic acids (II)  
XX CC encoding (I) are useful for diagnosing, monitoring disease and treating  
XX CC caused by altered expression of human POSHL1 including diagnosing and  
XX CC treating cancer, they are useful in the development of vaccines and (II) is  
XX CC useful in gene therapy. (II) is useful for constructing microarrays which  
XX CC are useful for measuring and for surveying gene expression and creating  
XX CC transgenic non-human animals capable of producing the proteins. The  
XX CC present sequence is that of a scanning oligonucleotide useful in examples  
XX CC of the invention. Note: The present sequence did not form part of the  
XX CC printed specification, but is based on sequence information supplied to  
XX CC Derwent by the European Patent Office  
XX CC Sequence 17 BP; 7 A; 2 C; 8 G; 0 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABV90749 (1-17)

Qy 21 AlaLysGlyArgArg 25

Db 1 GCAAAGGGAGAGG 15

RESULT 75

ABV90748

ID ABV90748 standard; DNA; 17 BP.

XX AC ABV90748;

XX DT 23-DEC-2002 (first entry)

XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1461.

XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
XX KW gene therapy; transgenic; ss.

XX OS Homo sapiens.

XX PN EP1239051-A2.

XX PD 11-SEP-2002.

XX PF 28-JAN-2002; 2002EP-00001165.

XX PR 30-JAN-2001; 2001WO-US0000663.

XX PR 30-JAN-2001; 2001WO-US0000664.

XX PR 30-JAN-2001; 2001WO-US0000665.

XX PR 30-JAN-2001; 2001WO-US0000666.

XX PR 30-JAN-2001; 2001WO-US0000667.

XX PR 30-JAN-2001; 2001WO-US0000668.

XX PR 30-JAN-2001; 2001WO-US0000669.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 10-OCT-2001; 2001US-0328205P.

XX PA (AEOM-) AEOMICA INC.

XX PI Shannon M;

XX WPI; 2002-684061/74.

XX DR Novel human SH3 domain (POSH)-like signalling protein 1 polypeptide, POSHL  
XX PT -1, useful for treating disorders associated with decreased expression or  
XX PT activity of human POSHL1.  
XX PS Example 2; SEQ ID NO 1461; 60pp + Sequence Listing; English.  
XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling  
XX CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino  
XX CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),  
XX CC (SI) having 95% deviations, especially conservative substitutions or a  
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.  
XX CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
XX CC adaptor protein that interacts with Rho family small GTPases as well as  
XX CC downstream components of the signal transduction pathway. (I) is useful  
XX CC for identifying a specific binding partner. (I) and nucleic acids (II)  
XX CC encoding (I) are useful for diagnosing, monitoring disease and treating  
XX CC caused by altered expression of human POSHL1 including diagnosing and  
XX CC treating cancer, they are useful in the development of vaccines and (II) is  
XX CC useful in gene therapy. (II) is useful for constructing microarrays which

CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 SQ Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Alignment Scores: Length: 17  
 Pred. No.: 8.13e+03  
 Score: 5.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 2.53%  
 DB: Indels: 0  
 Gaps: 0

US-09-966-880A-8 (1-198) x ABV90748 (1-17)

Qy 21 AlalysGlyArg 25

Db 2 GCAAAAGGGAGAGG 16

RESULT 76

ABV90747  
 ID ABV90747 standard; DNA; 17 BP.

AC ABV90747;

DT 23-DEC-2002 (first entry)

DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1460.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;  
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;  
 KW gene therapy; transgenic; ss.

XX Homo sapiens.

XX EPI239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 30-JAN-2001; 2001WO-US000670.

XX 23-MAY-2001; 2001US-00864761.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL

XX -1, useful for treating disorders associated with decreased expression or

XX activity of human POSHL1.

XX Example 2; SEQ ID NO 1460; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling

XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

XX acids (SI, ABB3999), a sequence having 65% sequence identity to (SI),

XX (SI) having 95% deviations, especially conservative substitutions or a

XX fragment of the sequences comprising at least 8 contiguous amino acids.

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an  
 CC adaptor protein that interacts with Rho family small GTPases as well as  
 CC downstream components of the signal transduction pathway. (I) is useful  
 CC for identifying a specific binding partner. (I) and nucleic acids (II)  
 CC encoding (I) are useful for diagnosing, monitoring disease and treating  
 CC caused by altered expression of human POSHL1 including diagnosing and  
 CC treating cancer, they useful in the development of vaccines and (II) is  
 CC useful in gene therapy. (II) is useful for constructing microarrays which  
 CC are useful for measuring and for surveying gene expression and creating  
 CC transgenic non-human animals capable of producing the proteins. The  
 CC present sequence is that of a scanning oligonucleotide useful in examples  
 CC of the invention. Note: The present sequence did not form part of the  
 CC printed specification, but is based on sequence information supplied to  
 CC Derwent by the European Patent Office  
 XX  
 SQ Sequence 17 BP; 7 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

Alignment Scores: Length: 17  
 Pred. No.: 8.13e+03  
 Score: 5.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 2.53%  
 DB: Indels: 0  
 Gaps: 0

US-09-966-880A-8 (1-198) x ABV90747 (1-17)

Qy 21 AlalysGlyArg 25

Db 3 GCAAAAGGGAGAGG 17

RESULT 77

ABL31617/C

ID ABL31617 standard; DNA; 17 BP.

XX ABL31617;

XX 21-MAR-2002 (first entry)

XX Human HLA genotyping oligonucleotide SEQ ID NO 1106.

XX Human; human leukocyte antigen; HLA; genotype; polymorphism;  
 KW immunogenetic; transplantation; genetic disease; ss.

XX Homo sapiens.

XX WO200192572-A1.

XX 06-DEC-2001.

XX 01-JUN-2001; 2001WO-JP004662.

XX 01-JUN-2000; 2000JP-00164798.

XX (NISR) NISSHINBO IND INC.

XX (SYST-) SYSTEM RES INC.

XX Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;

XX WPI; 2002-122074/16.

XX Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of  
 XX individuals e.g. by determining immunogenetic differences when  
 XX transplanting between them.

XX Claim 10; Page 303; 345pp; Japanese.

XX The invention relates to a typing kit for judging human leukocyte antigen  
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base  
 CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of  
 CC genes e.g. belonging to HLA class I antigens on human genome and  
 CC containing gene polymorphisms as alloantigens have been immobilised as  
 CC primers for amplification of cleaved nucleic acids relating to gene

CC polymorphisms. The method is useful for judging HLA genotypes of  
 CC individuals by determining immunogenetic differences before transplanting  
 CC between them, providing genetic information to decide compatibility of  
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,  
 CC pancreas, langerhans islet in pancreas and cornea, susceptibility  
 CC diagnosis of genetic diseases and identifying individuals  
 CC  
 SQ Sequence 17 BP; 7 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Alignment Scores: 8.13e+03 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservativity: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 6

US-09-966-880A-8 (1-198) x ABL31617 (1-17)

QY 112 ArgLeuTy-PheCys 116

DB 15 CGCTTGACTCTGT 1

RESULT 78

ABK57787/c  
 ID ABK57787 standard; RNA; 17 BP.

XX AC ABK57787;

XX DT 02-JUL-2002 (first entry)

XX DE Human CLCA1 gene enzymatic nucleic acid #2159.

XX KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KW acetylcysteine.

XX OS Homo sapiens.

XX PN WO200211674-A2.

XX PD 14-FEB-2002.

XX PF 09-AUG-2001; 2001WO-US024970.

XX PR 09-AUG-2000; 2000US-0224383P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (SYNT) SYNTEX USA LLC.

XX PA (THOM/) THOMPSON J.

XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

XX PI Grupe A;

XX DR WPI; 2002-217145/27.

XX PT Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX PS Claim 4; Page 136; 152pp; English.

XX CC The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition

CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention

XX SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Alignment Scores: 8.13e+03 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservativity: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 6

US-09-966-880A-8 (1-198) x ABK57787 (1-17)

QY 103 AsnLeuSerLeuArg 107

DB 16 AACTTGCTCTGAGA 2

RESULT 79

ABK5838/c  
 ID ABK5838 standard; RNA; 17 BP.

XX AC ABK5838;

XX DT 02-JUL-2002 (first entry)

XX DE Human CLCA1 gene enzymatic nucleic acid #209.

XX KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KW acetylcysteine.

XX OS Homo sapiens.

XX PN WO200211674-A2.

XX PD 14-FEB-2002.

XX PF 09-AUG-2001; 2001WO-US024970.

XX PR 09-AUG-2000; 2000US-0224383P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (SYNT) SYNTEX USA LLC.

XX PA (THOM/) THOMPSON J.

XX PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

XX PI Grupe A;

XX DR WPI; 2002-217145/27.

XX PT Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX PS Claim 4; Page 56; 152pp; English.

XX CC The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC that are related to or will respond to the levels of CLCA1 in a cell or

CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Alignment Scores: 17  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK55838 (1-17)

Qy 126 LeuArgLeuHis 130

Db 15 CTTGGAGATTGCAT 2

RESULT 80

ABK56396/c

ID ABK56396 standard; RNA; 17 BP.

XX AC ABK56396;

XX 02-JUL-2002 (first entry)

XX Human CLCA1 gene enzymatic nucleic acid #767.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KW acetylcysteine.

XX Homo sapiens.

XX WC200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US024970.

XX 09-AUG-2000; 2000US-0224383P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (SYNT) SYNTAX USA LLC.

XX (THOM/) THOMPSON J.

XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

XX Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX Claim 4; Page 69; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are  
 CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic

CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention  
 XX

SQ Sequence 17 BP; 6 A; 5 C; 3 G; 0 T; 3 U; 0 Other;

Alignment Scores: 17  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABK56396 (1-17)

Qy 126 LeuArgLeuHis 130

Db 15 CTTGGAGATTGCAT 1

RESULT 81

ABK57455/c

ID ABK57455 standard; RNA; 17 BP.

XX AC ABK57455;

XX 02-JUL-2002 (first entry)

XX Human CLCA1 gene enzymatic nucleic acid #1826.

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;  
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;  
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;  
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;  
 KW acetylcysteine.

XX Homo sapiens.

XX WO200211674-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US024970.

XX 09-AUG-2000; 2000US-0224383P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (SYNT) SYNTAX USA LLC.

XX (THOM/) THOMPSON J.

XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

XX Grupe A;

XX WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride  
 PT channel calcium activated gene, useful for treating Chronic obstructive  
 PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX Claim 4; Page 113; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down  
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes  
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are

CC useful as pharmaceutical agents for treating conditions such as chronic  
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic  
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions  
 CC that are related to or will respond to the levels of CLCA1 in a cell or  
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,  
 CC hence, are useful for treatment of a patient having a condition  
 CC associated with the level of CLCA1, where the invention further comprises  
 CC the use of one or more therapies under conditions suitable for the  
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,  
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The  
 CC nucleic acids of the invention are also used as diagnostic tools to  
 CC examine genetic drift and mutations within diseased cells or to detect  
 CC the presence of CLCA1 RNA in a cell. This sequence represents an  
 CC enzymatic nucleic acid molecule of the invention  
 XX  
 SQ Sequence 17 BP; 6 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Alignment Scores: 8.13e+03 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 6

US-09-966-880A-8 (1-198) x ABK57455 (1-17)

Qy 103 AsnLeuSerLeuArg 107  
 Db 15 AACTTGCTCTGAGA 1

RESULT 82  
 ABZ95623/c  
 ID ABZ95623 standard; DNA; 17 BP.

AC ABZ95623;

DT 17-OCT-2003 (first entry)

DE Human NF-kappaB antisense fragment no.1487.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;  
 XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 XX antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 XX lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

XX Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired  
 XX respiration, has oligo(s) antisense to specific gene(s) or its  
 XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 XX ubiquinone.

XX Disclosure; SEQ ID NO 10865; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;

Alignment Scores: 8.13e+03 Length: 17  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 7

US-09-966-880A-8 (1-198) x ABZ95623 (1-17)

Qy 36 ArgAspSerAlaThr 40

Db 15 CGGACAGCGCCACC 1

RESULT 83

ACC52922

ID ACC52922 standard; DNA; 17 BP.

XX AC ACC52922;

XX 27-JUN-2003 (first entry)

XX Human tumour suppressor sequence #1689.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
 XX tumour regression; apoptosis; virus resistance; diagnosis;  
 XX cellular degeneration.

OS Homo sapiens.

XX FR2826373-A1.

XX 27-DEC-2002.

XX 20-JUN-2001; 2001FR-00008139.

XX 20-JUN-2001; 2001FR-00008139.

XX (MOLE-) MOLECULAR ENGINES LAB SA.

XX Tuijnder M, Telerman A, Amson R;

XX WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression, regression,  
 XX apoptosis or virus resistance are useful to diagnose and treat viral  
 XX disease, development of tumor cells and cell degeneration.

XX Claim 1; Page 430; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated



CC with tumour suppression or regression, apoptosis or virus resistance. The  
 CC invention relates to these sequences or sequences having at least 80%  
 CC identity to them, and polypeptides encoded by the sequences or  
 CC polypeptides having 80% identity to the polypeptide sequences. The  
 CC invention is used to diagnose or treat viral disease or disease  
 CC characterized by development of tumour cells or cellular degeneration  
 XX  
 SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: Gaps: 0

US-09-966-880A-8 (1-198) x ACC52922 (1-17)

QY 169 SerValArgLeuSer 173

Db 3 TCCGTCGCTCAGC 17

RESULT 84

ACC53318  
 ID ACC53318 standard; DNA; 17 BP.

XX AC

AC ACC53318;

XX DT 27-JUN-2003 (first entry)

XX DE Human tumour suppressor sequence #2085.

XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;

XX KW tumour regression; apoptosis; virus resistance; diagnosis;  
 XX KW cellular degeneration.

XX OS Homo sapiens.

XX PN FR2826373-A1.

XX XX 27-DEC-2002.

XX PF 20-JUN-2001; 2001FR-00008139.

XX PR 20-JUN-2001; 2001FR-00008139.

XX PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX PI Tuijnder M, Telerman A, Amson R;

XX DR WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumour suppression, regression,  
 PT apoptosis or virus resistance are useful to diagnose and treat viral  
 PT disease, development of tumor cells and cell degeneration.  
 XX  
 PS Claim 1; Page 521; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated  
 CC with tumour suppression or regression, apoptosis or virus resistance. The  
 CC invention relates to these sequences or sequences having at least 80%  
 CC identity to them, and polypeptides encoded by the sequences or  
 CC polypeptides having 80% identity to the polypeptide sequences. The  
 CC invention is used to diagnose or treat viral disease or disease  
 CC characterized by development of tumour cells or cellular degeneration  
 XX

SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: Gaps: 0

US-09-966-880A-8 (1-198) x ACC53318 (1-17)

QY 118 AspArgLysAlaGlu 122

Db 1 GATCGCAAGCTGAG 15

RESULT 85

ACC52814

ID ACC52814 standard; DNA; 17 BP.

XX AC

AC ACC52814;

XX DT 27-JUN-2003 (first entry)

XX DE Human tumour suppressor sequence #1581.

XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
 XX KW tumour regression; apoptosis; virus resistance; diagnosis;  
 XX KW cellular degeneration.

XX OS Homo sapiens.

XX PN FR2826373-A1.

XX XX 27-DEC-2002.

XX PF 20-JUN-2001; 2001FR-00008139.

XX PR 20-JUN-2001; 2001FR-00008139.

XX PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX PI Tuijnder M, Telerman A, Amson R;

XX DR WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumour suppression, regression,  
 PT apoptosis or virus resistance are useful to diagnose and treat viral  
 PT disease, development of tumor cells and cell degeneration.  
 XX  
 PS Claim 1; Page 405; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated  
 CC with tumour suppression or regression, apoptosis or virus resistance. The  
 CC invention relates to these sequences or sequences having at least 80%  
 CC identity to them, and polypeptides encoded by the sequences or  
 CC polypeptides having 80% identity to the polypeptide sequences. The  
 CC invention is used to diagnose or treat viral disease or disease  
 CC characterized by development of tumour cells or cellular degeneration  
 XX

SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: Gaps: 0

US-09-966-880A-8 (1-198) x ACC52814 (1-17)

QY 43 SerLeuAspPheGly 47

Db 3 TCCCTGGACTTTGGA 17

RESULT 86

ACC51417

ID ACC51417 standard; DNA; 17 BP.

XX AC AC51417;  
 XX DT 27-JUN-2003 (first entry)  
 XX DE Human tumour suppressor sequence #184.  
 XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
 XX KW tumour regression; apoptosis; virus resistance; diagnosis;  
 XX KW cellular degeneration.  
 XX OS Homo sapiens.  
 XX PN FR2826373-A1.  
 XX PD 27-DEC-2002.  
 XX PF 20-JUN-2001; 2001FR-00008139.  
 XX PR 20-JUN-2001; 2001FR-00008139.  
 XX PA (MOLE-) MOLECULAR ENGINES LAB SA.  
 XX PI Tuijnder M, Telerman A, Amson R;  
 XX DR WPI; 2003-250498/25.  
 XX New nucleic acid sequences associated with tumor suppression, regression,  
 PT apoptosis or virus resistance are useful to diagnose and treat viral  
 PT disease, development of tumor cells and cell degeneration.  
 XX PS Claim 1; Page 82; 798pp; French.  
 XX CC This sequence represents an isolated nucleic acid sequence associated  
 CC with tumour suppression or regression, apoptosis or virus resistance. The  
 CC invention relates to these sequences or sequences having at least 80%  
 CC identity to them, and polypeptides encoded by the sequences or  
 CC polypeptides having 80% identity to the polypeptide sequences. The  
 CC invention is used to diagnose or treat viral disease or disease  
 CC characterized by development of tumour cells or cellular degeneration  
 XX Sequence 17 BP; 6 A; 3 C; 6 G; 2 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-966-880A-8 (1-198) x ACC51417 (1-17)  
 Qy 173 SerArgGlnLeuArg 177  
 Db 3 TCAAGGAGCTGAGA 17  
 RESULT 87  
 ACC53675/C  
 ID ACC53675 standard; DNA; 17 BP.  
 XX AC ACC53675;  
 XX DT 27-JUN-2003 (first entry)  
 XX DE Human tumour suppressor sequence #2442.  
 XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
 KW tumour regression; apoptosis; virus resistance; diagnosis;  
 KW cellular degeneration.  
 XX OS Homo sapiens.

PN FR2826373-A1.  
 XX 27-DEC-2002.  
 XX 20-JUN-2001; 2001FR-00008139.  
 XX 20-JUN-2001; 2001FR-00008139.  
 XX (MOLE-) MOLECULAR ENGINES LAB SA.  
 XX Tuijnder M, Telerman A, Amson R;  
 XX WPI; 2003-250498/25.  
 XX New nucleic acid sequences associated with tumor suppression, regression,  
 PT apoptosis or virus resistance are useful to diagnose and treat viral  
 PT disease, development of tumor cells and cell degeneration.  
 XX PS Claim 1; Page 604; 798pp; French.  
 XX CC This sequence represents an isolated nucleic acid sequence associated  
 CC with tumour suppression or regression, apoptosis or virus resistance. The  
 CC invention relates to these sequences or sequences having at least 80%  
 CC identity to them, and polypeptides encoded by the sequences or  
 CC polypeptides having 80% identity to the polypeptide sequences. The  
 CC invention is used to diagnose or treat viral disease or disease  
 CC characterized by development of tumour cells or cellular degeneration  
 XX Sequence 17 BP; 9 A; 3 C; 3 G; 2 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-966-880A-8 (1-198) x ACC53675 (1-17)  
 Qy 59 LeuLeuPheLeuArg 63  
 Db 17 CTCTGTTTGTAGA 3  
 RESULT 88  
 ACC54176  
 ID ACC54176 standard; DNA; 17 BP.  
 XX AC ACC54176;  
 XX DT 27-JUN-2003 (first entry)  
 XX DE Human tumour suppressor sequence #2943.  
 XX KW ss; tumour suppressor; antitumour; cytostatic; tumour suppression;  
 KW tumour regression; apoptosis; virus resistance; diagnosis;  
 KW cellular degeneration.  
 XX OS Homo sapiens.  
 XX PN FR2826373-A1.  
 XX PD 27-DEC-2002.  
 XX PF 20-JUN-2001; 2001FR-00008139.  
 XX PR 20-JUN-2001; 2001FR-00008139.  
 XX PA (MOLE-) MOLECULAR ENGINES LAB SA.  
 XX PI Tuijnder M, Telerman A, Amson R;  
 XX WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression, regression,  
PT apoptosis or virus resistance are useful to diagnose and treat viral  
PT disease, development of tumor cells and cell degeneration.  
XX  
PS Claim 1; Page 719; 798pp; French.  
XX  
CC This sequence represents an isolated nucleic acid sequence associated  
CC with tumor suppression or regression, apoptosis or virus resistance. The  
CC invention relates to these sequences or sequences having at least 80%  
CC identity to them, and polypeptides encoded by the sequences or  
CC polypeptides having 80% identity to the polypeptide sequences. The  
CC invention is used to diagnose or treat viral disease or disease  
CC characterized by development of tumor cells or cellular degeneration  
XX  
SQ Sequence 17 BP; 2 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC54176 (1-17)

QY 169 SerValArgLeuSer 173

Db 3 TCCTGTCGCTCAGC 17

RESULT 89

ABT36841/c

ID ABT36841 standard; DNA; 17 BP.

XX AC ABT36841;

DT 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 2478.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001PR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.

XX Disclosure; Page 322; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive  
CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement

CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterised by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention

SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABT36841 (1-17)

QY 132 AlaGlyValGlnIle 136

Db 15 GCTGGAGTGCAGATC 1

RESULT 90

ABT37905

ID ABT37905 standard; DNA; 17 BP.

XX AC ABT37905;

DT 12-JUN-2003 (first entry)

XX Tumour suppression related human fukutin oligo SEQ ID No 3542.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; protein chip; gene therapy; tumour suppression;  
KW human fukutin; ds.

XX Homo sapiens.

XX WO2003025175-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-IB004208.

XX 17-SEP-2001; 2001PR-00011978.

XX (MOLE-) MOLECULAR ENGINES LAB.

XX Telerman A, Amson R, Tuijnder M;

XX WPI; 2003-313353/30.

XX New isolated nucleic acid, useful for treating viral diseases associated  
PT with tumors and cell degeneration, also related polypeptides, antibodies  
PT and transfected cells.

XX Disclosure; Page 448; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
CC given in the specification, a sequence containing at least 15 consecutive

CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
CC hybridizes to them under highly stringent conditions, or the complement  
CC of any of them, or the corresponding RNA. The novel isolated nucleic  
CC acids of the invention are useful as probes and primers for detecting,  
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
CC component of a gene chip, in vitro as (anti)sense reagents, and for  
CC production of recombinant polypeptides. Any of the nucleic acids,  
CC polypeptides, vectors containing the nucleic acids, cells containing the  
CC vector or antibodies directed against the polypeptides are useful for  
CC preparation of pharmaceuticals for prevention and/or treatment of viral  
CC diseases that are characterized by development of tumours or cell  
CC degeneration, specifically cancer but also Alzheimer's disease and  
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
CC patient samples is useful for diagnosis and/or prognosis of these  
CC diseases. The polypeptides can also be used to generate antibodies, and  
CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABT37905 (1-17)

OY 118 AspArgLysAlaGlu 122  
Db 1 GATCGCAAGGCTGAG 15

RESULT 91  
ABT34570  
ID ABT34570 standard; DNA; 17 BP.  
AC ABT34570;  
XX  
XX 12-JUN-2003 (first entry)  
XX Tumour suppression related human fukutin oligo SEQ ID No 207.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
XX antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
XX schizophrenia; protein chip; gene therapy; tumour suppression;  
XX human fukutin; ds.  
XX  
XX Homo sapiens.  
XX WO2003025175-A2.  
XX  
XX 27-MAR-2003.  
XX  
XX 17-SEP-2002; 2002WO-IB004208.  
XX  
XX 17-SEP-2001; 2001FR-00011978.  
XX  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX  
XX Telerman A, Anson R, Tuijnder M;  
XX WPI; 2003-313353/30.  
XX  
XX New isolated nucleic acid, useful for treating viral diseases associated  
XX with tumors and cell degeneration, also related polypeptides, antibodies  
XX and transfected cells.  
XX  
XX Disclosure; Page 58; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
XX given in the specification, a sequence containing at least 15 consecutive  
XX nucleotides from the 17 mer sequence, a sequence with, after optimal  
XX alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
XX hybridizes to them under highly stringent conditions, or the complement  
XX of any of them, or the corresponding RNA. The novel isolated nucleic  
XX acids of the invention are useful as probes and primers for detecting,  
XX identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
XX component of a gene chip, in vitro as (anti)sense reagents, and for  
XX production of recombinant polypeptides. Any of the nucleic acids,  
XX polypeptides, vectors containing the nucleic acids, cells containing the  
XX vector or antibodies directed against the polypeptides are useful for  
XX preparation of pharmaceuticals for prevention and/or treatment of viral  
XX diseases that are characterized by development of tumours or cell  
XX degeneration, specifically cancer but also Alzheimer's disease and  
XX schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
XX patient samples is useful for diagnosis and/or prognosis of these  
XX diseases. The polypeptides can also be used to generate antibodies, and  
XX both the polypeptide and antibodies are useful as components of protein  
XX chips. The nucleic acid sequences of the invention can be used in gene  
XX therapy. This polynucleotide sequence represents a tumour suppression  
XX related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABT34570 (1-17)

OY 83 SerTyrSerProCys 87  
Db 3 TCCTGGAGCCCTGT 17

RESULT 92  
ABZ64654  
ID ABZ64654 standard; RNA; 17 BP.  
XX  
XX ABZ64654;  
XX  
XX 21-MAR-2003 (first entry)

XX Human HER2 DNAzyme substrate #111.  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;  
XX anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
XX WO200297114-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 29-MAY-2002; 2002WO-US016840.  
XX  
XX 29-MAY-2001; 2001US-0294140P.  
XX 06-JUN-2001; 2001US-0296249P.  
XX 10-SEP-2001; 2001US-0318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Mcswiggen J;  
XX WPI; 2003-140484/13.  
XX  
XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX  
PS Claim 4; Page 135; 185pp; English.  
XX  
CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC bladder, or pancreatic cancer, and HIV infection, AIDS. The sequences  
CC shown in AB259889 - AB262215, AB264544 - AB265531, AB266520 - AB266524,  
CC AB266530 - AB266585 represent substrate/target sequences for the human  
CC ribozymes of the invention  
XX  
SQ Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AB264654 (1-17)  
  
Qy 89 AspCysAlaArgHis 93  
Db 3 GAUUGUGCGAGGCAC 17  
  
RESULT 93  
ACD59843  
ID ACD59843 standard; RNA; 17 BP.  
XX  
AC ACD59843;  
XX  
XX 24-SEP-2003 (first entry)  
DT  
XX HCV DNazyme substrate sequence #1533.  
DE  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
XX RNA stability; RNA expression; RNA synthesis; antisense;  
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
XX HBV reverse transcriptase; Enhancer I region; viral replication;  
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
XX virucide; antiinflammatory; substrate; ss.  
XX  
XX Hepatitis C virus.  
XX  
XX WO200281494-A1.  
XX  
XX 17-OCT-2002.  
PD  
XX  
XX 26-MAR-2002; 2002WO-US009187.  
PF  
XX  
XX 26-MAR-2001; 2001US-00817879.  
PR  
XX 08-JUN-2001; 2001US-00877478.  
PR  
XX 08-JUN-2001; 2001US-0296876P.  
PR  
XX 24-OCT-2001; 2001US-0135059P.  
PR  
XX 05-DEC-2001; 2001US-0337055P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (NACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORA/) MORRISSEY D.  
PA (PAVC/) PAVCO P.

PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
DR  
XX  
PT Novel compound useful for treating cirrhosis, liver failure,  
PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
PT infection.  
XX  
PS Claim 1; Page 261; 387pp; English.  
XX  
CC The present invention relates to nucleic acid molecules which modulate  
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed  
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
CC DNA. The nucleic acids may be used to modulate the expression of HBV  
CC genes and HBV viral replication. Also disclosed is a method for screening  
CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HCV  
CC DNazyme or minus strand DNazyme sequences disclosed in the present  
CC invention  
XX  
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 0 T; 3 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0  
  
US-09-966-880A-8 (1-198) x ACD59843 (1-17)  
  
Qy 126 LeuArgArgLeuHis 130  
Db 1 CUGAGGAGGCGUCCAU 15  
  
RESULT 94  
ACD53202  
ID ACD53202 standard; RNA; 17 BP.  
XX  
AC ACD53202;  
XX  
XX 24-SEP-2003 (first entry)  
DT  
XX  
XX HBV G-cleaver substrate sequence #39.  
DE  
XX  
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
XX RNA stability; RNA expression; RNA synthesis; antisense;  
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;  
XX HBV reverse transcriptase; Enhancer I region; viral replication;  
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
XX virucide; antiinflammatory; substrate; ss.  
XX  
XX Hepatitis B virus.  
XX  
XX WO200281494-A1.

PD 17-OCT-2002.  
 XX 26-MAR-2002; 2002WO-US009187.  
 XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX Example 1; Page 165; 387pp; English.  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberszymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HCV. The compounds  
 CC that modulate the expression and/or replication of HCV. The compounds  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberszyme sequences  
 CC disclosed in the present invention  
 XX Sequence 17 BP; 4 A; 6 C; 1 G; 0 T; 6 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0  
 US-09-966-880A-8 (1-198) x ACD533202 (1-17)  
 Qy 172 LeuSerArgGlnLeu 176  
 Db 2 CUUUCUGCCCAACU 16  
 RESULT 95  
 ACD50977  
 ID ACD50977 standard; RNA; 17 BP.  
 XX  
 AC ACD50977;  
 XX  
 DT 23-SEP-2003 (first entry)

XX HBV hammerhead ribozyme substrate sequence #341.  
 DE  
 XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
 KW RNA stability; RNA expression; RNA synthesis; antisense;  
 KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
 KW amberszyme; G-cleaver ribozyme; decoy molecule; aptamer;  
 KW HBV reverse transcriptase; Enhancer I region; viral replication;  
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
 KW virucide; antiinflammatory; substrate; ss.  
 XX Hepatitis B virus.  
 OS  
 XX WO200281494-A1.  
 PN  
 XX 17-OCT-2002.  
 DD  
 XX 26-MAR-2002; 2002WO-US009187.  
 XX 26-MAR-2001; 2001US-00817879.  
 PR 08-JUN-2001; 2001US-00877478.  
 PR 08-JUN-2001; 2001US-0296876P.  
 PR 24-OCT-2001; 2001US-0335059P.  
 PR 05-DEC-2001; 2001US-0337055P.  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MACE/) MACEJAK D.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (MORR/) MORRISSEY D.  
 PA (PAVC/) PAVCO P.  
 PA (LEEP/) LEE P.  
 PA (DRAP/) DRAPER K.  
 PA (ROBE/) ROBERTS E.  
 XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
 PI Draper K, Roberts E;  
 XX WPI; 2003-229207/22.  
 XX Novel compound useful for treating cirrhosis, liver failure,  
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus  
 PT infection.  
 XX Example 1; Page 142; 387pp; English.  
 XX The present invention relates to nucleic acid molecules which modulate  
 CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
 CC inozymes, zinzymes, amberszymes, and G-cleaver ribozymes. Also disclosed  
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well  
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV  
 CC DNA. The nucleic acids may be used to modulate the expression of HBV  
 CC genes and HBV viral replication. Also disclosed is a method for screening  
 CC compounds and/or potential therapies directed against HCV. The compounds  
 CC that modulate the expression and/or replication of HCV. The compounds  
 CC methods of the invention are useful for the treatment of degenerative and  
 CC disease states related to HBV and HCV infection, replication and gene  
 CC expression such as cirrhosis, liver failure, and hepatocellular  
 CC carcinoma. The present sequence represents a substrate for one of the HBV  
 CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberszyme sequences  
 CC disclosed in the present invention  
 XX Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x ACD50977 (1-17)

QY 194 ArgThrLeuGlyLeu 198  
|||||  
DB 1 AGGACTUCUGGACUU 15

RESULT 96  
ACD50781  
ID ACD50781 standard; RNA; 17 BP.  
XX ACD50781;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HBV hammerhead ribozyme substrate sequence #247.  
XX

Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
RNA stability; RNA expression; RNA synthesis; antisense;  
enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
HBV reverse transcriptase; Enhancer I region; viral replication;  
degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
liver failure; hepatocellular carcinoma; hepatotropic; cyostatic;  
virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR  
PR 08-JUN-2001; 2001US-00877478.  
PR  
PR 08-JUN-2001; 2001US-0296876P.  
PR  
PR 24-OCT-2001; 2001US-0335059P.  
PR  
PR 05-DEC-2001; 2001US-0337055P.  
XX

(RIBO-) RIBOZYME PHARM INC.  
(BLAT/) BLATT L.  
(MACE/) MACEJAK D.  
(MCSW/) MCSWIGGEN J.  
(MORR/) MORRISSEY D.  
(PAVC/) PAVCO P.  
(LEEF/) LEE P.  
(DRAP/) DRAPER K.  
(ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
XX

Novel compound useful for treating cirrhosis, liver failure,  
hepatocellular carcinoma, or condition associated with hepatitis C virus  
infection.  
XX  
XX Example 1; Page 140; 387pp; English.  
XX

The present invention relates to nucleic acid molecules which modulate  
the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
transcriptase and/or HBV reverse transcriptase primer sequences, as well  
as oligonucleotides that specifically bind the Enhancer I region of HBV  
DNA. The nucleic acids may be used to modulate the expression of HBV  
genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV, and compounds  
CC that modulate the expression and/or replication of HCV. The compounds and  
CC methods of the invention are useful for the treatment of degenerative and  
CC disease states related to HBV and HCV infection, replication and gene  
CC expression such as cirrhosis, liver failure, and hepatocellular  
CC carcinoma. The present sequence represents a substrate for one of the HBV  
CC ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences  
CC disclosed in the present invention  
XX  
SQ Sequence 17 BP; 3 A; 6 C; 1 G; 0 T; 7 U; 0 Other;  
XX

Alignment Scores: Length: 17  
Pred. No.: 8.13e+03 Matches: 5  
Score: 5.00 Conservatives: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 7

US-09-966-880A-8 (1-198) x ACD50781 (1-17)

QY 172 LeuSerArgGlnLeu 176  
|||||  
DB 3 CUUUCUGGCCAACUU 17

RESULT 97  
ACD50976  
ID ACD50976 standard; RNA; 17 BP.  
XX ACD50976;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE HBV hammerhead ribozyme substrate sequence #340.  
XX

Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
RNA stability; RNA expression; RNA synthesis; antisense;  
enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;  
HBV reverse transcriptase; Enhancer I region; viral replication;  
degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
liver failure; hepatocellular carcinoma; hepatotropic; cyostatic;  
virucide; antiinflammatory; substrate; ss.  
XX  
OS Hepatitis B virus.  
XX  
PN WO200281494-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-US009187.  
XX  
PR 26-MAR-2001; 2001US-00817879.  
PR  
PR 08-JUN-2001; 2001US-00877478.  
PR  
PR 08-JUN-2001; 2001US-0296876P.  
PR  
PR 24-OCT-2001; 2001US-0335059P.  
PR  
PR 05-DEC-2001; 2001US-0337055P.  
XX

(RIBO-) RIBOZYME PHARM INC.  
(BLAT/) BLATT L.  
(MACE/) MACEJAK D.  
(MCSW/) MCSWIGGEN J.  
(MORR/) MORRISSEY D.  
(PAVC/) PAVCO P.  
(LEEF/) LEE P.  
(DRAP/) DRAPER K.  
(ROBE/) ROBERTS E.  
XX  
PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX  
XX WPI; 2003-229207/22.  
XX

Novel compound useful for treating cirrhosis, liver failure,  
hepatocellular carcinoma, or condition associated with hepatitis C virus  
infection.  
XX  
XX Example 1; Page 140; 387pp; English.  
XX

The present invention relates to nucleic acid molecules which modulate  
the synthesis, expression and/or stability of Hepatitis C virus (HCV) or  
Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense  
and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,  
inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed  
are nucleic acid decoy molecules and aptamers that bind to HBV reverse  
transcriptase and/or HBV reverse transcriptase primer sequences, as well  
as oligonucleotides that specifically bind the Enhancer I region of HBV  
DNA. The nucleic acids may be used to modulate the expression of HBV  
genes and HBV viral replication. Also disclosed is a method for screening

PT Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection.

XX Example 1; Page 142; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes, inozymes, zinzymes, amberszymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberszyme sequences disclosed in the present invention

SQ Sequence 17 BP; 4 A; 3 C; 5 G; 0 T; 5 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACD50976 (1-17)

Qy 194 ArgThrLeuGlyLeu 198  
Db 3 AGGACUUCUGGACUU 17

RESULT 98  
ACD52479  
ID ACD52479 standard; RNA; 17 BP.

AC ACD52479;  
XX 24-SEP-2003 (first entry)  
DE HBV inozyme substrate sequence #405.

XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;  
KW RNA stability; RNA expression; RNA synthesis; antisense;  
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;  
KW amberszyme; G-cleaver ribozyme; decoy molecule; aptamer;  
KW HBV reverse transcriptase; Enhancer I region; viral replication;  
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;  
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;  
KW virucide; antiinflammatory; substrate; ss.

XX Hepatitis B virus.

XX WO200281494-A1.

XX 17-OCT-2002.

XX 26-MAR-2002; 2002WO-US009187.

XX 26-MAR-2001; 2001US-00817879.

XX 08-JUN-2001; 2001US-00877478.

XX 08-JUN-2001; 2001US-0296876P.

XX 24-OCT-2001; 2001US-0335059P.

XX 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.  
PA (BLAT/) BLATT L.  
PA (MACE/) MACEJAK D.  
PA (MCSW/) MCSWIGGEN J.  
PA (MORR/) MORRISSEY D.  
PA (PAVC/) PAVCO P.  
PA (LEEP/) LEE P.  
PA (DRAP/) DRAPER K.  
PA (ROBE/) ROBERTS E.

XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;  
PI Draper K, Roberts E;  
XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure, hepatocellular carcinoma, or condition associated with hepatitis C virus infection.

XX Example 1; Page 158; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate the synthesis, expression and/or stability of Hepatitis C virus (HCV) or Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes, inozymes, zinzymes, amberszymes, and G-cleaver ribozymes. Also disclosed are nucleic acid decoy molecules and aptamers that bind to HBV reverse transcriptase and/or HBV reverse transcriptase primer sequences, as well as oligonucleotides that specifically bind the Enhancer I region of HBV DNA. The nucleic acids may be used to modulate the expression of HBV genes and HBV viral replication. Also disclosed is a method for screening compounds and/or potential therapies directed against HBV, and compounds that modulate the expression and/or replication of HCV. The compounds and methods of the invention are useful for the treatment of degenerative and disease states related to HBV and HCV infection, replication and gene expression such as cirrhosis, liver failure, and hepatocellular carcinoma. The present sequence represents a substrate for one of the HBV ribozyme, inozyme, G-cleaver, zinzyme, DNazyme or amberszyme sequences disclosed in the present invention

SQ Sequence 17 BP; 3 A; 3 C; 5 G; 0 T; 6 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.13e+03 Length: 17  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACD52479 (1-17)

Qy 194 ArgThrLeuGlyLeu 198  
Db 2 AGGACUUCUGGACUU 16

RESULT 99  
ACD68084  
ID ACC68084 standard; DNA; 17 BP.

XX ACC68084;

XX 01-JUL-2003 (first entry)

XX Murine oligonucleotide associated with tumour supression, SEQ ID 5331.

XX Cytostatic; virucide; neuroprotective; neuroleptic; murine;  
KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
KW schizophrenia; ss.

XX Mus musculus.



XX WO2003025176-A2.  
XX 27-MAR-2003.  
XX 17-SEP-2002; 2002WO-IB004210.  
XX 17-SEP-2001; 2001FR-00011979.  
XX (MOLE-) MOLECULAR ENGINES LAB.  
XX Telerman A, Amson R, Tuijnder M;  
XX WPI; 2003-333167/31.  
XX New isolated nucleic acid, useful for treating viral diseases associated  
XX with tumors and cell degeneration, also related polypeptides, antibodies  
XX and transfected cells.  
XX Disclosure; Page 654; 738pp; French.  
XX The present invention relates to murine oligonucleotides (ACC62754-  
XX ACC6806), which are associated with tumour suppression, tumour  
XX reversion, apoptosis and virus resistance. The oligonucleotides are  
XX useful as (1) as probes and primers for detecting, identifying,  
XX quantifying and/or amplifying nucleic acid, e.g. as one component of a  
XX gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
XX recombinant polypeptides. The oligonucleotides are useful for preparation  
XX of pharmaceuticals for prevention and/or treatment of viral diseases that  
XX are characterised by development of tumours or cell degeneration,  
XX specifically cancer but also Alzheimer's disease and schizophrenia  
XX Sequence 17 BP; 2 A; 8 C; 1 G; 6 T; 0 U; 0 Other;  
XX  
XX Alignment Scores: Length: 17  
XX Pred. No.: 8.13e+03 Matches: 5  
XX Score: 5.00 Conservative: 0  
XX Percent Similarity: 100.00% Mismatches: 0  
XX Best Local Similarity: 100.00% Indels: 0  
XX Query Match: 2.53% Gaps: 0  
XX DB: 7  
XX  
XX US-09-966-880A-8 (1-198) x ACC68084 (1-17)  
XX  
XX QY 179 IleleuLeuProLeu 183  
XX  
XX DB 2 ATCTTCTCCCACTC 16  
XX  
XX RESULT 100  
XX ACC63683  
XX ID ACC63683 standard; DNA; 17 BP.  
XX AC ACC63683;  
XX  
XX DT 01-JUL-2003 (first entry)  
XX  
XX DE Murine oligonucleotide associated with tumour suppression, SEQ ID 930.  
XX  
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
XX schizophrenia; ss.  
XX OS Mus musculus.  
XX PN WO2003025176-A2.  
XX  
XX PD 27-MAR-2003.  
XX  
XX PF 17-SEP-2002; 2002WO-IB004210.  
XX  
XX PR 17-SEP-2001; 2001FR-00011979.  
XX  
XX PT New isolated nucleic acid, useful for treating viral diseases associated  
XX with tumors and cell degeneration, also related polypeptides, antibodies  
XX and transfected cells.

PA (MOLE-) MOLECULAR ENGINES LAB.  
XX Telerman A, Amson R, Tuijnder M;  
XX WPI; 2003-333167/31.  
XX New isolated nucleic acid, useful for treating viral diseases associated  
XX with tumors and cell degeneration, also related polypeptides, antibodies  
XX and transfected cells.  
XX Disclosure; Page 139; 738pp; French.  
XX The present invention relates to murine oligonucleotides (ACC62754-  
XX ACC6806), which are associated with tumour suppression, tumour  
XX reversion, apoptosis and virus resistance. The oligonucleotides are  
XX useful as (1) as probes and primers for detecting, identifying,  
XX quantifying and/or amplifying nucleic acid, e.g. as one component of a  
XX gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
XX recombinant polypeptides. The oligonucleotides are useful for preparation  
XX of pharmaceuticals for prevention and/or treatment of viral diseases that  
XX are characterised by development of tumours or cell degeneration,  
XX specifically cancer but also Alzheimer's disease and schizophrenia  
XX Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 0 Other;  
XX  
XX Alignment Scores: Length: 17  
XX Pred. No.: 8.13e+03 Matches: 5  
XX Score: 5.00 Conservative: 0  
XX Percent Similarity: 100.00% Mismatches: 0  
XX Best Local Similarity: 100.00% Indels: 0  
XX Query Match: 2.53% Gaps: 0  
XX DB: 7  
XX  
XX US-09-966-880A-8 (1-198) x ACC63683 (1-17)  
XX  
XX QY 71 AspProGlyArgCys 75  
XX  
XX DB 1 GATCCAGGCAGGTGT 15  
XX  
XX RESULT 101  
XX ACC65317  
XX ID ACC65317 standard; DNA; 17 BP.  
XX AC ACC65317;  
XX  
XX DT 01-JUL-2003 (first entry)  
XX  
XX DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2564.  
XX  
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
XX schizophrenia; ss.  
XX OS Mus musculus.  
XX PN WO2003025176-A2.  
XX  
XX PD 27-MAR-2003.  
XX  
XX PF 17-SEP-2002; 2002WO-IB004210.  
XX  
XX PR 17-SEP-2001; 2001FR-00011979.  
XX  
XX PA (MOLE-) MOLECULAR ENGINES LAB.  
XX Telerman A, Amson R, Tuijnder M;  
XX WPI; 2003-333167/31.  
XX New isolated nucleic acid, useful for treating viral diseases associated  
XX with tumors and cell degeneration, also related polypeptides, antibodies  
XX and transfected cells.

XX Disclosure; Page 330; 738pp; French.  
 PS The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68806), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC65317 (1-17)  
 QY 43 SerLeuAspPheGly 47  
 Db 3 TCCTGGACTTGGT 17

RESULT 102  
 ACC67174  
 ID ACC67174 standard; DNA; 17 BP.  
 XX  
 AC ACC67174;  
 XX  
 DT 01-JUL-2003 (first entry)  
 XX  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 4421.  
 XX  
 KW Cytostatic; virucide; neuroprotective; notropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003025176-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004210.  
 XX  
 PR 17-SEP-2001; 2001PR-00011979.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-333167/31.  
 XX  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 PT  
 PS Disclosure; Page 547; 738pp; French.  
 XX  
 CC The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68806), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
 SQ

CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX Sequence 17 BP; 1 A; 8 C; 2 G; 6 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC67174 (1-17)  
 QY 179 IleLeuLeuProLeu 183  
 Db 2 ATCTCTCTCTCTCTG 16

RESULT 103  
 ACC64429  
 ID ACC64429 standard; DNA; 17 BP.  
 XX  
 AC ACC64429;  
 XX  
 DT 01-JUL-2003 (first entry)  
 XX  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1676.  
 XX  
 KW Cytostatic; virucide; neuroprotective; notropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003025176-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004210.  
 XX  
 PR 17-SEP-2001; 2001PR-00011979.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-333167/31.  
 XX  
 XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 PT  
 PS Disclosure; Page 227; 738pp; French.  
 XX  
 CC The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68806), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17

Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC64429 (1-17)

QY 179 IleLeuLeuProLeu 183  
 DB 2 ATCCTTGGCACTG 16

RESULT 104

ACC68311  
 ID ACC68311 standard; DNA; 17 BP.

XX  
 AC ACC68311;

DT 01-JUL-2003 (first entry)

DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5558.

XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizophrenia; ss.

OS Mus musculus.

PN WO2003025176-A2.

PD 27-MAR-2003.

PF 17-SEP-2002; 2002WO-IB004210.

PR 17-SEP-2001; 2001PR-00011979.

XX (MOLE-) MOLECULAR ENGINES LAB.

PI Telerman A, Amson R, Tuijnder M;

DR WPI; 2003-333167/31.

XX New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.

XX Disclosure; Page 680; 738pp; French.

XX The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68806), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration.  
 CC Specifically cancer but also Alzheimer's disease and schizophrenia

XX Sequence 17 BP; 1 A; 7 C; 2 G; 7 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC68311 (1-17)

QY 179 IleLeuLeuProLeu 183

Db 2 ATCCTTGGCACTT 16

RESULT 105

ADA15891/C

ID ADA15891 standard; DNA; 17 BP.

XX ADA15891;

DT 20-NOV-2003 (first entry)

XX Primer for amplification of GAPDH DNA #SEQ ID 70.

XX Human; beta-actin; GAPDH; loop-mediated isothermal amplification; LAMP;  
 KW glyceraldehyde-3-phosphate dehydrogenase; cancer; metastasis;  
 KW genetic engineering; PCR; primer; ss.

OS Homo sapiens.

PN WO2003070935-A1.

PD 28-AUG-2003.

PF 13-FEB-2003; 2003WO-JP001474.

PR 20-FEB-2002; 2002JP-00043866.

PR 20-FEB-2002; 2002JP-00043867.

XX (SYSM-) SYSMEX CORP.

XX Tada S;

XX WPI; 2003-679880/64.

XX Primers for nucleic acid amplification in detecting housekeeping gene  
 PT mRNAs to confirm amplification of beta-actin and glyceraldehyde-3-  
 PT phosphate dehydrogenase useful in diagnosis of cancer.

XX Claim 5; Page 25; 90pp; Japanese.

XX The invention relates to primers for nucleic acid amplification for  
 CC detecting a housekeeping gene and/or a housekeeping gene-related mRNA by  
 CC the loop-mediated isothermal amplification (LAMP) method. Particularly  
 CC referred to are primers for the amplification of beta-actin or GAPDH. The  
 CC primers of the invention are for nucleic acid amplification in detecting  
 CC housekeeping gene mRNAs, e.g. to confirm amplification of beta-actin and  
 CC glyceraldehyde-3-phosphate dehydrogenase (GAPDH), which are useful in  
 CC diagnosis of cancer and metastasis. By applying such primers, the  
 CC amplification of beta-actin and GAPDH can be used to confirm the presence  
 CC or absence of a tumour marker, e.g. cytokeratin, which can be used in the  
 CC control of data correction in the LAMP method, particularly in genetic  
 CC engineering, molecular biology and clinical medicine including disease  
 CC diagnosis. Using this method, diagnosis is fast (within 15 minutes) and  
 CC highly reliable. The required primers were designed based upon the gene  
 CC domain of e.g. beta-actin. After reaction by the reverse transcriptase-  
 CC loop-mediated isothermal amplification (RT-LAMP) method, the  
 CC amplification product was detected to confirm amplification of beta-actin  
 CC in the samples. The current sequence represents a primer for the  
 CC amplification of human GAPDH.

XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.13e+03 Length: 17  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x ADA15891 (1-17)

QY 82 ThrSerTrpSerPro 86

```
Db      15  ACCTCGTGGAGTCCA 1
RESULT 106
ADB42925
ID      ADB42925 standard; DNA; 17 BP.
XX
AC      ADB42925;
XX
DT      18-DEC-2003 (revised)
DT      04-DEC-2003 (first entry)
XX
DE      Tumour suppression/reversion associated nucleotide #3248.
XX
XX      cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW      primer; probe; tumour suppression; tumour reversion; apoptosis;
KW      virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW      diagnosis.
XX
OS      Homo sapiens.
XX
EN      WO2003040369-A2.
XX
XX      15-MAY-2003.
XX
PF      17-SEP-2002; 2002WO-IB004219.
XX
PR      17-SEP-2001; 2001FR-00011981.
XX
PA      (MOLE-) MOLECULAR ENGINES LAB.
XX
PI      Telerman A, Amson R, Tuijnder M;
XX
DR      WPI; 2003-441574/41.
XX
PT      New nucleic acid encoding human prostate membrane-specific antigen,
PT      useful e.g. for treatment of tumors and viral infection, also related
PT      polypeptide and antibodies.
XX
PS      Disclosure; Page 411; 771pp; French.
XX
XX      The invention relates to the isolation of 6327 nucleotide sequences,
XX      fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX      sequence having at least 80% identity, after optimal alignment with the
XX      nucleotides, a sequence that hybridizes under stringent conditions with
XX      the nucleotides, or the complement, or corresponding RNA, of the
XX      nucleotides. The nucleotides are used as probes or primers for detecting,
XX      identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX      sense and antisense sequences, of nucleotides involved in tumour
XX      suppression or reversion, apoptosis and or viral resistance, to produce
XX      recombinant polypeptides, and to prepare transgenic animals, as
XX      experimental models. The nucleotides (also vectors containing them and
XX      cells containing the vectors), the encoded polypeptides and antibodies
XX      (Ab) against the polypeptide are useful for prevention and/or treatment
XX      of viral infections or diseases characterized by development of tumours
XX      or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX      Analysis of the expression of the nucleotides can be used for diagnosis
XX      and/or prognosis of these diseases. The nucleotides and polypeptides can
XX      also be used to screen for their specific interactive molecules,
XX      potentially useful for treating diseases associated with abnormal
XX      expression of the nucleotides.
XX
SQ      Sequence 17 BP; 1 A; 8 C; 3 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8.13e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Conservatives: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      2.53%      Indels:      0
DB:              9          Gaps:      0

us-09-966-880a-8 (1-198) x ADB42925 (1-17)
```

```
Oy      179 IleleulenProJen 183
Db      2  ATCCTCTGCTCTG 16
RESULT 107
ADB43664
ID      ADB43664 standard; DNA; 17 BP.
XX
AC      ADB43664;
XX
DT      18-DEC-2003 (revised)
DT      04-DEC-2003 (first entry)
XX
DE      Tumour suppression/reversion associated nucleotide #3987.
XX
XX      cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
KW      primer; probe; tumour suppression; tumour reversion; apoptosis;
KW      virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW      diagnosis.
XX
OS      Homo sapiens.
XX
EN      WO2003040369-A2.
XX
XX      15-MAY-2003.
XX
PF      17-SEP-2002; 2002WO-IB004219.
XX
PR      17-SEP-2001; 2001FR-00011981.
XX
PA      (MOLE-) MOLECULAR ENGINES LAB.
XX
PI      Telerman A, Amson R, Tuijnder M;
XX
DR      WPI; 2003-441574/41.
XX
PT      New nucleic acid encoding human prostate membrane-specific antigen,
PT      useful e.g. for treatment of tumors and viral infection, also related
PT      polypeptide and antibodies.
XX
PS      Disclosure; Page 498; 771pp; French.
XX
XX      The invention relates to the isolation of 6327 nucleotide sequences,
XX      fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX      sequence having at least 80% identity, after optimal alignment with the
XX      nucleotides, a sequence that hybridizes under stringent conditions with
XX      the nucleotides, or the complement, or corresponding RNA, of the
XX      nucleotides. The nucleotides are used as probes or primers for detecting,
XX      identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX      sense and antisense sequences, of nucleotides involved in tumour
XX      suppression or reversion, apoptosis and or viral resistance, to produce
XX      recombinant polypeptides, and to prepare transgenic animals, as
XX      experimental models. The nucleotides (also vectors containing them and
XX      cells containing the vectors), the encoded polypeptides and antibodies
XX      (Ab) against the polypeptide are useful for prevention and/or treatment
XX      of viral infections or diseases characterized by development and/or treatment
XX      or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX      Analysis of the expression of the nucleotides can be used for diagnosis
XX      and/or prognosis of these diseases. The nucleotides and polypeptides can
XX      also be used to screen for their specific interactive molecules,
XX      potentially useful for treating diseases associated with abnormal
XX      expression of the nucleotides.
XX
SQ      Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8.13e+03      Length:      17
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Conservatives: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      2.53%      Indels:      0
DB:              9          Gaps:      0
```

```

US-09-966-880A-8 (1-198) x ADB43664 (1-17)
QY 179 TleLeuLeuProLeu 183
Db 2 ATCTTGTCCTTG 16

RESULT 108
ADB39967/C
ID ADB39967 standard; DNA; 17 BP.
XX AC ADB39967;
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX Tumour suppression/reversion associated nucleotide #290.
DE XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX Homo sapiens.
XX WO2003040369-A2.
XX 15-MAY-2003.
XX 17-SEP-2002; 2002WO-IB004219.
XX 17-SEP-2001; 2001FR-00011981.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX Disclosure; Page 66; 771pp; French.
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
SQ Sequence 17 BP; 7 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00% Mismatches: 0

```

```

Query Match: 2.53% Indels: 0
DB: 9 Gaps: 0
US-09-966-880A-8 (1-198) x ADB39967 (1-17)
QY 46 PheGlyTYrLeuArg 50
Db 17 TTGGATATCTCAGA 3

RESULT 109
ADB43195
ID ADB43195 standard; DNA; 17 BP.
XX AC ADB43195;
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX Tumour suppression/reversion associated nucleotide #3518.
DE XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX Homo sapiens.
XX WO2003040369-A2.
XX 15-MAY-2003.
XX 17-SEP-2002; 2002WO-IB004219.
XX 17-SEP-2001; 2001FR-00011981.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX Disclosure; Page 443; 771pp; French.
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.13e+03 Length: 17
Score: 5.00 Matches: 5

```





Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x AAN60649 (1-18)

QY 32 ValVallyeArgArg 36  
 DB 2 GTTGTAAACGACGG 16

RESULT 114

AAQ58760  
 ID AAQ58760 standard; DNA; 18 BP.

XX AC AAQ58760;

XX 25-MAR-2003 (revised)

DT 03-OCT-1994 (first entry)

XX Glucagon receptor primer ZC976.

DE XX Rat; human; glucagon receptor; transgenic animal; metabolism; model;  
 KW secretin; amplification; primer; polymerase chain reaction; PCR; ss.  
 KW Synthetic.

OS WO9405789-A1.

XX 17-MAR-1994.

XX 30-AUG-1993; 93WO-US008174.

XX 28-AUG-1992; 92US-00938331.

PR 01-JUL-1993; 93US-00086631.

XX (ZYMO) ZYMOGENETICS INC.

XX Kindsvogle WR, Jelinek LJ, Sheppard PO, Grant FJ, Kuitjer JL;

PI Foster DC, Lok S, Ohara PJ;

XX WPI; 1994-101194/12.

XX New recombinant glucagon receptors and antibodies - useful to produce  
 model transgenic animals for study and with therapeutic applications.

PS Example 4; Page 71; 112pp; English.

XX Rat and human glucagon receptor (GR) DNA was isolated. Primers for DNA  
 amplification are ZC4715 and ZC4701 (rat and human; corresp. to regions  
 of high conservation among the members of the secretin gene family); and  
 ZC4758 and ZC4778 (human). To screen transformants for a human GR  
 sequence, the insert DNA present in each transformant was amplified using  
 oligonucleotides ZC447 and ZC976, which were designed as universal pUC  
 sequencing primers and primed to pUC sequences flanking the PCR product  
 insert. One clone, G30, was shown to hybridise with the full length rat  
 cDNA probe. The nucleotide sequence of G30 is shown in AAQ67246. Host  
 cells contg. GR DNA may be used for the prodn. of recombinant GR. GR DNA  
 may also be expressed in non-human transgenic animals, pref. mice. Such  
 animals may be readily used as models to study the role of the glucagon  
 receptor in metabolism. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ58760 (1-18)

QY 32 ValVallyeArgArg 36  
 DB 2 GTTGTAAACGACGG 16

RESULT 115

AAQ65771  
 ID AAQ65771 standard; DNA; 18 BP.

XX AC AAQ65771;

XX 25-MAR-2003 (revised)

DT 19-DEC-1994 (first entry)

XX Type II procollagen sequencing primer CW-5.

XX Type II procollagen; COL2A1; amplification; primer;  
 KW polymerase chain reaction; PCR; osteoarthritis; cartilage; ss.  
 KW Synthetic.

OS WO9411532-A1.

XX 26-MAY-1994.

XX 12-NOV-1993; 93WO-US010964.

XX 13-NOV-1992; 92US-00977284.

XX (UYJE-) UNIV JEFFERSON THOMAS.

XX Prockop DJ, Ala-Kokko L, Williams CJ, Ritvaniemi P, Baldwin C;

PI Hopkinson I, Ahmad NN;

XX WPI; 1994-183530/22.

XX Detecting genetic pre-disposition to osteoarthritis - and other diseases  
 involving mutation in cartilage protein genes, by amplification and  
 analysis of DNA and comparison with standards.  
 Claim 18; Page 22; 112pp; English.

XX Claim 18 claims primers for use in detecting mutations in a mammalian  
 gene for a structural protein of cartilage comprising a sequence  
 identified in Table I (Page 18-31). Table I includes 179 primer sequences  
 (see AAQ65728-Q65906). The following details are given for primer CW-5:  
 CC Region/exon: 18 Direction: sense Primer position: 8351 (Updated on 25-MAR  
 CC -2003 to correct PN field.)

XX Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ65771 (1-18)

QY 69 AspLeuAspProGly 73

DB 3 GATCTGGATCTGGA 17

RESULT 116

AAQ72647/c  
 ID AAQ72647 standard; DNA; 18 BP.

XX AC AAQ72647;



XX 25-MAR-2003 (revised)  
DT 22-MAY-1995 (first entry)  
XX  
DE Probe 12, anneals to bases 189-206 of exon 2 of HLA-B\*4601.  
XX  
XX Polymerase chain reaction; PCR; primer; amplify; detection; HLA-B;  
KW human leukocyte antigen; B2P; allele; exon 2; B52(22); B52(5); B7801;  
KW B2(15); B75(15); B71(70); B46; B79; B53; B5102; B5103; B56(17);  
KW compatibility; donor; recipient; organ transplant; success-rate;  
KW bone-marrow transplant; disease susceptibility study; probe;  
KW forensic investigation; ss.  
XX  
XX Synthetic.  
XX  
XX WO9421818-A1.  
XX  
XX 29-SEP-1994.  
XX  
XX 07-MAR-1994; 94WO-EP000654.  
XX  
XX 18-MAR-1993; 93EP-00400700.  
XX  
XX (INNO-) INNOGENETICS NV SA.  
XX  
XX Andrien M, Dupont E, Rossau R, De Canck I;  
XX WPI; 1994-317037/39.  
XX  
XX DNA typing using primers and probes enabling discrimination of HLA-B  
PT alleles - esp. where difficult to discriminate by serological means.  
XX  
XX Claim 7; Page 39; 66pp; English.  
XX  
XX The sequences given in AAQ72636-55 are probes which were used to  
CC discriminate HLA-B alleles which are characterised by having the sequence  
CC 5'-GCCA-3' at position 30-33 of exon 2 of the HLA-B allele. Variants of  
CC these sequences which may also be used are given in AAQ72656- 81. These  
CC probes are used to identify the amplification products of the primers  
CC given in AAQ72630-35. These primers may be used to distinguish between  
CC HLA-B types which are serologically difficult to discriminate, eg.  
CC B54(22), B52(5), B7801, B62(15), B75(15), B71(70), B46, B79, B53, B5102,  
CC B5103 and B58(17). Using this method, HLA-B compatibility between donors  
CC and recipients of organ transplants can be increased, thereby having a  
CC beneficial impact on success-rate of organ and bone-marrow transplants.  
CC HLA-B typing may be used to improve or facilitate disease susceptibility  
CC studies and forensic investigations. (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
XX Sequence 18 BP; 8 A; 5 C; 4 G; 1 T; 0 U; 0 Other;

Alignment Scores:  
Pred. NO.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0  
US-09-966-880A-8 (1-198) x AAQ72647 (1-18)

QY 112 ArgLeuTyrPheCys 116  
DB 17 CGCTTGACTTCGT 3  
RESULT 117  
AAT36742  
ID AAT36742 standard; DNA; 18 BP.  
XX  
XX AAT36742;  
AC  
XX 18-APR-1997 (first entry)  
DT  
XX

DE Carnobacterium piscicola piscicolin 126 gene primer #1.  
XX  
XX Bacteriocin; Carnobacterium piscicola; Piscicolin 126; microorganism;  
KW anti-microbial activity; PCR; polymerase chain reaction; amplification;  
KW 16S rRNA gene; primer; probe; genomic library; phage lambda; nicin;  
KW pediocin; food-borne pathogen; spoilage; starter culture; preservation;  
KW beverage; ss.  
XX  
XX Synthetic.  
XX  
XX WO9626216-A1.  
XX  
XX 29-AUG-1996.  
XX  
XX 22-FEB-1996; 96WO-AU0000096.  
XX  
XX 22-FEB-1995; 95AU-00001310.  
XX  
XX (UYME) UNIV MELBOURNE.  
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.  
XX (AUFO-) AUSTRALIAN FOOD IND SCI CENT.  
XX  
XX Wetenhall REH, Davidson BE, Hillier AJ, Harmark K, Jack RW;  
XX Hickey MW, Coventry J, Wan J;  
XX WPI; 1996-402319/40.  
XX  
XX Bacteriocin active against food-borne pathogens and spoilage organisms,  
PT but not against beneficial bacteria - useful as preservative in foods and  
PT beverages and in cheese starter cultures.  
XX  
XX Example 5; Page 6; 25pp; English.  
XX  
XX The invention relates to the isolation of a novel bacteriocin designated  
CC Piscicolin 126 from the microbe Carnobacterium piscicola strain JG126  
CC (WO2211). The parent microorganism was isolated from a ham when a range  
CC of microorganisms were assayed for anti-microbial activity. Primers  
CC T36740-1 were used to identify the strain of microorganism by PCR  
CC amplifying a region of the cell's 16S rRNA gene. The resultant sequence  
CC was identical to a C. piscicola sequence (Genbank accession M5812). The  
CC protein was isolated by conventional chromatography techniques and  
CC subjected to amino acid sequencing. The degenerate primers (T36742-3)  
CC were synthesised based on the amino acid sequence. These were used to  
CC amplify a 107 bp fragment of the gene which was used as a probe to screen  
CC a genomic library in phage lambda. From this screen, a positive clone  
CC containing the piscicolin gene (T36876) was isolated. The new bacteriocin  
CC has a more limited range of activity than nicin or pediocin Pa-1 and is  
CC active against a range of food-borne pathogens or spoilage organisms but  
CC not against beneficial organisms e.g. starter cultures. The bacteriocin  
CC can thus be used to preserve food and beverages  
XX  
XX Sequence 18 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 6 Other;

Alignment Scores:  
Pred. NO.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0  
US-09-966-880A-8 (1-198) x AAT36742 (1-18)

QY 51 AsnLysAsnGlyCys 55  
DB 4 AAYAAAPAYGGTGY 18  
RESULT 118  
AAX64476/c  
ID AAX64476 standard; RNA; 18 BP.  
XX  
XX AAX64476;  
AC  
XX

DT 20-JUL-1999 (first entry)  
 XX Rabbit stromelysin hairpin target sequence SEQ ID NO:1108.  
 DE  
 XX  
 KW Arthritic condition; graft tolerance; immune response; target; cleavage;  
 KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;  
 KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;  
 KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;  
 KW diagnosis; ss.  
 XX  
 XX Oryctolagus cuniculus.  
 OS  
 XX  
 XX WO9618736-A2.  
 PN  
 XX  
 XX 20-JUN-1996.  
 PD  
 XX  
 XX 22-NOV-1995; 95WO-US015516.  
 PF  
 XX  
 XX 13-DEC-1994; 94US-00354920.  
 PR  
 XX 23-DEC-1994; 94US-00363253.  
 PR  
 XX 23-DEC-1994; 94US-00363254.  
 PR  
 XX 17-FEB-1995; 95US-00390850.  
 PR  
 XX 20-APR-1995; 95US-00426124.  
 PR  
 XX 02-MAY-1995; 95US-00432874.  
 PR  
 XX 04-MAY-1995; 95US-00434509.  
 PR  
 XX 07-JUL-1995; 95US-0000951P.  
 PR  
 XX 07-JUL-1995; 95US-0000974P.  
 PR  
 XX 07-AUG-1995; 95US-00512861.  
 PR  
 XX 05-OCT-1995; 95US-00541365.  
 PR  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA  
 XX Beigelman L, Stinchcomb DT, Jarvis T, Draper K, Pavco P;  
 PI Mesigian J, Gustofson J, Usman N, Wincott F, Matulic-Adamic J;  
 PI Karpelsky A, Thompson JD, Modak A, Burgin A;  
 PI  
 XX WPI; 1996-300653/30.  
 DR  
 XX  
 XX Enzymatic nucleic acid molecules having a hammer-head motif - used for  
 PT the treatment of arthritis, induction of graft tolerance or treatment of  
 PT auto-immune diseases.  
 PT  
 XX  
 XX Example 1; Page 165; 307pp; English.  
 PS  
 XX  
 CC The present invention describes a novel enzymatic nucleic acid (ENA)  
 CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose residues  
 CC ; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii) at least  
 CC ten 2'-O-methyl modifications; and (iv) a 3'-end modification. The ENA's  
 CC can inhibit collagenase and stromelysin production in the synovial  
 CC membrane of joints for the treatment or prevention of arthritis,  
 CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also  
 CC be used to treat antigen presenting cells of a donor to induce tolerance  
 CC in a recipient to an alloantigen of a donor. They can also be used for  
 CC enhancing graft tolerance or for treating autoimmune disease, and for  
 CC treating allergies and other inflammatory conditions. The ENA's can also  
 CC be used in diagnosis. Ribozyme therapy impacts on the expression of  
 CC stromelysin without introducing the non-specific effects upon gene  
 CC expression which accompany treatment with retinoids and dexamethasone.  
 CC The concentration of ribozyme required to affect a therapeutic treatment  
 CC is lower than that required of antisense molecules, and is highly  
 CC specific. The present sequence is used in the exemplification of the  
 CC present invention  
 CC  
 XX Sequence 18 BP; 2 A; 7 C; 3 G; 0 T; 6 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAY64476 (1-18)  
 QY 119 ArgLysalaGluPro 123  
 Db 15 AGAAGGCGGACCG 1  
 RESULT 119  
 AAT76355  
 ID AAT76355 standard; DNA; 18 BP.  
 XX  
 XX AC AAT76355;  
 XX  
 XX 15-SEP-1997 (first entry)  
 DT  
 XX Human fibronectin antisense oligonucleotide HUMFNA/HSFIB1AS23.  
 DE  
 XX Asthma; airway epithelium; adenosine free; cystic fibrosis;  
 KW chronic obstructive pulmonary disease; bronchitis; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9640162-A1.  
 PN  
 XX 19-DEC-1996.  
 PD  
 XX 06-JUN-1996; 96WO-US009306.  
 PF  
 XX 07-JUN-1995; 95US-00474497.  
 PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA  
 XX  
 XX Nyce JW, Metzger WJ;  
 PI  
 XX WPI; 1997-051871/05.  
 DR  
 XX Treatment of airway diseases such as asthma - by topically applying  
 PT adenosine-free antisense oligo:nucleotide to airway epithelium of  
 PT subject.  
 PT  
 XX Claim 5; Page 36; 71pp; English.  
 PS  
 XX A method for treating airway disease in a subject has been produced,  
 CC which involves the topical administration of an essentially adenosine  
 CC free antisense oligonucleotide (ON) to the airway epithelium of the  
 CC subject. The present sequence is an antisense oligonucleotide  
 CC HUMFNA/HSFIB1AS23 specific for the human fibronectin. The method can be  
 CC used to treat airway diseases such as cystic fibrosis, asthma, chronic  
 CC obstructive pulmonary disease, bronchitis and other airway diseases  
 CC characterised by an inflammatory response. By eliminating adenosine from  
 CC the antisense ON, its liberation upon antisense degradation is prevented,  
 CC thereby preventing adenosine- induced bronchoconstriction in patients  
 CC with hyper-reactive airways  
 CC  
 XX Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT76355 (1-18)  
 QY 59 LeuLeuPheLeuArg 63  
 Db 4 CTCCTGTTCCTCCGT 18  
 RESULT 120  
 AAV59406  
 ID AAV59406 standard; DNA; 18 BP.  
 XX

AC AAV59406;  
XX  
XX DT 21-JAN-1999 (first entry)  
XX DE  
XX PCR primer ZC976 used to amplify a zsig32 DNA fragment.  
XX  
XX Secreted salivary polypeptide; zsig32; salivary gland; human;  
KW mucous associated; digestive dysfunction; wound healing dysfunction;  
KW salivary gland carcinoma; sarcoidosis; pneumocystic carinii; PCR primer;  
KW emphysema; chronic bronchitis; cystic fibrosis; tumour; xerostomia;  
KW adult respiratory distress syndrome; ARDS; dental caries; osteomyelitis;  
KW sudden infant death syndrome; SIDS; oral candidiasis; prostate carcinoma;  
KW migraine; buccal mucosa infection; Sjogren's syndrome; mumps; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX WO9841628-A1.  
FN  
XX  
XX 24-SEP-1998.  
PD  
XX  
XX 18-MAR-1998; 98WO-US005255.  
PF  
XX  
XX 19-MAR-1997; 97US-0041263P.  
PR  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX Sheppard PO;  
PI  
XX WPI; 1998-531567/45.  
DR  
XX New isolated mucous-associated polypeptide, zsig32 - used to develop  
PT products for treating e.g. digestive or lung dysfunction, microbial  
PT infections, cystic fibrosis, inflammation or tumour metastasis.  
XX  
XX Example 8; Page 100; 118pp; English.  
PS  
XX PCR primers AAV59406-07 were used to amplify fragments of DNA encoding a  
CC secreted salivary polypeptide designated zsig32. The protein is involved  
CC in salivary gland and mucous associated functions. The products can be  
CC used in the treatment of e.g. digestive dysfunction, wound healing  
CC dysfunction, inadequate saliva production or composition, mucosal  
CC integrity breakdown, failure or diminished anti-microbial function.  
CC salivary gland carcinoma, sarcoidosis, pneumocystic carinii (particularly  
CC as associated with AIDS patients), emphysema, chronic bronchitis, cystic  
CC fibrosis, adult respiratory distress syndrome (ARDS), sudden infant death  
CC syndrome (SIDS), lung diseases, tumour metastasis, xerostomia, dental  
CC caries, osteomyelitis, oral candidiasis, buccal mucosa infections,  
CC chronic inflammation (Sjogren's syndrome), mumps, prostate carcinoma or  
CC migraine  
XX  
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV59406 (1-18)

QY 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16

RESULT 121  
AAV59324  
ID AAV59324 standard; cDNA; 18 BP.  
XX  
XX AAV59324;  
AC  
XX

DT 21-DEC-1998 (first entry)  
XX  
XX zsig10 primer ZC976.  
DE  
XX ss; human; mucous-mediated function; adhesion; tumour metastasis;  
KW bacterial colonisation; microbial infection; AIDS; cystic fibrosis;  
KW chronic obstructive pulmonary disease; asthma; Crohn's disease;  
KW sinonasal inflammatory disease; inflammatory bowel disease; bronchitis;  
KW PCR; primer; amplification.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX WO9841627-A1.  
FN  
XX  
XX 24-SEP-1998.  
PD  
XX  
XX 18-MAR-1998; 98WO-US005251.  
PF  
XX  
XX 19-MAR-1997; 97US-0039631P.  
PR  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX Sheppard PO;  
PI  
XX WPI; 1998-531566/45.  
DR  
XX New isolated mucous-associated polypeptide, zsig10 - used to develop  
PT products for treating e.g. tumour metastasis, microbial infections,  
PT cystic fibrosis, asthma, bronchitis or inflammatory bowel disease.  
XX  
XX Example 1; Page 85; 109pp; English.  
PS  
XX The primer AAV59321-V59327 were used in the production of a human  
CC polypeptide zsig10. zsig10 is involved in mucous-mediated functions such  
CC as adhesion. The products of the invention can be used in the study and  
CC treatment of e.g. tumour metastasis, bacterial colonisation,  
CC susceptibility to and persistence of infection, microbial infections,  
CC AIDS, cystic fibrosis, chronic obstructive pulmonary disease, asthma,  
CC sinonasal inflammatory disease, inflammatory bowel disease, bronchitis,  
CC or Crohn's disease. The products can also be used for detection,  
CC diagnosis and drug screening  
XX  
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
SQ

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV59324 (1-18)

QY 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16

RESULT 122  
AAV45453  
ID AAV45453 standard; cDNA; 18 BP.  
XX  
XX AAV45453;  
AC  
XX  
XX 02-FEB-1999 (first entry)  
DT  
XX Human chemokine ZSIG-35 PCR primer ZC976.  
DE  
XX ZSIG-35; beta-chemokine; human; ligand; lymphocyte migration;  
KW inflammation; ischaemia; reperfusion injury; baculovirus; vector;  
KW PFSGE35; PCR; primer; ss.  
XX

```

OS Synthetic.
XX Homo sapiens.
XX WO9844117-A1.
XX PD 08-OCT-1998.
XX XX
XX PF 27-MAR-1998; 98WO-US006115.
XX PR 28-MAR-1997; 97US-0042862P.
XX PR 09-MAY-1997; 97US-0046083P.
XX XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX XX
XX PI Sheppard PO;
XX DR WPI; 1998-557114/47.
XX XX
XX PT New human chemokine ZSIG-35 - used for, e.g. treating inflammatory
XX PT disease, lymphocyte migration and ischaemia/reperfusion injury.
XX XX
XX PS Example 7; Page 90; 105pp; English.
XX XX
XX CC Primer ZC976 and primer ZC447 (see AAV45454) were used in PCR
XX CC amplification of bacmid DNA isolated from DH5-alpha cells following
XX CC transformation with a baculovirus vector carrying human beta-chemokine
XX CC ZSIG-35 DNA (see also AAV45444). PCR was performed to screen for the
XX CC correct insert in positive colonies. Those having the correct insert were
XX CC used to transfect Spodoptera frugiperda Sf9 cells for production of
XX CC recombinant ZSIG35 polypeptides (see AAV30565). Novel ZSIG-35
XX CC polypeptides of the invention can be used in therapeutic compositions for
XX CC the regulation of acute and chronic inflammatory disease conditions,
XX CC lymphocyte migration and ischaemia/reperfusion injury
XX XX
XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV45453 (1-18)
QY 32 ValVallysArgArg 36
DB 2 GTTGTAAACGACGG 16

RESULT 123
AAV32961
XX ID AAV32961 standard; cDNA; 18 BP.
XX AC AAV32961;
XX XX
XX DT 26-OCT-1998 (first entry)
XX DE Human ZPPAR6 nuclear hormone receptor cDNA primer ZC976.
XX KW Human ZPPAR6 nuclear hormone receptor; ZPPAR6 NHR; transcription;
XX KW cell differentiation, cell proliferation; embryogenesis; cancer; PCR;
XX KW primer; amplification; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9831797-A1.
XX XX
XX PD 23-JUL-1998.
XX PF 15-JAN-1998; 98WO-US0000678.
XX XX

15-JAN-1997; 97US-0033762P.
(ZYMO ) ZYMOGENETICS INC.
Holloway JL;
WPI; 1998-414097/35.
Nuclear hormone receptor, ZPPAR6 - useful for developing products for
modulating transcription of target genes, cellular differentiation and
proliferation.
Example 1; Page 51; 58pp; English.
Primers ZC976 and ZC447 (AAV32962) were used to amplify the human ZPPAR6
nuclear hormone receptor (ZPPAR6 NHR) cDNA fragment (AAV32960) from an
EST present within a human brain cDNA library clone. The invention claims
for the ZPPAR6 NHR protein (AAW49094) which can be used to identify
compounds that modulate its activity. These compounds may be useful as
therapeutic agents for modulating transcription of target genes, for e.g.
agonists for such receptors are claimed to be useful for influencing
transcription, cellular differentiation, and/or proliferation during
development, in particular during embryogenesis while antagonists are
claimed to be useful for out-competing endogenous human ZPPAR6 ligands
and exert control over the receptor. Antagonists are also claimed to be
useful as research reagents for characterising sites of ligand receptor
interaction. The ZPPAR6 cDNA and protein are also claimed to be useful in
detection and diagnosis e.g. elevated or depressed levels of ligand or
receptor may be indicative of pathological conditions, including cancers
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV32961 (1-18)
QY 32 ValVallysArgArg 36
DB 2 GTTGTAAACGACGG 16

RESULT 124
AAV32155
XX ID AAV32155 standard; DNA; 18 BP.
XX AC AAV32155;
XX XX
XX DT 23-APR-1999 (first entry)
XX DE Human IVS17 3'-acceptor splice site PCR primer #3.
XX KW IVS17 acceptor splice site; PCR primer; detection; base-pair mutation;
XX KW heteroduplex; homoduplex; migration; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN US5874212-A.
XX XX
XX PD 23-FEB-1999.
XX PF 06-JUN-1995; 95US-00468551.
XX PR 13-MAY-1993; 93US-00061574.
XX XX
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX XX
XX PI Ganguly A, Rock MJ, Prockop DJ;

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XX WPI; 1999-179967/15.  
 XX Detection of nucleic acid mutations - by electrophoresis in  
 XX polyacrylamide gel that distinguishes heteroduplexes from homoduplexes.  
 PT Disclosure; Col 5; 16pp; English.  
 XX  
 XX AAX02153-X02161 are primers used in a method for detecting one or more  
 CC base-pair mutations in a nucleic acid sequence by differentiating  
 CC heteroduplexes from homoduplexes. The method involves generating  
 CC heteroduplexes and heteroduplexes in a sample and performing gel  
 CC electrophoresis on the sample using a polyacrylamide gel that causes  
 CC heteroduplexes to migrate more slowly than homoduplexes. The gel  
 CC comprises 3-20% polyacrylamide, 1-50% of at least one denaturing agent  
 CC selected from aliphatic alcohols, cyclic alcohols, alicyclic compounds,  
 CC amides, ureas and carbamates, 10-100 mM borate-free TE [Tris-HCl, EDTA]  
 CC buffer, and 10-100 mM taurine. The method has a high reliability and can  
 CC be improved by allowing for the presence of the mutations in domains with  
 CC high melting temperatures. These primers can specifically detect a  
 CC mutation in the human IVS17 3'-acceptor splice site  
 XX  
 SQ Sequence 18 BP; 3 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAX02155 (1-18)  
 QY 69 AspLeuAspProGly 73  
 DB 3 GATCTGAGCTCTGGA 17  
 RESULT 125  
 AAZ41011  
 ID AAZ41011 standard; DNA; 18 BP.  
 XX  
 AC AAZ41011;  
 XX  
 DT 26-JAN-2000 (first entry)  
 XX  
 DE Cellular inhibitor of apoptosis-2 phosphorothioate antisense oligo #3.  
 XX  
 XX Identification; genetic target; gene modulation; human; probe;  
 KW antisense oligonucleotide; phosphorothioate; PCR primer;  
 KW nucleotide sequence-based technology; antisense drug discovery;  
 KW target validation; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9953101-A1.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 13-APR-1999; 99WO-US008268.  
 XX  
 PR 13-APR-1998; 98US-0081483P.  
 PR 28-APR-1998; 98US-00067638.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 PI Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;  
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;  
 XX  
 DR WPI; 1999-620446/53.  
 XX  
 XX Identifying compounds which modulate expression of nucleic acids, used to

PT provide compounds having defined physical, chemical or bioactive  
 XX properties, e.g. antisense activity.  
 XX  
 PS Example 21; Page 100; 264pp; English.  
 XX  
 CC A method has been developed of defining a set of compounds that modulate  
 CC the expression of a target nucleic acid (tNA) sequence via binding of the  
 CC compounds with the tNA sequence. The method comprises generating a  
 CC library of virtual compounds in silico according to defined criteria, and  
 CC evaluating in silico the binding of the virtual compounds with the tNA  
 CC according to defined criteria. Also described are: (1) a method of  
 CC defining a set of oligonucleotides (ONs) that modulate the expression of  
 CC a tNA sequence via binding of the ONs with the tNA sequence comprising  
 CC generating a library of virtual compounds in silico according to defined  
 CC criteria, and evaluating in silico the binding of the virtual ONs with  
 CC the tNA according to defined criteria; and (2) a method of defining a set  
 CC of compounds that modulate the expression of a tNA sequence via binding  
 CC of the compounds with the tNA. The methods can be used for the generation  
 CC and identification of synthetic compounds having defined physical,  
 CC chemical or bioactive properties. Information gathered from assays of  
 CC such compounds is used to identify nucleic acid sequences that are  
 CC tractable to a variety of nucleotide sequence-based technologies, e.g.  
 CC antisense drug discovery and target validation. AAZ40852 to AAZ41220, and  
 CC AAY52701 to AAY52706, represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 18 BP; 4 A; 3 C; 2 G; 9 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAZ41011 (1-18)  
 QY 59 LeuLeuPheLeuArg 63  
 DB 4 CTTTATTCTTAGA 18  
 RESULT 126  
 AAZ41043  
 ID AAZ41043 standard; DNA; 18 BP.  
 XX  
 AC AAZ41043;  
 XX  
 DT 26-JAN-2000 (first entry)  
 XX  
 DE Cellular inhibitor of apoptosis-2 phosphorothioate antisense oligo #35.  
 XX  
 XX Identification; genetic target; gene modulation; human; probe;  
 KW antisense oligonucleotide; phosphorothioate; PCR primer;  
 KW nucleotide sequence-based technology; antisense drug discovery;  
 KW target validation; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9953101-A1.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 13-APR-1999; 99WO-US008268.  
 XX  
 PR 13-APR-1998; 98US-0081483P.  
 PR 28-APR-1998; 98US-00067638.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 PI Cowsert LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;  
 PI Ohasi C, Wyatt JR, Borchers AH, Vickers TA;

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XX DR WPI; 1999-620446/53.
XX PT Identifying compounds which modulate expression of nucleic acids, used to
XX PT provide compounds having defined physical, chemical or bioactive
XX PT properties, e.g. antisense activity.
XX PS Example 21; Page 101; 264pp; English.
XX CC A method has been developed of defining a set of compounds that modulate
XX CC the expression of a target nucleic acid (tNA) sequence via binding of the
XX CC compounds with the tNA sequence. The method comprises generating a
XX CC library of virtual compounds in silico according to defined criteria, and
XX CC evaluating in silico the binding of the virtual compounds with the tNA
XX CC according to defined criteria. Also described are: (1) a method of
XX CC defining a set of oligonucleotides (ONS) that modulate the expression of
XX CC a tNA sequence via binding of the ONS with the tNA sequence comprising
XX CC generating a library of virtual compounds in silico according to defined
XX CC criteria, and evaluating in silico the binding of the virtual ONS with
XX CC the tNA according to defined criteria; and (2) a method of defining a set
XX CC of compounds that modulate the expression of a tNA sequence via binding
XX CC of the compounds with the tNA. The methods can be used for the generation
XX CC and identification of synthetic compounds having defined physical,
XX CC chemical or bioactive properties. Information gathered from assays of
XX CC such compounds is used to identify nucleic acid sequences that are
XX CC tractable to a variety of nucleotide sequence-based technologies, e.g.
XX CC antisense drug discovery and target validation. AA240852 to AA241220, and
XX CC AA152701 to AA152706, represent sequences used in the exemplification of
XX CC the present invention
XX SQ Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      Length:      18
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     2.53%       Indels:       0
DB:              Gaps:       0

US-09-966-880A-8 (1-198) x AA241043 (1-18)
QY 38 SerAlaThrSerPhe 42
DB 4 AGTGTACTCTCTTTT 18

RESULT 127
AAZ41092/C
ID AAZ41092 standard; DNA; 18 BP.
XX AC AAZ41092;
XX DT 26-JAN-2000 (first entry)
XX DE Human ELK-1 phosphorothioate antisense oligonucleotide SEQ ID NO:244.
XX KW Identification; genetic target; gene modulation; human; probe;
XX KW antisense oligonucleotide; phosphorothioate; PCR primer;
XX KW nucleotide sequence-based technology; antisense drug discovery;
XX KW target validation; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX WO9953101-AL.
XX PN 21-OCT-1999.
XX PD 13-APR-1999; 99WO-US008268.
XX PF 13-APR-1998; 98US-0081483P.
XX PR 28-APR-1998; 98US-00067638.
XX PR

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PA (ISIS-) ISIS PHARM INC.
XX CS Cowsett LM, Baker BF, Mcneil J, Freier SM, Sasmor HM, Brooks DG;
XX PI Chasi C, Wyatt JR, Borchers AH, Vickers TA;
XX DR WPI; 1999-620446/53.
XX PT Identifying compounds which modulate expression of nucleic acids, used to
XX PT provide compounds having defined physical, chemical or bioactive
XX PT properties, e.g. antisense activity.
XX PS Example 24; Page 105; 264pp; English.
XX CC A method has been developed of defining a set of compounds that modulate
XX CC the expression of a target nucleic acid (tNA) sequence via binding of the
XX CC compounds with the tNA sequence. The method comprises generating a
XX CC library of virtual compounds in silico according to defined criteria, and
XX CC evaluating in silico the binding of the virtual compounds with the tNA
XX CC according to defined criteria. Also described are: (1) a method of
XX CC defining a set of oligonucleotides (ONS) that modulate the expression of
XX CC a tNA sequence via binding of the ONS with the tNA sequence comprising
XX CC generating a library of virtual compounds in silico according to defined
XX CC criteria, and evaluating in silico the binding of the virtual ONS with
XX CC the tNA according to defined criteria; and (2) a method of defining a set
XX CC of compounds that modulate the expression of a tNA sequence via binding
XX CC of the compounds with the tNA. The methods can be used for the generation
XX CC and identification of synthetic compounds having defined physical,
XX CC chemical or bioactive properties. Information gathered from assays of
XX CC such compounds is used to identify nucleic acid sequences that are
XX CC tractable to a variety of nucleotide sequence-based technologies, e.g.
XX CC antisense drug discovery and target validation. AA240852 to AA241220, and
XX CC AA152701 to AA152706, represent sequences used in the exemplification of
XX CC the present invention
XX SQ Sequence 18 BP; 5 A; 1 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      Length:      18
Score:          5.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     2.53%       Indels:       0
DB:              Gaps:       0

US-09-966-880A-8 (1-198) x AA241092 (1-18)
QY 103 AenLeuSerLeuArg 107
DB 17 AACCTTTCTCTCAGA 3

RESULT 128
AAZ02856
ID AAZ02856 standard; DNA; 18 BP.
XX AC AAZ02856;
XX DT 14-MAY-1999 (first entry)
XX DE Human zsig46 PCR primer ZC976.
XX KW Secreted protein; zsig46; human; chromosome 13; thyroid; disease;
XX KW hypothyroidism; Graves' disease; thyrotoxicosis; thyroid cancer;
XX KW Hirschprung's disease; neuronal ceroid-lipofucinosi; Wilson disease;
XX KW Reiger syndrome; immunoassay; detection; anti-idiotypic antibody;
XX KW therapy; diagnostic; PCR primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX XX WO9905275-A1.
XX XX 04-FEB-1999.
XX XX

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PF 24-JUL-1998; 98WO-US015431.  
 XX  
 PR 24-JUL-1997; 97US-0053613P.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 PI Sheppard PO, Gilbertson DG;  
 XX  
 DR WPI; 1999-142930/12.  
 XX  
 XX New secreted polypeptide, zsig46, and its fragments, related fusion  
 PT proteins - used for diagnosis and treatment of thyroid disorders or  
 PT diseases involving genes on chromosome 13.  
 XX  
 PS Example 1; Page 92; 101pp; English.  
 XX  
 CC This invention describes the isolation of a novel human secreted protein,  
 CC zsig46 encoded by a gene on chromosome 13 which is mainly expressed in  
 CC the thyroid. This product can be used to study secretion of proteins from  
 CC cells and also to treat or prevent deficient expression of zsig46, which  
 CC may be associated with thyroid diseases (e.g. hypothyroidism, Graves'  
 CC disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that  
 CC involve genes in the same region of chromosome 13 (e.g. Hirschsprung's  
 CC disease, neuronal ceroid-lipofuscinosis, Wilson disease and Reiger  
 CC syndrome). Antibodies and other binding proteins, are used as immunoassay  
 CC reagents to detect zsig46 or cells expressing it, e.g. for assessing  
 CC thyroid function to produce anti-idiotypic antibodies, for affinity  
 CC purification of zsig46, to screen expression libraries, to neutralise  
 CC zsig46 activity, and to deliver toxins, radioisotopes etc. for  
 CC therapeutic or diagnostic purposes. Agonists of the product can be used  
 CC to promote growth, differentiation and proliferation of specific cell  
 CC types, e.g. for treating (extra)thyroid diseases or as additive to cell  
 CC cultures  
 XX  
 SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAX02856 (1-18)  
 QY 32 ValVallyVArgArg 36  
 Db 2 GTTGTAAACGACGG 16  
 RESULT 129  
 AAX54157  
 ID AAX54157 standard; DNA; 18 BP.  
 AC AAX54157;  
 XX  
 XX 05-JUL-1999 (first entry)  
 DE Human fibronectin antisense oligonucleotide fragment.  
 XX  
 KW Antisense oligonucleotide; multiple target; antisense treatment;  
 KW impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;  
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 XX  
 XX Synthetic.  
 OS  
 XX

PN WO9913886-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 17-SEP-1998; 98WO-US019419.  
 XX  
 PR 17-SEP-1997; 97US-0059160P.  
 PR 09-JUN-1998; 98US-00093972.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 XX Nyce JW;  
 XX  
 DR WPI; 1999-229400/19.  
 XX  
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 PT vasoconstriction.  
 PT  
 PS Disclosure; Page 55; 120pp; English.  
 XX  
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
 CC end and the juxta-section between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived  
 CC from sequences AAX55272-74. These multiple target oligonucleotides  
 CC (specifically AAX55180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX  
 SQ Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAX54157 (1-18)  
 QY 59 LeuLeuPheLeuArg 63  
 Db 4 CTCCTGTTTCTCCGT 18  
 RESULT 130  
 AAX22137  
 ID AAX22137 standard; DNA; 18 BP.  
 AC AAX22137;  
 XX  
 XX 26-NOV-1999 (first entry)  
 DE Human c-IAP-2 mRNA inhibiting antisense oligo ISIS #23446.  
 XX  
 KW Cellular Inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;  
 KW c-IAP-2; prophylaxis; infection; inflammation; tumor formation; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX Homo sapiens.  
 XX

PN US958771-A.  
 XX  
 PD 28-SEP-1999.  
 XX  
 PF 03-DEC-1998; 98US-00205144.  
 XX  
 PR 03-DEC-1998; 98US-00205144.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Cowsett LM, Ackermann EJ;  
 XX  
 DR WPI; 1999-561046/47.  
 XX  
 PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2  
 XX useful for e.g. diagnostics, therapeutics, and as research reagents.  
 XX  
 SQ Claim 3; Col 39; 33pp; English.  
 XX  
 CC The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2 (c-IAP-  
 CC 2). The antisense compounds may be used for diagnostics, therapeutics  
 CC (for modulating the expression of c-IAP-2), prophylaxis (e.g. to prevent  
 CC or delay infection, inflammation, or tumor formation), as research  
 CC reagents (e.g. to distinguish between members of a biological pathway)  
 CC and in kits. Sequences AA22103-142 represent phosphorothioate  
 CC oligonucleotides used for antisense inhibition of cellular inhibitor of  
 CC apoptosis-2  
 XX  
 SQ Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AA222137 (1-18)  
 QY 38 SerAlaThrSerPhe 42  
 Db 4 AGTGCTACCTCTTT 18  
 RESULT 131  
 AA222105  
 ID AA222105 standard; DNA; 18 BP.  
 XX  
 AC AA222105;  
 XX  
 DT 26-NOV-1999 (first entry)  
 XX  
 DE Human c-IAP-2 mRNA inhibiting antisense oligo ISIS #23414.  
 XX  
 KW Cellular Inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;  
 KW c-IAP-2; prophylaxis; infection; inflammation; tumor formation; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US958771-A.  
 XX  
 PD 28-SEP-1999.  
 XX  
 PF 03-DEC-1998; 98US-00205144.  
 XX  
 PR 03-DEC-1998; 98US-00205144.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Cowsett LM, Ackermann EJ;  
 XX  
 DR WPI; 1999-561046/47.  
 XX  
 PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2  
 XX useful for e.g. diagnostics, therapeutics, and as research reagents.  
 XX  
 SQ Claim 3; Col 39; 33pp; English.  
 XX  
 CC The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2 (c-IAP-  
 CC 2). The antisense compounds may be used for diagnostics, therapeutics  
 CC (for modulating the expression of c-IAP-2), prophylaxis (e.g. to prevent  
 CC or delay infection, inflammation, or tumor formation), as research  
 CC reagents (e.g. to distinguish between members of a biological pathway)  
 CC and in kits. Sequences AA22103-142 represent phosphorothioate  
 CC oligonucleotides used for antisense inhibition of cellular inhibitor of  
 CC apoptosis-2  
 XX  
 SQ Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AA222137 (1-18)  
 QY 38 SerAlaThrSerPhe 42  
 Db 4 AGTGCTACCTCTTT 18  
 RESULT 131  
 AA222105  
 ID AA222105 standard; DNA; 18 BP.  
 XX  
 AC AA222105;  
 XX  
 DT 26-NOV-1999 (first entry)  
 XX  
 DE Human c-IAP-2 mRNA inhibiting antisense oligo ISIS #23414.  
 XX  
 KW Cellular Inhibitor of Apoptosis-2; antisense; diagnostic; therapeutic;  
 KW c-IAP-2; prophylaxis; infection; inflammation; tumor formation; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US958771-A.  
 XX  
 PD 28-SEP-1999.  
 XX  
 PF 03-DEC-1998; 98US-00205144.  
 XX  
 PR 03-DEC-1998; 98US-00205144.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bennett CF, Cowsett LM, Ackermann EJ;  
 XX  
 DR WPI; 1999-561046/47.  
 XX  
 PT Antisense compounds complementary to Cellular Inhibitor of Apoptosis-2  
 XX useful for e.g. diagnostics, therapeutics, and as research reagents.  
 XX  
 SQ Claim 3; Col 39; 33pp; English.  
 XX  
 CC The invention provides antisense compounds of 8-30 nucleotides that  
 CC inhibit the expression of human Cellular Inhibitor of Apoptosis-2 (c-IAP-  
 CC 2). The antisense compounds may be used for diagnostics, therapeutics  
 CC (for modulating the expression of c-IAP-2), prophylaxis (e.g. to prevent  
 CC or delay infection, inflammation, or tumor formation), as research  
 CC reagents (e.g. to distinguish between members of a biological pathway)  
 CC and in kits. Sequences AA22103-142 represent phosphorothioate  
 CC oligonucleotides used for antisense inhibition of cellular inhibitor of  
 CC apoptosis-2  
 XX  
 SQ Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AA222105 (1-18)  
 QY 59 LeuLeuPheLeuArg 63  
 Db 4 CTTTATTCTTAGA 18  
 RESULT 132  
 AA223878  
 ID AA223878 standard; DNA; 18 BP.  
 XX  
 AC AA223878;  
 XX  
 DT 25-JUN-1999 (first entry)  
 XX  
 DE PCR primer ZC976.  
 XX  
 KW Chromosomal mutagenesis; chromosomal loci; genotype; enzyme production;  
 KW lipase; cellulase; protease; enzyme inhibitor; growth factor; cytokine;  
 KW platelet derived growth factor; fibroblast growth factor; hormone;  
 KW epidermal growth factor; erythropoietin; thrombopoietin; insulin; leptin;  
 KW glucagon; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Pichia methanolica.  
 XX  
 PN WO9914320-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 11-SEP-1998; 98WO-US019448.  
 XX  
 PR 15-SEP-1997; 97US-00929748.  
 PR 30-DEC-1997; 97US-00001141.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 PI Raymond CK;  
 XX  
 DR WPI; 1999-229528/19.  
 XX  
 PT Altering a selected chromosomal locus to produce strains with desired  
 XX genotypes.  
 XX  
 PS Example 4; Page 68; 72pp; English.  
 XX  
 SQ This invention describes a novel method for introducing mutations into



CC chromosomal loci of Pichia methanolica to produce strains having desired  
CC genotypes. P. methanolica strains having altered target loci are useful  
CC as hosts for the expression of heterologous genes. Proteins that can be  
CC produced in P. methanolica included proteins of industrial and  
CC pharmaceutical interest, e.g. enzymes (lipases, cellulases, proteases),  
CC enzyme inhibitors, growth factors such as a platelet derived growth  
CC factor, fibroblast growth factor and epidermal growth factor, cytokines  
CC such as erythropoietin and thrombopoietin, and hormones such as insulin,  
CC leptin and glucagon. Directed mutagenesis allows the introduction of  
CC mutations into predetermined genomic loci, permitting the selective  
CC alteration of gene activity. However, some mutation methods are  
CC unsuitable for Pichia methanolica cells, e.g. the pop-in/pop-out method  
CC which requires selection against 5-fluoro orotic acid to which P.  
CC methanolica cells are resistant. The methods can be used to easily and  
CC readily mutate P. methanolica cells

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX23878 (1-18)

OY 32 ValVallysArgArg 36  
DB 2 GTTGTAAACGACGG 16

RESULT 133

AAX32591  
ID AAX32591 standard; DNA; 18 BP.

XX AC AAX32591;

XX DT 24-JUN-1999 (first entry)

XX DE PCR primer ZC376.

XX KW Pichia methanolica; vacuolar protease; genetic defect; proteinase; ss;  
XX industrial; pharmaceutical; enzyme; enzyme inhibitor; growth factor;  
XX cytokine; hormone; insulin; leptin; glucagon; proteolysis; PCR primer.

XX OS Synthetic.

XX PN WO9914347-A1.

XX PD 25-MAR-1999.

XX PF 11-SEP-1998; 98WO-US019449.

XX PR 15-SEP-1997; 97US-00929748.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Raymond CK, Vanaja E;

XX DR WPI; 1999-244037/20.

XX PI Pichia methanolica defective in vacuolar protease.

XX PS Example 3; Page 50; 54pp; English.

XX CC The invention relates to Pichia methanolica cell which are functionally  
XX defective in a vacuolar protease. The functional deficiency is due to a  
XX genetic defect in the parent gene, wherein said parent gene encodes  
XX proteinase A or proteinase B. The new cells are hosts for production of  
XX heterologous proteins of industrial or pharmaceutical value, e.g. a wide  
XX range of enzymes, enzyme inhibitors, growth factors, cytokines and  
XX hormones (such as insulin, leptin and glucagon). The protease-defective

CC cells should show reduced proteolysis of recombinant proteins. Sequences  
CC AAX32582-595 represent PCR primers used during the course of the  
CC invention

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX32591 (1-18)

OY 32 ValVallysArgArg 36

DB 2 GTTGTAAACGACGG 16

RESULT 134

AAX34800  
ID AAX34800 standard; DNA; 18 BP.

XX AC AAX34800;

XX DT 06-JUL-1999 (first entry)

XX DE Human ZSIG-11 DNA amplifying primer ZC976.

XX KW Secretory protein; ZSIG-11; ligand polypeptide; testis; endoprotease;  
XX prohormone convertase; fertility; therapeutic; human; PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO9916870-A1.

XX PD 08-APR-1999.

XX PF 23-SEP-1998; 98WO-US020449.

XX PR 29-SEP-1997; 97US-0060327P.

XX PR 29-SEP-1997; 97US-00939897.

XX PR 19-MAY-1998; 98US-00081310.

XX PR 19-MAY-1998; 98US-0085966P.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Sheppard PO;

XX DR WPI; 1999-263692/22.

XX PT Polynucleotide encoding a human secretory protein, ZSIG-II.

XX PS Example 1; Page 105; 113pp; English.

XX CC The invention relates to a human secretory protein, ZSIG-11. Host cells  
XX containing a vector comprising the ZSIG-11 nucleic acid are used for the  
XX recombinant expression of the protein. ZSIG-11 is a novel ligand  
XX polypeptide and specific antibodies can be used to detect its presence in  
XX a biological sample. Probes derived from ZSIG-11 nucleotide sequences can  
XX also be used in detection of ZSIG-11 RNA. ZSIG-11 is expressed at high  
XX levels in testis, and could be used to identify/study prohormone  
XX convertases or endoproteases that exhibit testis specificity.

XX CC Antagonists, including antibodies, are useful for inhibiting or  
XX eliminating the function of ZSIG-11. It is possible that ZSIG-11 and its  
XX antagonists will be useful as fertility inducing therapeutics. Sequences  
XX AAX34800-21 represent PCR primers for amplifying the ZSIG-11 DNA

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores: 8.57e+03 Length: 18  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservatives: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 2

US-09-966-880A-8 (1-198) x AA224778 (1-18)

QY 32 ValVallyArgArg 36  
 AA224778  
 ID AAZ24778 standard; DNA; 18 BP.  
 AC AAZ24778;  
 XX 31-JAN-2000 (first entry)  
 DT Human soluble protein ZTMPO-1 DNA sequencing primer ZC976.  
 DE Soluble protein; ZTMPO-1; thymopietin-emerin family; human; cancer;  
 KW nuclear membrane protein; cardiac disorder; autoimmune disorder; testis;  
 KW infectious disease; cellular proliferation; skeletal muscle; thyroid;  
 KW adrenal gland; tumor; spermatogenesis; sperm activation; PCR primer;  
 KW contraception; immune response; humoral response; vaccination; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9954468-A1.  
 PN 28-OCT-1999.  
 PD 19-APR-1999; 99WO-US008601.  
 PF 21-APR-1998; 98US-00063838.  
 PR (ZYMO) ZYMOGENETICS INC.  
 PA Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;  
 PI WPI; 1999-634003/54.  
 DR New isolated ZTMPO-1 polypeptides used for diagnosis and treatment of  
 XX e.g. cancer, cardiac and autoimmune disorders and infectious diseases and  
 XX for developing contraceptives.  
 XX Example 1; Page 98; 110pp; English.

The invention provides a human soluble protein ZTMPO-1 which has homology  
 to the thymopietin-emerin family of nuclear membrane proteins. The ZTMPO  
 -1 protein can be expressed by standard recombinant methodology. Altered  
 levels of ZTMPO-1 receptor polypeptides may be indicative of pathological  
 conditions including cancer, cardiac and autoimmune disorders and  
 infectious diseases. The nucleic acid can be used as a source of  
 hybridization probes for detecting a genetic abnormality in a patient.  
 The ZTMPO-1 polypeptides can be used to modulate cellular proliferation  
 and differentiation in a diverse array of tissues such as testis,  
 skeletal muscle, thyroid and adrenal gland. Antagonists of ZTMPO-1 can be  
 used in modulating cellular proliferation and differentiation such as in  
 tumor growth and development. They can also be used for inhibiting  
 spermatogenesis and sperm activation. Such ZTMPO-1 antagonists can be used  
 for contraception in humans and animals, and in particular, domestic and  
 zoological animals and livestock, where they would act to prevent  
 fertilization of an egg. ZTMPO-1 antagonists could also be used to  
 mediate immune response, e.g. by boosting the humoral response in  
 individuals at risk for an infectious disease or as a supplement to  
 vaccination. Sequences AAZ24777-791 represent primers used for sequencing  
 the ZTMPO-1 DNA

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores: 8.57e+03 Length: 18  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservatives: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 2

US-09-966-880A-8 (1-198) x AAX34800 (1-18)

QY 32 ValVallyArgArg 36  
 AA224778  
 ID AAZ24778 standard; DNA; 18 BP.  
 AC AAZ24778;  
 XX 31-JAN-2000 (first entry)  
 DT Human soluble protein ZTMPO-1 DNA sequencing primer ZC976.  
 DE Soluble protein; ZTMPO-1; thymopietin-emerin family; human; cancer;  
 KW nuclear membrane protein; cardiac disorder; autoimmune disorder; testis;  
 KW infectious disease; cellular proliferation; skeletal muscle; thyroid;  
 KW adrenal gland; tumor; spermatogenesis; sperm activation; PCR primer;  
 KW contraception; immune response; humoral response; vaccination; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9954468-A1.  
 PN 28-OCT-1999.  
 PD 19-APR-1999; 99WO-US008601.  
 PF 21-APR-1998; 98US-00063838.  
 PR (ZYMO) ZYMOGENETICS INC.  
 PA Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;  
 PI WPI; 1999-634003/54.  
 DR New isolated ZTMPO-1 polypeptides used for diagnosis and treatment of  
 XX e.g. cancer, cardiac and autoimmune disorders and infectious diseases and  
 XX for developing contraceptives.  
 XX Example 1; Page 98; 110pp; English.

The invention provides a human soluble protein ZTMPO-1 which has homology  
 to the thymopietin-emerin family of nuclear membrane proteins. The ZTMPO  
 -1 protein can be expressed by standard recombinant methodology. Altered  
 levels of ZTMPO-1 receptor polypeptides may be indicative of pathological  
 conditions including cancer, cardiac and autoimmune disorders and  
 infectious diseases. The nucleic acid can be used as a source of  
 hybridization probes for detecting a genetic abnormality in a patient.  
 The ZTMPO-1 polypeptides can be used to modulate cellular proliferation  
 and differentiation in a diverse array of tissues such as testis,  
 skeletal muscle, thyroid and adrenal gland. Antagonists of ZTMPO-1 can be  
 used in modulating cellular proliferation and differentiation such as in  
 tumor growth and development. They can also be used for inhibiting  
 spermatogenesis and sperm activation. Such ZTMPO-1 antagonists can be used  
 for contraception in humans and animals, and in particular, domestic and  
 zoological animals and livestock, where they would act to prevent  
 fertilization of an egg. ZTMPO-1 antagonists could also be used to  
 mediate immune response, e.g. by boosting the humoral response in  
 individuals at risk for an infectious disease or as a supplement to  
 vaccination. Sequences AAZ24777-791 represent primers used for sequencing  
 the ZTMPO-1 DNA

Sequence AAZ06571-206607 are antisense polynucleotides targeted to a  
 nucleic acid molecule encoding human ELK-1 (also known as p62TCF). ELK-1  
 is a member of the ternary complex factor subfamily of Ets-domain  
 transcription factor proteins. The polynucleotides inhibit the expression  
 of human ELK-1, and this sequence targets the 3' untranslated region of  
 the ELK-1 RNA. Sequences AAZ06571-206607 all cause at least 30%  
 inhibition of ELK-1 expression. The antisense sequences can be used to  
 inhibit the expression of human ELK-1 in human cells or tissues in vitro.  
 ELK-1 uses a bipartite recognition mechanism mediated by both protein-DNA

CC and protein-protein interactions to regulate genes by direct and indirect  
CC DNA binding and has been shown to control various signal transduction  
CC pathways and other cell functions including apoptosis. This means that  
CC antisense compounds inhibiting expression of ELK-1 can be used to treat  
CC diseases associated with its expression in animals, particularly humans  
CC and to prevent or delay infection, inflammation or tumour formation. The  
CC compounds can also be used for diagnosis, as research reagents and in  
CC kits.  
XX  
SQ Sequence 18 BP; 5 A; 1 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAZ06607 (1-18)

QY 103 AsnLeuSerLeuArg 107  
Db 17 AACCTTCTCTCAGA 3

RESULT 137  
AAZ44028  
ID AAZ44028 standard; DNA; 18 BP.

AC AAZ44028;

DT 20-MAR-2000 (first entry)

XX P. methanolica ADE2 PCR primer ZC976.

XX Alcohol oxidase; industrial enzyme; pharmaceutical protein; ADE2;  
KW PCR primer; ss.

XX Pichia methanolica.

OS US6001597-A.

PN 14-DEC-1999.

XX 15-DEC-1998; 98US-00211631.

XX 09-NOV-1995; 95US-0006397P.

PR 17-JUL-1996; 96US-0042910P.

PR 26-AUG-1996; 96US-00703807.

PR 15-SEP-1997; 97US-0058822P.

PR 11-SEP-1998; 98US-00152180.

XX (ZYMO ) ZYMOGENETICS INC.

XX Vanaaja E, Raymond CK;

XX WPI; 2000-071656/06.

XX Pichia cell with disrupted genes, useful for producing polypeptides of  
XX economic importance, including industrial enzymes and pharmaceutical  
XX proteins.

XX Example 9; Col 39-40; 27pp; English.

XX This invention describes a novel Pichia methanolica cell in which an  
XX alcohol oxidase gene has been disrupted. The cell is useful for producing  
XX polypeptides of economic importance, including industrial enzymes and  
XX pharmaceutical proteins. This sequence represents a PCR primer used in  
XX the amplification of the ADE2 gene described in the method of the  
XX invention

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAZ44028 (1-18)

QY 32 ValVallysArgArg 36  
Db 2 GTTGTAACGACGG 16

RESULT 138

AAA75596

ID AAA75596 standard; DNA; 18 BP.

XX AAA75596;

XX 22-JAN-2001 (first entry)

XX PCR primer for DNA encoding a human zalphall ligand fragment.

XX zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;  
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour; PCR primer; ss.

XX Homo sapiens.

OS WO200053761-A2.

PN 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US006067.

XX 09-MAR-1999; 99US-00264908.

PR 11-MAR-1999; 99US-00265992.

PR 01-JUL-1999; 99US-0142013P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX WPI; 2000-565600/52.

XX New human cytokine, designated zalphall ligand, useful for stimulating  
XX the proliferation and/or development of hematopoietic cells in vitro and  
XX in vivo, and for treating tumorigenesis.

XX Example 30; Page 228; 256pp; English.

XX PCR primers AAA75595-96 were used to amplify DNA encoding a fragment of  
XX human zalphall ligand polypeptide. Zalphall ligand is a cytokine. The  
XX zalphall ligand is useful for stimulating the proliferation and  
XX development of haematopoietic cells in vitro and in vivo. Zalphall ligand  
XX polynucleotides can be used as primers or probes for cloning the zalphall  
XX gene. The zalphall ligand is useful for treating tumorigenesis. A  
XX zalphall ligand-saporin fusion toxin may be used for treating leukaemias  
XX and lymphomas. Antagonists against zalphall ligand are useful as research  
XX reagents for characterizing ligand-receptor interaction. Antagonists are  
XX also useful for inhibiting expansion, proliferation, activation and  
XX differentiation of cells involved in regulating hematopoiesis. The  
XX zalphall ligand may also be used to stimulate an immune response against  
XX B cell tumour, a virus, a parasite or a bacterium. The zalphall  
XX polypeptides, polynucleotides, antagonists, agonists and antibodies are  
XX also useful for the detection, diagnosis, prevention, and treatment of  
XX diseases associated with a zalphall ligand genetic defect

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA75596 (1-18)

QY 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16

RESULT 139

AAZ44774/C

ID RAZ44774 standard; DNA; 18 BP.

XX AC AAZ44774;

XX XX

DT 19-APR-2000 (first entry)

XX XX

DE Human FADD primer ISIS #23874.

XX XX

XX FADD; human; antisense; inhibitor; Fas-associated death domain; primer; probe; ss.

KW KW

XX XX

OS Homo sapiens.

XX XX

PN US6015712-A.

XX XX

PD 18-JAN-2000.

XX XX

PF 19-JUL-1999; 99US-00357072.

XX XX

PR 19-JUL-1999; 99US-00357072.

XX XX

PA (ISIS-) ISIS PHARM INC.

XX XX

PI Monia BP, Cowseert LM, Baker BP, Zhang H;

XX XX

DR WPI; 2000-126316/11.

XX XX

PT Antisense oligonucleotides, useful for inhibiting human Fas-associated death domain (FADD) expression are targeted to the 3' untranslated region of the FADD gene.

PT PT

XX XX

XX XX

PS Example 16; Col 53-54; 37pp; English.

XX XX

CC This invention describes novel antisense oligonucleotides (OCNs) (I) 8-20 nucleotides in length that specifically hybridize with and inhibit nucleic acids encoding human Fas-associated death domain (FADD), targeted to the 3' untranslated region (3'UTR). (I) can be used to treat animals, especially humans, suspected of having or being prone to a disease or condition associated with FADD expression. AAZ44746-244831 represent primers and probes used in the method of the invention

XX XX

SQ Sequence 18 BP; 6 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ44774 (1-18)

QY 43 SerLeuAspPheGly 47

Db 17 AGCCTGGACTTGGT 3

RESULT 140

AAA33601

ID AAA33601 standard; DNA; 18 BP.  
XX XX  
AC AAA33601;  
XX XX  
DT 28-JUL-2000 (first entry)  
XX XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:1290.  
XX XX

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary asoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX OS Homo sapiens.

XX PN WO200009525-A2.

XX XX

PD 24-FEB-2000.

XX XX

PF 03-AUG-1999; 99WO-US017712.

XX XX

PR 03-AUG-1998; 98US-0095212P.

XX XX

PA (UYEC-) UNIV EAST CAROLINA.

XX XX

PI Nyce JW;

XX XX

WPI; 2000-205971/18.

XX XX

PT New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.

XX XX

PS Claim 18; Page 426; 1343pp; English.

XX XX

CC The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytosstatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONS from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

SQ Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA33601 (1-18)

QY 59 LeuLeuPheLeuArg 63  
|||||  
4 CTCCTGTTCTCCGT 18

Db  
RESULT 141  
AAZ35164  
ID AAZ35164 standard; DNA; 18 BP.  
AC AAZ35164;  
XX  
XX  
DT 13-MAR-2000 (first entry)  
XX  
DE Human immunomodulator zsig57 primer ZC976.  
XX  
XX Immunomodulator; zsig57; human; transcytosis receptor; immunostimulant;  
KW antiviral; virucide; wound healing; vulnery; gene therapy; primer; ss.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX  
XX WO9966040-A1.  
PN  
XX  
XX  
PD 23-DEC-1999.  
XX  
XX 20-MAY-1999; 99WO-US011337.  
XX  
XX 18-JUN-1998; 98US-00099600.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX Sheppard PO;  
PI  
XX  
XX WPI; 2000-097745/08.  
DR  
XX Polynucleotides encoding the polypeptide zsig57 useful for regulating the  
PT immune system.  
PT  
XX  
XX Example 1; Page 131; 144pp; English.  
PS  
XX This primer, termed ZC976, was used in the sequence analysis of an EST  
CC clone that had been obtained by querying an EST database for sequences  
CC homologous to proteins having a secretory signal sequence. Primers  
CC designed from the isolated EST clone were used in the isolation of full-  
CC length cDNA (see AAZ35141) coding for zsig57 (see AAZ32397). Zsig57 is a  
CC novel human immunomodulator that is a member of the immunoglobulin  
CC superfamily of proteins and which may act as a transcytosis receptor. The  
CC invention provides zsig57 polypeptides, polynucleotides and antibodies  
CC that may be useful in the treatment of human disease states  
XX  
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ35164 (1-18)

QY 32 ValVallyeArgArg 36  
|||||  
2 GTTGTAAACGACGG 16

Db  
RESULT 142  
AAZ44135  
ID AAZ44135 standard; DNA; 18 BP.

XX AAZ44135;  
AC  
XX 24-MAR-2000 (first entry)  
DT  
XX Human EGR-1 DNA antisense primer #24157.  
XX  
XX EGR-1, early growth response 1; antisense; inhibition; human; primer;  
KW anti-inflammatory; cytostatic; antiviral; detection; diagnosis;  
KW viral infection; inflammation; tumor; ss.  
XX  
XX Homo sapiens.  
OS  
XX US6008048-A.  
PN  
XX 28-DEC-1999.  
PD  
XX 04-DEC-1998; 98US-00205921.  
XX  
XX 04-DEC-1998; 98US-00205921.  
PR  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Monia BP, Cowser LM;  
PI  
XX WPI; 2000-096375/08.  
DR  
XX  
XX Antisense oligonucleotides that inhibit expression of human early growth  
PT response-1, useful for diagnosis, treatment and prevention of tumors,  
PT inflammation and infection.  
PT  
XX Claim 1; Col 37-38; 31pp; English.  
PS  
XX This invention describes novel antisense oligonucleotides (I) capable of  
CC inhibiting expression of human EGR-1 (early growth response-1). The  
CC products of the invention have anti-inflammatory, cytostatic and  
CC antiviral activity. (I) was tested for its effects on EGR-1 mRNA levels  
CC by real-time polymerase chain reaction (PCR), results indicated that 60%  
CC inhibition was achieved. When (I) was modified by 2'-O-methoxyethyl  
CC substitution of the first 4 and last 4 residues, and by replacing any C  
CC in these flanking regions with 5-methyl-C, the degree of inhibition was  
CC increased to 71%. (I) is used to inhibit expression of EGR-1 in cells and  
CC tissues in vitro, for research or diagnosis, e.g. detecting EGR-1  
CC encoding nucleic acid. (I) may also be used to treat or prevent EGR-1-  
CC associated diseases, particularly viral infections, inflammation and  
CC tumors. AAZ44134-244159 represent antisense primers used to inhibit the  
CC human EGR-1 protein  
XX  
SQ Sequence 18 BP; 1 A; 13 C; 3 G; 1 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ44135 (1-18)

QY 127 ArgArgLeuHisArg 131  
|||||  
4 CGCCGCTCCACCGC 18

Db  
RESULT 143  
AAZ75987  
ID AAZ75987 standard; DNA; 18 BP.  
XX  
XX AAZ75987;  
AC  
XX 10-SEP-2001 (first entry)  
DT  
XX Human biallelic marker downstream amplification primer SEQ ID NO:10343.  
DE

XX Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.  
 XX Homo sapiens.  
 OS  
 PN WO9954500-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 21-APR-1999; 99WO-IB000822.  
 XX  
 PR 21-APR-1998; 98US-0082614P.  
 PR 23-NOV-1998; 98US-0109732P.  
 XX  
 XX (GEST ) GENSET.  
 PA

XX Cohen D, Blumenfeld M, Chumakov I;  
 PI WPI; 2000-013267/01.  
 DR Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.  
 XX  
 PS Claim 9; Page 2435; 2745pp; English.  
 XX  
 CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention  
 XX  
 SQ Sequence 18 BP; 7 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ75987 (1-18)

QY 34 LysArgArgAspSer 38  
 DB 4 AAGAGACGAGACTCC 18

RESULT 144  
 AAZ72263  
 ID AAZ72263 standard; DNA; 18 BP.  
 XX  
 AC AAZ72263;  
 XX  
 XX 10-SEP-2001 (first entry)  
 DT

DE Human biallelic marker upstream amplification primer SEQ ID NO:6619.  
 XX  
 KW Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.  
 XX Homo sapiens.  
 OS  
 PN WO9954500-A2.  
 XX  
 PD 28-OCT-1999.  
 XX  
 PF 21-APR-1999; 99WO-IB000822.  
 XX  
 PR 21-APR-1998; 98US-0082614P.  
 PR 23-NOV-1998; 98US-0109732P.  
 XX  
 XX (GEST ) GENSET.  
 PA Cohen D, Blumenfeld M, Chumakov I;  
 PI WPI; 2000-013267/01.  
 DR Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.  
 XX  
 PS Claim 9; Page 1642; 2745pp; English.  
 XX  
 CC AAZ65654 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention  
 XX  
 SQ Sequence 18 BP; 5 A; 8 C; 0 G; 5 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ72263 (1-18)

QY 102 ProAsnLeuSerLeu 106  
 DB 4 CCAATCTATCCCTC 18

RESULT 145  
 AAZ52254  
 ID AAZ52254 standard; DNA; 18 BP.  
 XX  
 AC AAZ52254;  
 XX  
 XX 18-JUL-2000 (first entry)  
 DT

DE Primer ZC976 for sequencing human stomach protein zsig28 cDNA.

XX Human; stomach; zsig28 protein; chromosome 3q22.1-3q22.2; gene therapy;  
 KW claudin; oligodendrocyte-specific protein; OSP; apoptosis; RVP.1;  
 KW rat androgen-withdrawal apoptosis protein; growth factor receptor;  
 KW cell-cell signalling molecule; cytostatic; antibacterial; food poisoning;  
 KW Botulism; diarrhoea; inflammation; cramping; cancer; gastric ulcer;

KW diagnosis; prevention; treatment; primer; ss.

OS Homo sapiens.

PN WC200015659-A2.

XX 23-MAR-2000.

XX 14-SEP-1999; 99WO-US021023.

XX 16-SEP-1998; 98US-00154444.

XX (ZYMO ) ZYMOGENETICS INC.

XX Sheppard PO, Foley KP;

XX WPI; 2000-271379/23.

XX New isolated polynucleotide encoding a stomach zsig28 polypeptide used for diagnosis, prevention and treatment of stomach disorders caused by bacteria, gastric ulcers or cancer.

PS Example 1; Page 121; 121pp; English.

XX The present sequence is a primer ZC976 used for sequencing a cDNA corresponding to an expressed sequence tag identified in a human lung library' to obtain full length clone of polynucleotide encoding stomach protein zsig28. The zsig28 gene is located at 3q22.1-3q22.2 region of human chromosome 3. The zsig28 protein shows homology to a diverse family of receptor proteins containing e.g. human claudin 1 and 2, human and murine oligodendrocyte-specific protein (OSP) and rat androgen-withdrawal apoptosis protein RVP.1. It is thought to be a cell-cell signalling molecule, a growth factor receptor or extracellular matrix associated protein with growth factor hormone activity and may be involved in an apoptotic cellular pathway. The protein may act as an anti-microbial agent and may bind toxins produced by bacteria which cause food poisoning, Botulism, severe diarrhoea, inflammation and cramping. zsig28 agonists are useful for promoting apoptosis in cells over-expressing zsig28 e.g. in cancer cells. They are also useful for stimulating cell growth or differentiation. Altered levels of zsig28 protein in a test sample such as saliva, serum, sweat or biopsy can be monitored as an indication of digestive function, gastric ulcer or cancer. zsig28 expression can be used as a differentiation marker to determine the stage of tumour or cell maturity, particularly in epithelial cells. CC Polynucleotides encoding zsig28 can be used in gene therapy applications to increase or inhibit zsig28 activity

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ52254 (1-18)

QY 32 ValVallysArgArg 36

DB 2 GTTGTAACGACGG 16

RESULT 146

AAZ30211

ID AAA30211 standard; DNA; 18 BP.

XX AAA30211;

XX 16-AUG-2000 (first entry)

DE Human RING finger protein zapop3 gene sequencing primer ZC976.

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KW

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XX

Human; RING finger; leucine rich repeat; LRR; zapop3; chromosome 9q34.11; myocardial infarction; dilated myopathy; retinitis pigmentosa-deafness syndrome 1; apoptosis inhibition; angiogenesis; hyperplasia; pulmonary hypertension; gene therapy; sequencing primer; ss.

OS Homo sapiens.

PN WC200029430-A1.

XX 25-MAY-2000.

XX 04-NOV-1999; 99WO-US026104.

XX 12-NOV-1998; 98US-00191500.

XX (ZYMO ) ZYMOGENETICS INC.

XX Venezia D, Grossmann A;

XX WPI; 2000-387737/33.

XX Polynucleotides encoding zapop3 polypeptides useful for detecting chromosomal abnormalities comprising a sequence identical to a specific amino acid sequence, identity being determined by a specific program.

PS Example 1; Page 99; 104pp; English.

XX The present sequence is a sequencing primer for the human zapop3 gene. The Zapop3 protein was isolated by searching an EST database for proteins similar to proteins with a RING finger sequence, with the full length clone being obtained from a peripheral blood granulocyte library. BRCA1 is an example of a RING finger protein. The gene is found on chromosome 9q43.11, and its locus is associated with retinitis pigmentosa-deafness syndrome 1. In addition to gene therapy for this disease, the protein, nucleic acid and antibodies can be used to diagnose and treat myocardial infarction, congestive heart failure, hypertrophic cardiomyopathy, dilated myopathy, to limit infarct size following a heart attack, to aid recovery after heart transplantation, to promote angiogenesis and wound healing, to develop coronary collateral circulation, for revascularisation in the eye, for complications related to poor circulation, for stroke, induction of skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and treatment of systemic and pulmonary hypertension. In addition to a RING finger domain, the protein also contains eight leucine rich repeat motifs

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA30211 (1-18)

QY 32 ValVallysArgArg 36

DB 2 GTTGTAACGACGG 16

RESULT 147

AAF19723

ID AAF19723 standard; DNA; 18 BP.

XX AAF19723;

XX 14-MAR-2001 (first entry)

DE Human fibronectin polynucleotide fragment #1290.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 OS Homo sapiens.  
 XX WO200062736-A2.  
 PN 26-OCT-2000.  
 PD 24-MAR-2000; 2000WO-US008020.  
 XX 06-APR-1999; 99US-0127958P.  
 PF (UYEC-) UNIV EAST CAROLINA.  
 XX (NYCE/) NYCE J W.  
 PA Nyce JW;  
 PI WPI; 2000-679539/86.  
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.  
 XX Claim 14; Page 221; 1592pp; English.  
 XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors and  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention  
 XX SQ Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAF19723 (1-18)  
 Qy 59 Leuleupheleuarg 63  
 Db 4 CTCCTGTTCTCGT 18  
 RESULT 148  
 AAA29424/c  
 ID AAA29424 standard; DNA; 18 BP.  
 XX AC AAA29424;  
 XX DT 08-AUG-2000 (first entry)  
 XX DE Primer extension product modulating module #1.  
 XX KW Primer extension product; modular oligonucleotide; identification;  
 KW hybridisation; probe; ss.  
 XX Unidentified.  
 OS WO200015842-A1.  
 XX PN 23-MAR-2000.  
 PD 15-SEP-1999; 99WO-GB003056.  
 XX 15-SEP-1998; 98US-00153242.  
 PF 16-SEP-1998; 98GB-00020185.  
 XX (DYNA-) DYNAL AS.  
 PA (JONE/) JONES E L.  
 PI Lundeberg J, Uhlen M;  
 XX WPI; 2000-271472/23.  
 DR Isolating primer extension products using modular oligonucleotides.  
 XX Claim 13; Page 15; 74pp; English.  
 XX A method (I) has been developed of isolating primer extension products,  
 CC produced from template vectors and containing sequences corresponding to  
 CC or complementary to (i) to (iii) below, where the method comprises  
 CC binding a modular oligonucleotide, comprising 2 parts (or modules), to  
 CC adjacent stretches on the primer extension products (the modular  
 CC oligonucleotide is complementary to and capable of binding to the vector  
 CC derived sequences of the primer extension products and at least 1 module  
 CC (the capture module) is immobilized or can be immobilised: (i) a primer  
 CC binding region; (ii) an insert; and (iii) vector derived sequence(s).  
 CC Also described is a method for determining the nucleotide sequence of a  
 CC nucleic acid insert in a vector, in which sequencing products are  
 CC generated by performing appropriate extension reaction on the vector, the  
 CC sequencing products are isolated via (i) and the isolated products are  
 CC separated by an appropriate technique and the labels carried on the  
 CC sequencing products are visualised to allow determination of the sequence  
 CC of the insert or a portion of it. (i) may be used for isolating primer  
 CC extension products, particularly sequencing reaction products in which  
 CC the products contain sequences corresponding or complementary to primer  
 CC binding regions, inserts and vector derived sequences. The present  
 CC sequence represents a specifically claimed modular oligonucleotide which  
 CC is used in the exemplification of the present invention  
 XX SQ Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0



US-09-966-880A-8 (1-198) x AAZ29424 (1-18)

QY 32 ValVallyeArgArg 36  
 Db 17 GTTGTAAACGACGG 3

RESULT 149

AAZ58580  
 ID AAZ58580 standard; cDNA; 18 BP.

XX AC AAZ58580;

XX 05-JUN-2000 (first entry)

XX zsig58 cDNA PCR primer ZC976.

XX Human; zsig58; vulnery; gonadotropin activity enhancer; osteopathic;  
 KW antitumor; hormone dependent tumour growth inhibitor; gene therapy;  
 KW PCR primer; ss.

XX OS Homo sapiens.

XX PN WC200008154-A1.

XX PD 17-FEB-2000.

XX PF 03-AUG-1999; 99WO-US017552.

XX PR 03-AUG-1998; 98US-00128372.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Sheppard PO, Chandrasekher Y;

XX WPI; 2000-205709/18.

XX New polynucleotide encoding a member of trabecular meshwork-induced  
 PT glucocorticoid response protein for treating ovarian, pancreatic, ocular,  
 PT blood and bone disorders such as osteoporosis and Paget's disease.

XX Example 9; Page 119; 138pp; English.

XX The present sequence is that of primer ZC986, which was used with primer  
 CC ZC447 (see AAZ58581) to screen Escherichia coli DH5 alpha cells following  
 CC transformation with a baculovirus expression vector including zsig58  
 CC cDNA. Clones having the correct insert were used to transfect Sf9 insect  
 CC cells. zsig58 (see AAY79147) is a novel cell-cell signalling molecule,  
 CC growth factor, or secreted extracellular matrix associated protein with  
 CC growth factor/hormone activity, that is a novel member of the trabecular  
 CC meshwork-induced glucocorticoid response protein (TIGR) family of  
 CC proteins. It is strongly expressed in ovary, pancreas and small  
 CC intestine. zsig58 nucleic acids (see AAZ58586) can be used in gene  
 CC therapy to increase or inhibit zsig58 activity and to identify regions of  
 CC the genome associated with disease states

XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e-03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ58580 (1-18)

QY 32 ValVallyeArgArg 36  
 Db 2 GTTGTAAACGACGG 16

RESULT 150

AAZ93482/c

ID XX AAZ93482 standard; DNA; 18 BP.  
 XX AC AAZ93482;  
 XX DT 24-JUL-2000 (first entry)  
 XX DE TRADD antisense oligonucleotide.  
 XX KW TRADD; TNF; tumour necrosis factor; NF-kappa-B; apoptosis;  
 KW programmed cell death; antisense; inhibition; treatment; therapy;  
 KW septic shock; inflammation; cancer; antiinflammatory; human; ss.  
 XX OS Synthetic.  
 XX FH Key Location/Qualifiers  
 FT misc\_binding complement(1..18)  
 FT /\*tag= a  
 FT /note= "Complementary to bases 702-685 of the human TRADD  
 FT sequence described in GENESEQ record AAZ93431"  
 XX PN WC2000012527-A1.  
 XX PD 09-MAR-2000.  
 XX PF 25-AUG-1999; 99WO-US019614.  
 XX PR 28-AUG-1998; 98US-00143212.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, Cowsert LM;  
 XX WPI; 2000-237846/20.  
 XX New antisense compounds that limit the expression of human TRADD protein,  
 XX useful in the treatment and diagnosis of cancer, inflammation and septic  
 XX shock.  
 XX Claim 3; Page 52; 85pp; English.  
 XX The intracellular protein TRADD has been identified as a critical link  
 CC between tumour necrosis factor (TNF) receptor binding and downstream  
 CC activation of NF-kappa-B. Overexpression of native TRADD activates NF-  
 CC kappa-B in the absence of TNF and dominant negative mutants of TRADD  
 CC block TNF-induced NF-kappa-B activation. A second effect of TNF in many  
 CC cell types is the induction of apoptosis (programmed cell death). TRADD  
 CC overexpression has been shown to mimic TNF induction of apoptosis as  
 CC well. Data indicates that TRADD and other downstream effector proteins  
 CC are the rate limiting step of TNF action and would therefore serve as the  
 CC most efficient targets for inhibition of TNF-induced events. Antisense  
 CC oligonucleotides capable of inhibiting TRADD function may therefore be  
 CC useful in a number of therapeutic, diagnostic and research applications.  
 CC Inhibiting expression of TRADD by contacting human cells or tissues with  
 CC the antisense compound may be used to treat a disease or condition  
 CC associated with TRADD expression, for example, septic shock,  
 CC inflammation, or cancer. TRADD antisense oligonucleotides of varying  
 CC inhibitory capabilities are listed in GENESEQ records AAZ93438-293517.  
 CC The antisense oligonucleotides exhibit enhanced inhibitory capabilities  
 CC when they have 2'-MOE wings and a deoxy gap

SQ Sequence 18 BP; 2 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e-03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ93482 (1-18)

QY 121 AlaGluProGluGly 125

Db 16 GCTGAGCCTGAAGGA 2

RESULT 151  
AAC64070  
ID AAC64070 standard; DNA; 18 BP.  
XX AC AAC64070;  
XX AC AAC64070;  
DT 19-FEB-2001 (first entry)  
XX DE Baculovirus expression vector pZBV32L PCR primer, SEQ ID NO:19.  
XX Human zacr3p3; adipocyte complement related protein homologue; ACRP30;  
KW Clq domain; collagen-like domain; energy balance modulation;  
KW cellular metabolism; metabolic disorder; obesity; anorexia;  
KW antimicrobial agent; infection; platelet aggregation inhibition;  
KW adhesion; activation; vascular injury; antibacterial; antiviral;  
KW PCR primer; ss.  
XX OS Synthetic.  
XX PN WO200063377-A1.  
XX PD 26-OCT-2000.  
XX PF 19-APR-2000; 2000WO-US010454.  
XX PR 20-APR-1999; 99US-00294943.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
XX PI Piddington CS, Bishop PD;  
XX DR WPI; 2000-665243/64.  
XX DR Novel zacr3p3 polypeptides used to treat or prevent bacterial or viral  
PT infections, for wound healing, improving blood flow, and to analyze  
PT energy efficiency in mammals.  
XX Example 2; Page 120; 123pp; English.

XX The invention relates to the human zacr3p3 protein (AA29590) and to  
CC nucleic acids which encode it (AAC64058, AAC64063). Zacr3p3 is a homologue  
CC of adipocyte complement related protein (ACRP30) and contains a collagen-  
CC like domain comprising Gly-Xaa-Xaa or Gly-Xaa-Pro repeats, and a C-  
CC terminal Clq domain comprising 10 beta-strands. The zacr3p3 gene is  
CC located on chromosome 5p12. The invention also relates to zacr3p3-  
CC fragments, fusion proteins containing zacr3p3 polypeptides, zacr3p3-  
CC specific antibodies, expression constructs and host cells comprising  
CC zacr3p3 nucleic acids, and methods of recombinant production of zacr3p3.  
CC Human zacr3p3, and its agonists and antagonists may be used in the study  
CC and modulation of cellular metabolism and energy balance in mammals, and  
CC may therefore be used to treat disorders such as obesity and anorexia,  
CC and conditions associated with these disorders. Due to its Clq like  
CC domain, zacr3p3 and zacr3p3-containing fusion proteins may be useful as  
CC antimicrobial agents, promoting lysis or phagocytosis of infectious  
CC organisms such as bacteria or viruses. Zacr3p3, its fragments, fusion  
CC proteins, antibodies and activity modulators may also be used to inhibit  
CC collagen-induced platelet aggregation, adhesion, or activation, and may  
CC therefore have potential for promoting blood flow within the vasculature  
CC of a mammal e.g., to treat injury to the vasculature or other collagenous  
CC tissue. Human zacr3p3 and its antibodies may additionally be used to study  
CC dimerisation and oligomerisation. The present sequence represents a PCR  
CC primer used in an exemplification of the invention

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAC64070 (1-18)

Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16

RESULT 152  
AAC65144  
ID AAC65144 standard; DNA; 18 BP.  
XX AC AAC65144;  
XX DT 12-FEB-2001 (first entry)  
XX DE Human adipocyte complement related protein homologue zacr2p2 primer #10.  
XX KW Human; zacr2p2; adipocyte complement related protein; ACRP30;  
KW energy balance; metabolism; haemostasis; anti-microbial; PCR primer; ss.  
XX OS Homo sapiens.  
XX PN WO200063376-A1.  
XX PD 26-OCT-2000.  
XX PF 19-APR-2000; 2000WO-US010452.  
XX PR 20-APR-1999; 99US-00295072.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
XX PI Piddington CS, Bishop PD;  
XX DR WPI; 2000-647517/62.  
XX DR Human DNA sequence encoding a zacr2p2 polypeptide which has homology to an  
PT adipocyte complement related protein (ACRP30), useful in gene therapy  
PT applications for inhibiting or increasing zacr2p2 activity.  
XX Example 3; Page 122; 125pp; English.

XX The present invention is related to the isolation and uses of a homologue  
CC to the adipocyte complement related protein ACRP30, known as zacr2p2. The  
CC zacr2p2 protein is involved in energy balance, and the protein, its  
CC antibodies and coding sequence can be used to modulate energy balance,  
CC haemostasis, calcium ion concentration, muscle contraction, hormone  
CC secretion, DNA synthesis and cell growth, inositol phosphate turnover,  
CC arachidonate release, phospholipase-C activation, gastric emptying, human  
CC neutrophil activation or ADCC capability and superoxide anion production.  
CC They may also have uses in antimicrobial applications

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAC65144 (1-18)

Qy 32 ValVallysArgArg 36  
Db 2 GTTGTAAACGACGG 16

RESULT 153  
AAC90239  
ID AAC90239 standard; DNA; 18 BP.

XX AAC90239;  
 XX 14-MAR-2001 (first entry)  
 XX Primer ZC976.  
 XX Vacuolar protease; proteinase A; proteinase B; protein production; ss.  
 XX Pichia methanolica.  
 XX US6153424-A.  
 XX 28-NOV-2000.  
 XX 09-MAR-1999; 99US-00265628.  
 XX 09-NOV-1995; 95US-0006397P.  
 XX 17-JUL-1996; 96US-0042910P.  
 XX 26-AUG-1996; 96US-00703807.  
 XX 15-SEP-1997; 97US-0058822P.  
 XX 11-SEP-1998; 98US-00152180.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Sheppard PO;  
 XX WPI; 2001-040516/05.  
 XX A new Pichia methanolica cell with functional deficiency in vacuolar  
 XX protease, useful as hosts for production of proteins of interest.  
 XX Example 4; Col 39; 27pp; English.  
 XX The present invention relates to a Pichia methanolica cell with a  
 XX functional deficiency in a vacuolar protease, resulting from a genetic  
 XX defect, where the defect is an insertion, deletion, or substitution of at  
 XX least 4 contiguous base pairs in a parent gene, which encodes proteinase  
 XX A or proteinase B. The invention can be used for the production of a  
 XX protein of industrial and pharmaceutical interest. These include enzymes,  
 XX enzyme inhibitors, growth factors, cytokines and hormones  
 XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 8.57e+03 Length: 18  
 XX Score: 5.00 Matches: 5  
 XX Percent Similarity: 100.00% Conservative: 0  
 XX Best Local Similarity: 100.00% Mismatches: 0  
 XX Query Match: 2.53% Indels: 0  
 XX DB: 4 Gaps: 0  
 XX  
 XX US-09-966-880A-8 (1-198) x AAC90239 (1-18)  
 XX  
 XX Qy 32 ValVallylsArgArg 36  
 XX 2 GTTGTAACGACGCG 16  
 XX  
 XX Db  
 XX  
 XX RESULT 154  
 XX AAD07920  
 XX ID AAD07920 standard; DNA; 18 BP.  
 XX  
 XX AC AAD07920;  
 XX  
 XX 03-AUG-2001 (first entry)  
 XX ZC976 primer related to human Zsig87 protein.  
 XX  
 XX Human; Zsig87 protein; cardiovascular disease; infertility; cytostatic;  
 XX male reproductive dysfunction; ovarian disorder; testicular; pancreatic;  
 XX lymphatic; bone; blood; uterine; stomach; cancer; inflammatory disorder;  
 XX immunoc contraceptive; anti-fertility vaccine; spermatogenesis; arthritis;  
 XX sperm capacitation; wound healing; diabetes; vulnary; ocular; asthma;  
 XX

KW chromosomal abnormality; forensic DNA profiling; leukaemia; gene therapy;  
 KW vasotropic; gynaecological; gastrointestinal-gen; primer; ss.  
 XX Homo sapiens.  
 XX WO200142292-A2.  
 XX 14-JUN-2001.  
 XX 08-DEC-2000; 2000WO-US033539.  
 XX 08-DEC-1999; 99US-00456641.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Sheppard PO;  
 XX WPI; 2001-381639/40.  
 XX Novel secreted protein, zsig87 polypeptides and polynucleotides for  
 XX detecting human chromosomal abnormalities, as immunoc contraceptive and  
 XX for diagnosing, treating cancer, cardiovascular and inflammatory  
 XX diseases.  
 XX Disclosure; Page 107; 107pp; English.  
 XX The present invention relates to polynucleotides and polypeptides for  
 XX zsig87, a novel secreted protein. Zsig87 polypeptides are useful for  
 XX producing antibodies, which are useful for detecting cancer. Zsig87  
 XX modulators are useful for treating cardiovascular diseases, infertility,  
 XX in vitro fertilisation, birth control, treating impotence or other male  
 XX reproductive dysfunctions. Zsig87 polypeptides are useful for promoting  
 XX wound healing for e.g. in the pancreas, for anti-microbial applications  
 XX and for diagnosing, preventing and treating ovarian, ocular, testicular,  
 XX pancreatic, immune, lymphatic, bone or blood disorders, uterine, stomach  
 XX cancer and disorders associated with gastrointestinal mobility and  
 XX dysfunction, as components in immunoc contraceptive or anti-fertility  
 XX vaccines and for modulating spermatogenesis and sperm capacitation.  
 XX Zsig87 sequence and its modulators are useful for treating diabetes,  
 XX pancreatic cancer and inflammatory diseases, such as asthma and  
 XX arthritis. Zsig87 polynucleotide sequences are useful for detecting human  
 XX chromosomal abnormalities and as diagnostics in forensic DNA profiling.  
 XX Zsig87-cytokine fusion proteins or antibody-cytokine fusion proteins are  
 XX useful for enhancing in vivo killing of target tissue for e.g. leukaemia,  
 XX blood and bone marrow cancers. Zsig87 DNA is used in gene therapy. The  
 XX present sequence is a primer related to human Zsig87 protein  
 XX  
 XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Alignment Scores:  
 XX Pred. No.: 8.57e+03 Length: 18  
 XX Score: 5.00 Matches: 5  
 XX Percent Similarity: 100.00% Conservative: 0  
 XX Best Local Similarity: 100.00% Mismatches: 0  
 XX Query Match: 2.53% Indels: 0  
 XX DB: 4 Gaps: 0  
 XX  
 XX US-09-966-880A-8 (1-198) x AAD07920 (1-18)  
 XX  
 XX Qy 32 ValVallylsArgArg 36  
 XX 2 GTTGTAACGACGCG 16  
 XX  
 XX Db  
 XX  
 XX RESULT 155  
 XX AAF69050  
 XX ID AAF69050 standard; DNA; 18 BP.  
 XX  
 XX AC AAF69050;  
 XX  
 XX 12-APR-2001 (first entry)  
 XX COXI PCR primer #26.  
 XX

KW Mitochondria; cytochrome C oxidase; COX; Alzheimer's disease; PCR primer;  
 XX ss.  
 XX Homo sapiens.  
 OS  
 XX  
 PN US6171859-B1.  
 XX  
 XX 09-JAN-2001.  
 PD  
 XX  
 PF 30-MAR-1995; 95US-00413740.  
 XX  
 PR 30-MAR-1994; 94US-00219842.  
 XX  
 PA (MITO-) MITOKOR.  
 XX  
 PI Herrstadt C, Parker WD;  
 XX  
 XX WPI; 2001-136875/14.  
 DR  
 XX  
 XX Targeting conjugate molecule to mitochondria having defective cytochrome  
 PT C oxidase activity for diagnosing Alzheimer's disease, involves  
 PT contacting mitochondria with a conjugate of targeting molecule and toxin.  
 XX  
 XX Example 2; Col 41-42; 88pp; English.  
 XX  
 XX The present invention relates to a method for selectively accumulating a  
 CC mitochondrial disabling or destructive amount of a conjugate molecule in  
 CC mitochondria having defective cytochrome C oxidase (COX) activity or  
 CC displaying increased membrane potential. The method involves contacting  
 CC mitochondria with a conjugate molecule comprising a targeting molecule  
 CC conjugated to a toxin, where the conjugate or targeting molecule selected  
 CC accumulates in the mitochondria. The method is useful for diagnosis of  
 CC Alzheimer's disease (AD), especially sporadic AD. The present sequence is  
 CC a PCR primer used in the method of the present invention  
 XX  
 SQ Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAF69050 (1-18)

Qy 125 GlyLeuArgLeu 129  
 Db 2 GGCTACGGAGGCTC 16  
 RESULT 156  
 AAH45321  
 ID AAH45321 standard; DNA; 18 BP.  
 XX  
 AC AAH45321;  
 XX  
 XX 01-OCT-2001 (first entry)  
 DT  
 XX Human MHC S DNA PCR primer S2\_02a (R).  
 DE  
 XX Human; MHC S; major histocompatibility complex S; vulgar psoriasis;  
 KW diagnosis; primer; SEEK1; HCR; a-helix coiled-coil rod homologue;  
 KW polymorphism; PCR primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200142458-A1.  
 FN  
 XX 14-JUN-2001.  
 PD  
 XX  
 PF 06-DEC-2000; 2000WO-JP008624.  
 XX

PR 06-DEC-1999; 99JP-00346867.  
 XX  
 PA (INOK/) INOKO H.  
 XX  
 PI Inoko H, Tamiya G;  
 XX  
 DR WPI; 2001-381680/40.  
 XX  
 XX New primer DNA, useful for detecting vulgar psoriasis.  
 PT  
 XX Example 1; Page 13; 106pp; Japanese.  
 FS  
 XX The invention relates to a method of diagnosing vulgar psoriasis using  
 CC primers based on the sequences of the human MHC S, SEEK1 and HCR genes.  
 CC By analysing the sequences of these genes in Japanese patients with  
 CC psoriasis and in normal subjects, it has been found that some of the  
 CC examined polymorphisms correlate significantly to the group of patients  
 CC with psoriasis. Vulgar psoriasis can therefore be diagnosed by analysing  
 CC these gene polymorphisms. The present sequence is a primer designed to  
 CC detect a genetic polymorphism in the human major histocompatibility  
 CC complex (MHC) S gene  
 XX  
 SQ Sequence 18 BP; 4 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH45321 (1-18)

Qy 128 ArgLeuHisArgAla 132  
 Db 4 CGCCTCCACAGAGCT 18

RESULT 157  
 AAD02427  
 ID AAD02427 standard; DNA; 18 BP.  
 XX  
 AC AAD02427;  
 XX

DT 24-APR-2001 (first entry)

XX PCR primer, ZC976 used to generate Pichia methanolica PRB1 probe.  
 DE  
 XX Glyceraldehyde 3-phosphate dehydrogenase 1; GAP1; GAPDH-1; promoter;  
 KW terminator; industrial enzyme; unglycosylated pharmaceutical protein;  
 KW cellulase; enzyme inhibitor; protease inhibitor; growth factor;  
 KW platelet derived growth factor; PGDF; glutamic acid decarboxylase; GAD;  
 KW cytokine; interleukin; hormone; insulin; PRB1; PCR primer; ss.  
 XX  
 OS Pichia methanolica.  
 XX  
 XX WO200078978-A1.  
 FN  
 XX 28-DEC-2000.  
 PD  
 XX 16-JUN-2000; 2000WO-US016671.  
 PF  
 XX 24-JUN-1999; 99US-0140703P.  
 PR  
 XX (ZYMO ) ZYMOGENETICS INC.  
 PA (MILL/) MILLER B G.  
 PA (SLOA/) SLOAN J S.  
 XX  
 XX Miller BG, Sloan JS, Raymond CK, Vanaja E;  
 PI  
 XX WPI; 2001-102728/11.  
 DR  
 XX New Pichia methanolica glyceraldehyde 3-phosphate dehydrogenase-1 (GAPDH-

PT 1) promoter for producing industrial enzymes and (unglycosylated)  
 PT pharmaceutical proteins.  
 XX Example 4; Page 36; 39pp; English.  
 XX The invention relates to transcription promoter and terminator sequences  
 CC of Pichia methanolica glyceraldehyde 3-phosphate dehydro- Genase 1 (GAPDH  
 CC -1) gene, designated as GAP1. These sequences are used within DNA  
 CC constructs for the production of proteins of interest in cultured P.  
 CC methanolica cells. The protein of interest includes industrial enzymes  
 CC and (unglycosylated) pharmaceutical proteins e.g. enzymes such as  
 CC cellulases, enzyme inhibitors such as protease inhibitors, growth factors  
 CC such as platelet derived growth factor (PDGF), glutamic acid  
 CC decarboxylase (GAD), cytokines such as interleukins, hormones such as  
 CC insulin, and receptors expressed as truncated forms or as fusion  
 CC proteins. The present sequence is PCR primer, ZC976 used to generate  
 CC Pichia methanolica PR1 probe. This primer is specifically used for  
 CC amplifying the desired region of PR1 gene in pCZR150 plasmid  
 XX  
 SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAD02427 (1-18)  
 QY 32 ValVallysArgArg 36  
 Db 2 GTTGTAACGACGG 16  
 RESULT 158  
 AAD09752  
 ID AAD09752 standard; DNA; 18 BP.  
 XX  
 AC AAD09752;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE ZC976 PCR primer, to construct zCytol8-CBE/pZBV32L expression vector.  
 XX  
 KW Mouse; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;  
 KW cancer; inflammation; gene therapy; PCR primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN W0200146422-A1.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 22-DEC-2000; 2000WO-US035308.  
 XX  
 PR 23-DEC-1999; 99US-00471767.  
 PR 01-DEC-2000; 2000US-0250841P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Presnell SR, Kindavogel W;  
 XX  
 DR WPI; 2001-408648/43.  
 XX  
 PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.  
 XX  
 PS Example 18A; Page 163; 167pp; English.  
 XX  
 CC The patent discloses novel human cytokine, ZCYTO18 protein and its  
 CC corresponding DNA. ZCYTO18 protein induces proliferation of cells  
 CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in  
 CC X5626 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in

CC a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer  
 CC and inflammation. ZCYTO18 protein is useful for killing cancer cells. It  
 CC is useful for increasing platelets in a patient or injured tissue. It is  
 CC also used in gene therapy. The present sequence is PCR primer, ZC976  
 CC which is used in the construction of C-terminal Glu-Glu (CEE) tagged  
 CC zCytol8/pZBV32L expression vector  
 XX  
 SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAD09752 (1-18)  
 QY 32 ValVallysArgArg 36  
 Db 2 GTTGTAACGACGG 16  
 RESULT 159  
 AAF57008  
 ID AAF57008 standard; DNA; 18 BP.  
 XX  
 AC AAF57008;  
 XX  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE P. methanolica PRB1 DNA amplifying primer ZC976.  
 XX  
 KW Pichia methanolica; auxotrophic; chromosomal locus; protease; PRB1;  
 KW proteinase A; proteinase B; alcohol oxidase; fermentation; PCR primer;  
 KW nutritional marker; ss.  
 XX  
 OS Pichia methanolica.  
 XX  
 PN US6183953-B1.  
 XX  
 PD 06-FEB-2001.  
 XX  
 PF 30-DEC-1997; 97US-00001141.  
 PR 15-SEP-1997; 97US-0058822P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Raymond CK;  
 XX  
 DR WPI; 2001-201998/20.  
 XX  
 PT Altering chromosomal locus in Pichia methanolica cells for large-scale  
 PT protein production, by transforming the cells with DNA construct  
 PT comprising target locus having altered nucleotide pair and selectable  
 PT marker.  
 XX  
 PS Example 3; Col 39-40; 27pp; English.  
 XX  
 CC The invention relates to altering a chromosomal locus in Pichia  
 CC methanolica cells (C) auxotrophic for adenine that comprises introducing  
 CC a DNA construct containing a segment with a portion of target locus  
 CC having an altered nucleotide pair and a selectable marker that  
 CC complements adenine auxotrophy, into (C) and identifying a subset of (C)  
 CC in which the DNA construct has been chromosomally integrated, thereby  
 CC altering the locus. The method is useful for altering a selected  
 CC chromosomal locus, especially a nutritional marker or a locus that  
 CC encodes a protease, such as proteinase A or B and/or an alcohol oxidase  
 CC of P. methanolica cells. The method is thus useful for designing strains  
 CC of P. methanolica for use in large-scale fermentation for protein  
 CC production. Sequences AAF57007-57008 represents PCR primers for  
 CC amplifying the P. methanolica PRB1 DNA

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAP57008 (1-18)  
 QY 32 ValVallysArgArg 36  
 DB 2 GTTGTAAACGACGG 16

RESULT 160  
 AAH47591/C  
 ID AAH47591 standard; DNA; 18 BP.  
 XX AC AAH47591;  
 XX 30-NOV-2001 (first entry)  
 XX Human Her-3 mRNA inhibiting antisense oligo ISIS # 19606.  
 XX Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;  
 XX antiinflammatory; cytostatic; antibacterial; antisense; ss.  
 XX Synthetic.  
 XX Homo sapiens.  
 XX US6277640-B1.  
 XX 21-AUG-2001.  
 XX 31-JUL-2000; 2000US-00630706.  
 XX 31-JUL-2000; 2000US-00630706.  
 XX (ISIS-) ISIS PHARM INC.  
 XX Bennett CF, Cowser LM;  
 XX WPI; 2001-535134/59.  
 XX Antisense compounds capable of modulating expression of human Her-3.  
 XX member of epidermal growth factor family of receptor/tyrosine kinases,  
 XX useful for preventing or delaying infection, inflammation or tumor  
 XX formation.  
 XX Claim 1; Col 43-44; 49pp; English.

XX CC The invention provides antisense compounds capable of inhibiting the  
 XX expression of human Her-3, a member of epidermal growth factor (EGF)  
 XX family of receptor/tyrosine kinases. The antisense oligonucleotides are  
 XX useful for inhibiting the expression of Her-3 in cells or tissues. They  
 XX are commonly used as research reagents and in diagnostics for example, to  
 XX elucidate the function of particular genes. The antisense compounds are  
 XX also useful for distinguishing between functions of various members of a  
 XX biological pathway and for research use. They are also utilized for  
 XX diagnostics, therapeutics, prophylaxis and in kits. They are useful  
 XX prophylactically, e.g. to prevent or delay infection, inflammation or  
 XX tumor formation. Sequences AAH4752-47615 represent chimeric antisense  
 XX phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap,  
 XX used for the inhibition of Her-3 mRNA expression

XX SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH47591 (1-18)  
 QY 186 ValAspAspleuArg 190  
 DB 17 GTTGATGACCTCGG 3

RESULT 161  
 AAC91084  
 ID AAC91084 standard; DNA; 18 BP.  
 XX AC AAC91084;  
 XX 19-MAR-2001 (first entry)  
 XX Primer ZC976.  
 XX Cytokine; zsig 81; wound healing; proliferation; differentiation;  
 XX migration; metabolism; ss.  
 XX Unidentified.  
 XX OS  
 XX WO200073459-A1.  
 XX 07-DEC-2000.  
 XX 01-JUN-2000; 2000WO-US015002.  
 XX 01-JUN-1999; 99US-00323582.  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX Piddington CS, West JR, Holly RD, Burkhead SK;  
 XX WPI; 2001-061540/07.  
 XX New zsig81 polypeptides and polynucleotides useful for e.g. promoting  
 XX wound healing, or in diagnosing or treating disorders associated with  
 XX cell loss or abnormal cell proliferation, such as cancer.  
 XX Example 5; Page 105; 109pp; English.

XX CC The present invention relates to zsig81 and fragments thereof. The  
 XX invention is useful for promoting wound healing, for modulating the  
 XX proliferation, differentiation, migration or metabolism of responsive  
 XX cell types that includes both primary and cultured cell lines, and for  
 XX stimulating the proliferation of cells expressing markers associated with  
 XX dendritic lineage cells

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAC91084 (1-18)  
 QY 32 ValVallysArgArg 36  
 DB 2 GTTGTAAACGACGG 16

RESULT 162  
 AAP55422  
 ID AAP55422 standard; DNA; 18 BP.  
 XX

AC AAF55422;  
 XX  
 DT 29-MAY-2001 (first entry)  
 XX  
 DE PCR primer for a probe for the PRB1 gene.  
 XX  
 DE Glyceraldehyde-3-phosphate dehydrogenase; GAPDH; GAP2; GAP1; PRB1;  
 KW GAPDH promoter; GAPDH terminator; methylotrophic yeast; PCR primer; ss.  
 XX  
 XX Saccharomyces cerevisiae.  
 OS  
 XX WO200118182-A1.  
 PN  
 XX 15-MAR-2001.  
 XX  
 PD 01-SEP-2000; 2000WO-US024110.  
 XX  
 PF 08-SEP-1999; 99US-00391951.  
 XX  
 PR (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PA Raymond CK;  
 XX  
 PI WPI; 2001-235197/24.  
 XX  
 DR New transcription promoter and terminator sequences from Pichia  
 XX methanolica, useful within DNA constructs for producing proteins of  
 PT economic importance, e.g. industrial enzymes, proteins for research or  
 PT pharmaceutical proteins.  
 PT  
 XX Example 4; Page 40; 43pp; English.  
 XX  
 XX PCR primers AAF55421-22 were used to amplify a probe for the PRB1 gene.  
 CC The amplified sequence was used to construct a Pichia methanolica strain  
 CC deficient for vacuolar proteases. The specification describes GAP1 and  
 CC GAP2 gene fragments. GAP gene encode glyceraldehyde-3-phosphate  
 CC dehydrogenase (GAPDH). GAPDH transcription promoter and terminator  
 CC sequences are useful, within DNA constructs, in methylotrophic yeast for  
 CC producing polypeptides of economic importance, including industrial  
 CC enzymes, proteins for research or pharmaceutical proteins. In particular,  
 CC these proteins include lipases, cellulases or proteases, enzyme  
 CC inhibitors (e.g. protease inhibitors), growth factors (e.g. platelet  
 CC derived growth factor, fibroblast growth factors, epidermal growth  
 CC factor, or vascular endothelial growth factors), glutamic acid  
 CC decarboxylase (GAD); cytokines (e.g. erythropoietin, colony stimulating  
 CC factors, interleukins or interleukin antagonists); hormones (e.g.  
 CC insulin, proinsulin, leptin or glucagon), or receptors (e.g. growth  
 CC factor receptors)  
 XX  
 SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 5 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAF55422 (1-18)  
 QY 32 ValVallysArgArg 36  
 Db 2 GTTGTAACGACGCG 16  
 RESULT 163  
 AAH26911  
 ID AAH26911 standard; DNA; 18 BP.  
 XX  
 XX AAH26911;  
 AC  
 XX 21-DEC-2001 (first entry)  
 DT  
 XX

DE Fluorescent oligonucleotide target for electronic hybridisation.  
 XX  
 KW Capture probe; hybridisation; electronics; photonics; nanotechnology; ss.  
 XX  
 XX Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1/\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "fluorescent dye with 493 nm absorption and 503 nm  
 FT emission"  
 XX  
 PN WO200153799-A1.  
 XX  
 XX 26-JUL-2001.  
 PD  
 XX 12-JAN-2001; 2001WO-US000926.  
 PF  
 XX 24-JAN-2000; 2000US-00489855.  
 XX  
 XX (NANO-) NANOGEN INC.  
 PA  
 XX Edman CF, Heller MJ, Gurtner C, Formosa R;  
 PI WPI; 2001-607116/69.  
 XX  
 DR Device for photoelectric transport of charged materials in liquid  
 XX environment for micro- and opto- electronic devices, has a substrate  
 PT generating light induced current, conductor, permeation layer and light  
 PT source to illuminate substrate.  
 PT  
 XX Disclosure; Page 60; 119pp; English.  
 XX  
 XX The present sequence is that of fluorescent target oligonucleotide T2,  
 CC which was used to demonstrate an electron hybridisation method of the  
 CC invention. Mn2O3 stabilised n-type silicon photoelectrodes coated with a  
 CC streptavidin-agarose permeation layer were shown to constitute a simple  
 CC platform for rapid manipulation of DNA oligonucleotides by electron  
 CC hybridisation. In this process, a set of unlabelled oligonucleotides  
 CC (capture strands) are first targeted to specific locations and anchored.  
 CC A second set of fluorescent labeled oligonucleotides (target strands) is  
 CC then targeted to the same locations and actively hybridised to the  
 CC capture strands. In the example provided, 2 sets of biotinylated capture  
 CC probes, C1 (see AAH26908) and C2 (see AAH26909), were successively  
 CC transported and anchored to 4 different locations on a streptavidin-  
 CC agarose and Mn2O3 coated amorphous silicon substrate. 2 Fluorescence  
 CC labeled target sequences, T1 (see AAH26910) and T2 (present sequence),  
 CC were then transported to a location with complementary capture probes and  
 CC a location with non-complementary capture probes. This step produced 2  
 CC clearly detectable fluorescence signals at the 2 locations with matching  
 CC sequences. The ratio between signal and non-specific background was  
 CC better than 4. The method allows for detection of DNA oligonucleotides in  
 CC an extremely short time. The invention generally provides systems and  
 CC devices for photoelectroretro transport and hybridisation of  
 CC oligonucleotides. The techniques of the invention have wide use in  
 CC manufacture of micro electronic and opto electronic devices. Self-  
 CC assembly fabrication techniques based on DNA polymers enables micron, sub  
 CC -micron or nanoscale devices to be fabricated  
 XX  
 SQ Sequence 18 BP; 5 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 5 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAH26911 (1-18)  
 QY 56 HisValGluteuLeu 60

Db	2	CACGTAGAACTGCTA 16	3	CTCCACAGAGCTGGA 17
RESULT 164	RESULT 165			
AAS43573	AAS43571			
ID AAS43573 standard; DNA; 18 BP.	ID AAS43571 standard; DNA; 18 BP.			
XX AC AAS43573;	XX AC AAS43571;			
XX DT 18-DEC-2001 (first entry)	XX DT 18-DEC-2001 (first entry)			
XX DE Corneodesmosin PCR primer #43.	XX DE Corneodesmosin PCR primer #41.			
XX KW Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;	XX KW Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;			
XX KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.	XX KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.			
XX OS Homo sapiens.	XX OS Homo sapiens.			
XX FN WO200162788-A2.	XX FN WO200162788-A2.			
XX PD 30-AUG-2001.	XX PD 30-AUG-2001.			
XX PF 23-FEB-2001; 2001WO-GB000795.	XX PF 23-FEB-2001; 2001WO-GB000795.			
XX PR 23-FEB-2000; 2000GB-00004312.	XX PR 23-FEB-2000; 2000GB-00004312.			
XX PA (OXAG-) OXAGEN LTD.	XX PA (OXAG-) OXAGEN LTD.			
XX PI Olaveson M, Lench N, Allen M, Tazi-Ahmini R;	XX PI Olaveson M, Lench N, Allen M, Tazi-Ahmini R;			
XX DR WPI; 2001-570627/64.	XX DR WPI; 2001-570627/64.			
XX CC Corneodesmosin protein and polynucleotide encoding it, having one or more	XX CC Corneodesmosin protein and polynucleotide encoding it, having one or more			
XX PT polymorphisms useful in treating, diagnosing or determining	XX PT polymorphisms useful in treating, diagnosing or determining			
XX PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory	XX PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory			
XX PS diseases.	XX PS diseases.			
XX PS Disclosure; Page 36; 60pp; English.	XX PS Disclosure; Page 36; 60pp; English.			
XX CC The invention relates to corneodesmosin protein (I) and nucleic acid (II)	XX CC The invention relates to corneodesmosin protein (I) and nucleic acid (II)			
XX CC encoding the corneodesmosin gene, where the gene comprises a base	XX CC encoding the corneodesmosin gene, where the gene comprises a base			
XX CC substitution, deletion or insertion at one or more positions. (I) and	XX CC substitution, deletion or insertion at one or more positions. (I) and			
XX CC (II) are useful for screening for agents for use in prognosis, diagnosis	XX CC (II) are useful for screening for agents for use in prognosis, diagnosis			
XX CC and treatment of individuals having or being susceptible to	XX CC and treatment of individuals having or being susceptible to			
XX CC corneodesmosin-mediated disease, by monitoring the reaction between the	XX CC corneodesmosin-mediated disease, by monitoring the reaction between the			
XX CC molecules and the agents. The nucleotide and amino acid polymorphisms are	XX CC molecules and the agents. The nucleotide and amino acid polymorphisms are			
XX CC useful for diagnosing or determining susceptible to corneodesmosin-	XX CC useful for diagnosing or determining susceptible to corneodesmosin-			
XX CC mediated disease, which facilitates subsequent treatment of the disease	XX CC mediated disease, which facilitates subsequent treatment of the disease			
XX CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)	XX CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)			
XX CC are useful in diagnostic, prognostic or therapeutic methods and as	XX CC are useful in diagnostic, prognostic or therapeutic methods and as			
XX CC research tools for e.g. in drug screening. (II) is useful as probes or	XX CC research tools for e.g. in drug screening. (II) is useful as probes or			
XX CC primers for detecting an allele of the polymorphism or in the regulation	XX CC primers for detecting an allele of the polymorphism or in the regulation			
XX CC of corneodesmosin gene. Antibodies which binds to (I) are useful for	XX CC of corneodesmosin gene. Antibodies which binds to (I) are useful for			
XX CC screening DNA clone libraries for cells secreting the antigen. (II) is	XX CC screening DNA clone libraries for cells secreting the antigen. (II) is			
XX CC useful as a model to investigate the role of corneodesmosin in normal	XX CC useful as a model to investigate the role of corneodesmosin in normal			
XX CC skin function. AAS43492-AAS43749 represent corneodesmosin coding	XX CC skin function. AAS43492-AAS43749 represent corneodesmosin coding			
XX CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the	XX CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the			
XX CC invention	XX CC invention			
XX SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 0 Other;	XX SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 0 Other;			
Alignment Scores:	Alignment Scores:			
Pred. No.: 8.57e+03	Pred. No.: 8.57e+03			
Score: 5.00	Score: 5.00			
Length: 18	Length: 18			
Matches: 5	Matches: 5			
Conservative: 0	Conservative: 0			
Percent Similarity: 100.00%	Percent Similarity: 100.00%			
Best Local Similarity: 100.00%	Best Local Similarity: 100.00%			
Mismatches: 0	Mismatches: 0			
Query Match: 2.53%	Query Match: 2.53%			
Indels: 0	Indels: 0			
Gaps: 0	Gaps: 0			
DB:	DB:			
US-09-966-880A-8 (1-198) x AAS43573 (1-18)	US-09-966-880A-8 (1-198) x AAS43571 (1-18)			
QY 129 LeuHisArgAlaGly 133	QY 129 LeuHisArgAlaGly 133			
Db 3 CTCCACAGAGCTGGA 17	Db 3 CTCCACAGAGCTGGA 17			



RESULT 166  
AA543567  
ID AA543567 standard; DNA; 18 BP.  
XX  
AC AA543567;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Corneodesmosin PCR primer #37.  
XX  
KW Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;  
KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200162788-A2.  
XX  
PD 30-AUG-2001.  
XX  
PF 23-FEB-2001; 2001WO-GB000795.  
XX  
PR 23-FEB-2000; 2000GB-00004312.  
XX  
PA (OXAG-) OXAGEN LTD.  
XX  
PI Olaveson M, Lench N, Allen M, Tazi-Ahmini R;  
XX  
DR WPI; 2001-570627/64.  
XX  
XX Corneodesmosin protein and polynucleotide encoding it, having one or more  
PT polymorphisms useful in treating, diagnosing or determining  
PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory  
PT diseases.  
XX  
PS Disclosure; Page 36; 60pp; English.  
XX  
CC The invention relates to corneodesmosin protein (I) and nucleic acid (II)  
CC encoding the corneodesmosin gene, where the gene comprises a base  
CC substitution, deletion or insertion at one or more positions. (I) and  
CC (II) are useful for screening for agents for use in prognosis, diagnosis  
CC and treatment of individuals having or being susceptible to  
CC corneodesmosin-mediated disease, by monitoring the reaction between the  
CC molecules and the agents. The nucleotide and amino acid polymorphisms are  
CC useful for diagnosing or determining susceptibility to corneodesmosin-  
CC mediated disease, which facilitates subsequent treatment of the disease  
CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)  
CC are useful in diagnostic, prognostic or therapeutic methods and as  
CC research tools for e.g. in drug screening. (II) is useful as probes or  
CC primers for detecting an allele of the polymorphism or in the regulation  
CC of corneodesmosin gene. Antibodies which binds to (I) are useful for  
CC screening DNA clone libraries for cells secreting the antigen. (II) is  
CC useful as a model to investigate the role of corneodesmosin in normal  
CC skin function. AA543492-AA543749 represent corneodesmosin coding  
CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the  
CC invention  
XX  
SQ Sequence 18 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 5 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AA543567 (1-18)  
  
QY 129 LeuHisArgAlaGly 133  
DB 3 CTCACAGACTGGA 17

RESULT 167  
AAK98893  
ID AAK98893 standard; DNA; 18 BP.  
XX  
AC AAK98893;  
XX  
DT 24-MAY-2002 (first entry)  
XX  
DE PCR primer ZC976 for amplification of Pichia methanolica gene PRB1.  
XX  
KW Glyceraldhyde-3-phosphate dehydrogenase 2; GAP2; industrial; cytokine;  
KW pharmaceutical; unglycosylated; enzyme; hormone; growth factor; PCR;  
KW primer; ss.  
XX  
OS Unidentified.  
XX  
PN US6348331-B1.  
XX  
PD 19-FEB-2002.  
XX  
PF 01-SEP-2000; 2000US-00653403.  
XX  
PR 08-SEP-1999; 99US-0152744P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Raymond CK;  
XX  
DR WPI; 2002-266520/31.  
XX  
XX New Pichia methanolica glyceraldhyde-3-phosphate dehydrogenase 2 gene  
PT promoter, useful for producing desired protein in cultured yeast cell  
PT which is functionally deficient in vacuolar proteases proteinase A and  
PT proteinase B.  
XX  
PS Example 4; Col 35; 20pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising Pichia  
CC methanolica glyceraldhyde-3-phosphate dehydrogenase 2 gene (GAP2)  
CC promoter, of up to 5000 nucleotides comprising nucleotide 93-1080 of a  
CC fully defined nucleotide sequence of 3333 base pairs as given in the  
CC specification. A Pichia methanolica cell containing a DNA construct is  
CC useful for producing a desired protein by culturing the cell, where a DNA  
CC segment (other than GAP2) is expressed and desired protein is produced,  
CC and recovering the desired protein from the cultured cell, where the  
CC proteins are preferably of research, industrial, or pharmaceutical  
CC interest e.g. unglycosylated pharmaceutical proteins. Proteins include  
CC enzymes, cytokines, hormones and growth factors. This polynucleotide  
CC sequence represents a PCR primer for amplification of the Pichia  
CC methanolica gene PRB1  
XX  
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAK98893 (1-18)  
  
QY 32 ValVallyysArgArg 36  
DB 2 GTTGTAAACGACGG 16

RESULT 168  
ABK91359  
ID ABK91359 standard; DNA; 18 BP.  
XX  
AC ABK91359;  
XX

DT 15-NOV-2002 (first entry)  
XX Pichia methanolica PRB1 gene, PCR primer ZC976.  
DE  
DE Glyceraldehyde-3 phosphate dehydrogenase; GAPDH; PRB1; yeast; primer; ss;  
XX enzyme production; enzyme inhibitor production; growth factor; PCR;  
KW cytokine; interleukin; hormone; unglycosylated pharmaceutical protein.  
XX  
XX Pichia methanolica.  
OS  
XX  
XX US2002086366-A1.  
PN  
XX 04-JUL-2002.  
PD  
XX  
XX 07-DEC-2001; 2001US-00013784.  
PF  
XX  
XX 08-SEP-1999; 99US-0152744P.  
PR  
XX 01-SEP-2000; 2000US-00653403.  
PR  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX  
XX Raymond CK;  
PI  
XX  
XX WPI; 2002-635677/68.  
DR  
XX  
XX Novel isolated DNA molecule useful within DNA constructs for producing  
PT polypeptides of economical importance including industrial enzymes and  
PT pharmaceutical proteins, in cultured Pichia methanolica cells.  
PT  
XX  
XX Example 4; Page 19; 21pp; English.  
PS  
XX  
XX The invention relates to an isolated DNA molecule comprising a DNA  
CC construct comprising operably linked elements of a first DNA segment with  
CC a functional transcription promoter or Pichia methanolica gene  
CC  
CC transcription promoter, a second DNA segment encoding a protein of  
CC interest other than P. methanolica glyceraldehyde-3-phosphate  
CC dehydrogenase or P. methanolica protein, and a third DNA segment  
CC comprising a transcription terminator. A P. methanolica cell containing  
CC the DNA construct is useful for producing protein of interest, where the  
CC second DNA segment is expressed and the protein of interest is produced  
CC and recovered from the cultured cell. The transformed cell is useful for  
CC producing polypeptides of economical importance including industrial  
CC enzymes and pharmaceutical proteins, for producing proteins of research,  
CC industrial, or pharmaceutical interest. The proteins include enzymes such  
CC as lipase, cellulase, and protease, enzyme inhibitor including protease  
CC inhibitors, growth factors such as platelet derived growth factor (PDGF),  
CC fibroblast growth factors (FGF), epidermal growth factor (EGF), vascular  
CC endothelial growth factors (VEGFs), glutamic acid decarboxylase (GAD),  
CC cytokines, such as erythropoietin, thrombopoietin, colony stimulating  
CC factors, interleukins, and interleukin antagonist, hormones such as  
CC insulin, proinsulin, leptin, and glucagon, and receptors, including  
CC growth factor receptors, which are expressed in truncated form or as  
CC fusion proteins with, e.g., immunoglobulin constant region sequences. The  
CC transformed cell is also useful for producing unglycosylated  
CC pharmaceutical proteins. The present sequence represents a P. methanolica  
CC PRB1 gene, PCR primer  
XX  
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x ABK91359 (1-18)  
QY 32 ValVallVsAysAgx 36  
Db 2 GTTGTAAACGACGG 16

RESULT 169  
ABK49997  
ID ABK49997 standard; DNA; 18 BP.  
XX  
XX AC ABK49997;  
AC  
XX 15-JUL-2002 (first entry)  
DI  
XX Human ZTMPO-1 sequencing primer ZC976.  
DE  
XX ZTMPO; human; immunosuppressive; inotropic; cardiac; leukaemia; cardiac;  
KW cytostatic; antidiabetic; hypotensive; immunological; ss; reproductive;  
KW muscle pathology; diabetes; muscular dystrophy; haematopoietic disorder;  
KW hypertension; chromosome 12q24.33; sequencing; primer; ZC976.  
XX  
OS Homo sapiens.  
XX  
XX US6372889-B1.  
FN  
XX 16-APR-2002.  
PD  
XX 19-APR-1999; 99US-00294531.  
PF  
XX 21-APR-1998; 98US-0082513P.  
PR  
XX (ZYMO ) ZYMOGENETICS INC.  
PA  
XX Sheppard PO, Conklin DC, Farrah TM, Maurer MF, Grossmann A;  
PI  
XX WPI; 2002-350566/38.  
DR  
XX Novel isolated ZTMPO-1 polypeptide, useful for modulating cell  
PT proliferation, and for treating disorders such as diabetes, muscular  
PT dystrophy and hypertension.  
PT  
XX Example 1; Col 59; 40pp; English.  
PS  
XX This invention relates to the cDNA and protein sequences of a novel  
CC isolated ZTMPO-1 polypeptide. ZTMPO-1 is a soluble protein with homology  
CC to the nuclear membrane proteins emerin and thymoposins. The protein of  
CC the invention may have immunosuppressive, inotropic, cardiac,  
CC cytosolic, antidiabetic and hypotensive activities. The invention also  
CC comprises antibodies to ZTMPO-1 proteins which can be used to detect  
CC ZTMPO proteins and may be used to regulate the function of the protein.  
CC The sequences of the invention may be used for modulating cellular  
CC proliferation and differentiation, and for diagnostic purposes. The  
CC polypeptides can be used to treat immunological, reproductive, cardiac,  
CC and muscle pathologies, such as diabetes, muscular dystrophy,  
CC haematopoietic disorders, leukaemias, and hypertension. The present  
CC sequence represents a human ZTMPO-1 gene sequencing primer used to  
CC sequence the ZTMPO gene of the invention  
XX  
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0  
US-09-966-880A-8 (1-198) x ABK49997 (1-18)  
QY 32 ValVallVsAysAgx 36  
Db 2 GTTGTAAACGACGG 16  
RESULT 170  
AAS20707  
ID AAS20707 standard; DNA; 18 BP.  
XX  
XX AAS20707;  
AC

```

XX 09-APR-2002 (first entry)
XX Human zalphall Ligand bacmid DNA, transposable element PCR primer ZC976.
XX
XX Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation;
XX B-cell proliferation; anti-tumour response; immune system;
XX immunostimulant; cytostatic; human; PCR primer; ss.
XX
XX Synthetic.
XX
XX US6307024-B1.
XX
XX 23-OCT-2001.
XX
XX 09-MAR-2000; 2000US-00522217.
XX
XX 09-MAR-1999; 99US-01233547P.
XX
XX 11-MAR-1999; 99US-0123304P.
XX
XX 01-JUL-1999; 99US-0142013P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI; 2002-040208/05.
XX
XX New zalphall ligand polypeptides and polynucleotides, useful for
XX stimulating proliferation, activation, differentiation and/or induction
XX of inhibition of specialized cell function, or for stimulating an
XX antigenic response.
XX
XX Example 30; Col 155; 105pp; English.
XX
XX The present invention relates to the isolation of a novel cytokine,
XX zalphall Ligand and the polynucleotide encoding it. The invention also
XX gives the sequence for the zalphall receptor and the polynucleotide
XX encoding it. The zalphall Ligand polypeptide stimulates proliferation of
XX natural killer (NK) cells or NK cell progenitors, the activation of NK
XX cells, proliferation of T-cells, proliferation of B-cells stimulated with
XX anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
XX reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
XX zalphall Ligand polypeptide is also useful in preparing antibodies that
XX bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
XX be used as probes or primers to clone regions of a zalphall Ligand gene,
XX and in gene therapy. Zalphall Ligand may also be used to identify
XX inhibitors of its activity, to enhance the generation of anti-tumour
XX responses with or without the infusion of donor lymphocytes, and to
XX activate or stimulate the immune system. The present sequence represents
XX a PCR primer used in the methods of the present invention
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAS20707 (1-18)
XX
XX Qy 32 ValValValysArgArg 36
XX
XX Db 2 GTTGTAAACGACGG 16
XX
XX RESULT 171
XX ABK91070
XX ID ABK91070 standard; DNA; 18 BP.
XX

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AC ABK91070;
XX
XX 05-NOV-2002 (first entry)
XX
XX Rice Hd3a gene associated primer #2.
XX
XX Rice; Hd3a; linkage analysis; flowering time; improved plant breed;
XX cultivation region; cultivation time; rice cultivar; primer; ss.
XX
XX Unidentified.
XX
XX WO200242475-A1.
XX
XX 30-MAY-2002.
XX
XX 22-NOV-2001; 2001WO-JP010237.
XX
XX 24-NOV-2000; 2000JP-00356839.
XX
XX (NAAAG-) NAT INST AGRICULTURAL SCI.
XX (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
XX
XX Yano M, Kojima S;
XX
XX WPI; 2002-490207/52.
XX
XX Hd3a gene for inducing flowering of plants with modification to flowering
XX time by transferring the gene or controlling its expression, useful in
XX improving plant breeds, e.g. rice to adapt cultivation region and time.
XX
XX Example 6; Page 20; 66pp; Japanese.
XX
XX The present invention relates to the isolation of a rice gene and the
XX encoding Hd3a protein. The Hd3a gene is isolated by linkage analysis. The
XX Hd3a gene induces flowering in plants. The Hd3a gene can be used for
XX improving plant breeds, e.g. rice to adapt cultivation region and time,
XX with modification to flowering time by transferring the Hd3a gene or
XX controlling its expression. By applying this gene, a rice cultivar can be
XX obtained conveniently with reliability in a short period of time. The
XX present sequence represents a primer used in the examples of the present
XX invention
XX
XX Sequence 18 BP; 4 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x ABK91070 (1-18)
XX
XX Qy 38 SerAlaThrSerPhe 42
XX
XX Db 4 TCAGCAACGAGTTTC 18
XX
XX RESULT 172
XX AAD38796
XX ID AAD38796 standard; DNA; 18 BP.
XX
XX AC AAD38796;
XX
XX 23-SEP-2002 (first entry)
XX
XX Zlmda24 amplifying PCR primer, ZC976.
XX
XX Zlmda24; alpha-helical protein; cytokine-like polypeptide; gene therapy;
XX educational tool; molecular biology; immunocontraceptive;
XX protein chemistry; sperm capacitation; proliferation; differentiation;
XX antifertility vaccine; induction; haematopoiesis; immune function; PCR;
XX primer; ss.

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XX OS Unidentified.
XX PN WO200234917-A2.
XX PD 02-MAY-2002.
XX PF 19-OCT-2001; 2001WO-US045508.
XX PR 20-OCT-2000; 2000US-0242023P.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Conklin DC, Gao Z, Lofton-Day CE, Whitmore TE;
XX PS WPI; 2002-471440/50.
XX DR Novel Zlmda24 polypeptide, a cytokine-like polypeptide with antiparallel
XX PT alpha helical structure, useful as a diagnostic to detect the presence of
XX PT disease in testis tissue.
XX PS Example 5; Page 131; 133pp; English.
XX CC The invention relates to secreted alpha-helical protein, zlmda24 which is
XX CC a cytokine-like polypeptide, and its corresponding nucleic acid. Zlmda24
XX CC is useful for identifying and isolating Zlmda24 ligands, and as antigen
XX CC to produce anti-Zlmda24 antibodies. Zlmda24 DNA is used gene therapy.
XX CC Zlmda24 DNA is also useful as educational tool in laboratory practical
XX CC kits for courses related to genetics, molecular biology, protein
XX CC chemistry, and antibody production and analysis. It is also useful as an
XX CC aid to prepare expression constructs for bacterial, viral or mammalian
XX CC expression, including fusion constructs, for determining the restriction
XX CC endonuclease cleavage sites of the polynucleotides, determining mRNA and
XX CC DNA localisation of zlmda24 polynucleotides in tissues, and for
XX CC identifying related polynucleotides and polypeptides by nucleic acid
XX CC hybridisation. Zlmda24 is also useful as an aid to teach preparation of
XX CC antibodies, identifying proteins by Western blotting, protein
XX CC purification, determining the weight of expressed zlmda24 polypeptides as
XX CC a ratio of total protein expressed, identifying peptide cleavage sites,
XX CC coupling amino and carboxyl terminal tags, amino acid sequence analysis,
XX CC for teaching analytical skills, and for monitoring biological activities
XX CC of both the native and tagged protein in vitro and in vivo. Zlmda24 is
XX CC useful for modulating sperm capacitation, and as germ-cell specific
XX CC antigens for used as immunoc contraceptive or antiferility vaccines to
XX CC induce formation of Ab and/or cell mediated immunity to selectively
XX CC inhibit reproduction in humans or animals. Zlmda24 is also useful for
XX CC stimulating proliferation activation, differentiation and/or induction
XX CC or inhibition of specialised cell function of cells involved in
XX CC haematopoiesis and immune function. The present sequence is a PCR primer
XX CC used for amplifying zlmda24 cDNA. This sequence is used for viral
XX CC generation of zlmda24-CEB/pZBV32L
XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AAD38796 (1-18)
QY 32 ValVallysArgArg 36
Db 2 GTTGTAAACGACGG 16
RESULT 173
ABSS4171
ID ABSS4171 standard; DNA; 18 BP.
XX ABSS4171;
AC

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XX 26-NOV-2002 (first entry)
XX Human RING finger protein zapop3, sequencing primer #2.
XX Human; ss; zapop3; RING finger; chromosome 9q34.11; gene therapy;
XX myeloid leukaemia; chronic myelogenous leukaemia; myelocytic leukaemia;
XX lymphoblastic leukaemia; retinitis pigmentosa-deafness syndrome 1;
XX myocardial infarction; congestive heart failure; heart attack;
XX heart transplantation; angiogenesis; wound healing; angioplasty;
XX endarterectomy; coronary collateral circulation; revascularisation;
XX diabetic foot ulcer; stroke; cancer; coronary reperfusion; primer;
XX cardiac function; skeletal muscle neogenesis; hyperplasia;
XX kidney regeneration; systemic hypertension; pulmonary hypertension.
XX OS Homo sapiens.
XX PN US6440697-B1.
XX PD 27-AUG-2002.
XX PF 04-NOV-1999; 99US-00434408.
XX PR 12-NOV-1998; 98US-0108258P.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Venezia D, Grossmann A;
XX DR WPI; 2002-705357/76.
XX PT Novel expression vector comprising DNA segment encoding zapop3
XX PT polypeptide, useful for producing transformed cells expressing zapop3
XX PT polypeptide (a RING finger protein).
XX PS Example 1; Col 55; 48pp; English.
XX CC The invention relates to an expression vector comprising the following
XX CC operably linked elements: a transcription promoter; a DNA segment
XX CC encoding a polypeptide having a zapop3 (a RING finger protein) sequence;
XX CC and a transcription terminator, where the promoter is operably linked to
XX CC the DNA segment which is in turn operably linked to the transcription
XX CC terminator. The vector introduced into a cell and the protein expressed.
XX CC The cell is useful for producing the zapop3 polypeptide. The vector is
XX CC useful in gene therapy techniques to increase or inhibit zapop3 activity.
XX CC zapop3 polypeptide is useful for treating disorders associated with
XX CC myocardial infarction, congestive heart failure, hypertrophic
XX CC cardiomyopathy and dilated cardiomyopathy, for limiting infarct size
XX CC following a heart attack, aiding in recovery after heart transplantation,
XX CC promoting angiogenesis, and wound healing following angioplasty or
XX CC endarterectomy, to develop coronary collateral circulation, for
XX CC revascularisation in the eye, for complications related poor circulation
XX CC such as diabetic foot ulcer, for stroke, cancer, following coronary
XX CC reperfusion, and other indications, where angiogenesis is desired. The
XX CC polypeptide is also useful for improving cardiac function, inducing
XX CC skeletal muscle neogenesis and/or hyperplasia, kidney regeneration and/or
XX CC for treating systemic and pulmonary hypertension. The polypeptide is also
XX CC useful for identifying modulators of zapop3 activity, and for producing
XX CC antibodies. The gene for zapop3 is located on chromosome 9q34.11 an area
XX CC associated with myeloid leukaemia, chronic myelogenous leukaemia,
XX CC myelocytic leukaemia, lymphoblastic leukaemia and retinitis pigmentosa-
XX CC deafness syndrome 1. The present sequence is a sequencing primer for the
XX CC cDNA encoding zapop3
XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 8.57e+03 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

```

US-09-966-880A-8 (1-198) x ABS54171 (1-18)

QY 32 ValVallysArgArg 36  
 Db 2 GTTGTAACGACGG 16

RESULT 174

ABZ95417  
 ID ABZ95417 standard; DNA; 18 BP.

AC ABZ95417;

DT 17-OCT-2003 (first entry)

DE Human fibronectin antisense fragment no.1281.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

PN WO200285308-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013135.

PR 24-APR-2001; 2001US-0286137P.

PA (EPIC-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.

PS Disclosure; SEQ ID NO 10659; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 18 BP; 0 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Alignment Scores: 8.57e+03 Length: 18  
 Pred. No.:

Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABZ95417 (1-18)

QY 59 LeuLeuPheLeuArg 63

Db 4 CTCCTGTTCTCCGT 18

RESULT 175

ABX93718

ID ABX93718 standard; DNA; 18 BP.

AC ABX93718;

DT 04-JUN-2003 (first entry)

DE Human zsig58 cDNA sequencing primer #1.

KW Human; zsig58; ss; gonadal development; pregnancy; pubertal change;  
 KW menopause; ovarian cancer; fertility; ovarian function; pancreas; primer;  
 KW polycystic ovarian syndrome; diabetes; eye disease; pituitary function;  
 KW osteoporosis; bone disease; wound healing; bacterial infection;  
 KW viral infection; fungal infection; analgesic; antidiabetic; vulneryary;  
 KW gynaecological; osteopathic; cytostatic; ophthalmological; sequencing.

OS Homo sapiens.

PN US2002182677-A1.

PD 05-DEC-2002.

PF 26-FEB-2002; 2002US-00086135.

PR 03-AUG-1998; 98US-0095199P.

PR 03-AUG-1999; 99US-00366448.

PA (ZYMO) ZYMOGENETICS INC.

PI Sheppard PO, Chandrasekher YA;

DR WPI; 2003-328618/31.

PT New pancreatic and ovarian zsig58 polypeptides useful for diagnosing or  
 PT treating disorders associated with gonadal development, pregnancy, or  
 PT pubertal changes, menopause, ovarian cancer, fertility, and ovarian or  
 PT pancreatic function.

XX Example 1; Page 35; 49pp; English.

CC The invention relates to an isolated pancreatic and ovarian zsig58  
 CC polypeptide and the polynucleotide encoding it. The polypeptide,  
 CC polynucleotide and an antibody to the polypeptide are useful in  
 CC diagnosing or treating disorders associated with gonadal development,  
 CC pregnancy, pubertal changes, menopause, ovarian cancer, fertility,  
 CC ovarian function, polycystic ovarian syndrome, pancreas, diabetes, eye  
 CC disease, pituitary function, osteoporosis and other bone diseases. The  
 CC zsig58 polypeptide may also be used in promoting wound healing, in anti-  
 CC microbial applications, as a cell culture reagent in in vitro studies of  
 CC exogenous microorganism infections (e.g. bacterial, viral or fungal  
 CC infection), as an analgesic (e.g. bone pain), in identifying cells,  
 CC tissues or cell lines that respond to a zsig58-stimulated pathway, in  
 CC identifying agonists and antagonists of its activity and in preparing  
 CC antibodies. The antibody may be used for tagging cells that express  
 CC zsig58, for isolating zsig58 and for other diagnostic and therapeutic  
 CC applications. The polynucleotide is also useful in identifying a region  
 CC of the genome associated with human disease states. This sequence the human  
 CC represents a sequencing primer used to sequence cDNA encoding the human  
 CC zsig58 polypeptide

SQ Sequence 18 BP; 5 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABX93718 (1-18)

QY 32 ValVallysArgArg 36

DB 2 GTTGTAACGACGG 16

RESULT 176

ABX10645/c

ID ABX10645 standard; DNA; 18 BP.

XX AC ABX10645;

XX DT 22-APR-2003 (first entry)

XX DE DNA encoding the mouse PDGF-A proteolytic cleavage site.

XX KW Mouse; trans-dominant suppressor gene; growth factor; oligomeric state;  
XX KW suppressor gene; cell proliferation; autocrine loop; paracrine loop;  
XX KW cancer; tumour; atherosclerosis; coronary artery disease;  
XX KW rheumatoid arthritis; gene therapy; platelet derived growth factor; PDGF;  
XX KW PDGF-A; PDGF-B; transforming growth factor beta; TGF-beta; TGF-beta1;  
XX KW TGF-beta2; proteolytic cleavage site; mitogenic activity;  
XX KW propeptide processing; cytostatic; cardiant; ds.

XX OS Mus musculus.

XX US6475781-B1.

XX PN 05-NOV-2002.

XX PD 21-DEC-1993; 93US-00171384.

XX PF 17-MAY-1990; 90US-00525245.

XX PR 06-MAR-1992; 92US-00846972.

XX PA (DAND ) DANA FARRER CANCER INST INC.

XX PI Mercola MK, Deininger PL, Stiles CD;

XX DR WPI; 2003-208835/20.

XX DR P-PSDB; ABG75586.

XX PT New eukaryotic trans-dominant suppressor gene encoding a protein  
XX PT translation product which suppresses the activity of a growth factor,  
XX PT useful for inhibiting unwanted cell proliferation e.g., cancer.

XX PS Disclosure; Fig 1; 23pp; English.

XX CC The invention discloses a eukaryotic trans-dominant suppressor gene  
XX CC encoding a protein translation product which suppresses the activity of a  
XX CC growth factor that requires an oligomeric state for function, by forming  
XX CC an inactive oligomer with a wildtype subunit of the growth factor, the  
XX CC protein translation product being a mutant form of a wildtype subunit of  
XX CC the growth factor. The suppressor gene is useful for inhibiting unwanted  
XX CC cell proliferation in a mammalian patient, where the proliferation is  
XX CC stimulated in part by the presence of an autocrine or paracrine loop, and  
XX CC the unwanted cell is cancer, and is also useful for treating patient  
XX CC having atherosclerosis, coronary artery disease or rheumatoid arthritis  
XX CC (e.g. gene therapy). The suppressor gene is further useful for creating a  
XX CC transgenic laboratory animal which will serve as a disease model for  
XX CC medical research. A vector comprising the suppressor gene is useful for  
XX CC the production of dominant suppressor protein and also to transfect the  
XX CC suppressor gene into mammalian cells such as COS (Simian fibroblasts)

CC cells. Examples of growth factors to target are the dimeric protein,  
CC platelet derived growth factor (PDGF), comprising the sub-units PDGF-A  
CC and PDGF-B, and the transforming growth factor beta (TGF-beta) subfamily  
CC (e.g. TGF-beta1 or TGF-beta2). Target regions of the growth factors to  
CC mutate are the proteolytic cleavage sites and cysteine residues essential  
CC for mitogenic activity. The sequence presented is the DNA encoding the  
CC wild-type mouse PDGF-A proteolytic cleavage site  
XX SQ Sequence 18 BP; 7 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABX10645 (1-18)

QY 59 LeuLeuPheLeuArg 63

DB 17 CTTCCTCTCTCGCA 3

RESULT 177

ACC47946

ID ACC47946 standard; DNA; 18 BP.

XX AC ACC47946;

XX DT 11-AUG-2003 (first entry)

XX DE Nucleotide sequence of PCR primer ZC976.

XX KW Platelet-derived growth factor-D; PDGF-D; osteopathic; vulnery; bone;  
XX KW connective tissue; PCR; primer; ss.

XX OS Synthetic.

XX PN WO2003033677-A2.

XX PD 24-APR-2003.

XX PF 18-OCT-2002; 2002WO-US033563.

XX PR 19-OCT-2001; 2001US-0346117P.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Moore MD, Fox BA;

XX DR WPI; 2003-421322/39.

XX PT New protein consisting of two platelet-derived growth factor-D  
XX PT polypeptide chains, useful for stimulating the production of bone and/or  
XX PT connective tissue in both humans and animals, e.g. in treating fractures  
XX PT or osteoporosis.

XX PS Example 1; Page 47; 47pp; English.

XX CC The invention relates to a protein consisting of two platelet-derived  
XX CC growth factor-D (PDGF-D) polypeptide chains. The protein is useful in  
XX CC enhanced production of PDGF-D growth factor domain dimers. It may be used  
XX CC to stimulate production of bone and/or connective tissue in both humans  
XX CC and animals, such as in cases of fractures, bone grafts, implants, repair  
XX CC of bony defects arising from surgery, surgical reconstruction following  
XX CC traumatic injury, repair of hereditary or other physical abnormalities,  
XX CC or in treatment of osteoporosis. The present sequence represents a PCR  
XX CC primer used in the course of the invention

SQ Sequence 18 BP; 5 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 18  
Score: 8.57e+03  
Length: 18  
Matches: 5  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatches: 0  
Query Match: 2.53%  
Indels: 0  
Gaps: 0  
DB:

US-09-966-880A-8 (1-198) x ACC47946 (1-18)

Qy 32 ValVallyysArgArg 36  
Db 2 GTTGTAAACGACGG 16

RESULT 178

ADA49993  
ID AAD50482 standard; DNA; 18 BP.

XX AC AAD50482;

XX DT 24-MAR-2003 (first entry)

XX DE ZC976 PCR primer used to amplify human zcyto20 DNA.

XX Human; leukaemia; carcinoma; acquired immune deficiency syndrome; AIDS;  
KW melanoma; Kaposi's sarcoma; multiple myeloma; non-Hodgkin's lymphoma;  
KW hepatitis; infection; myocarditis; blood vessel formation; gene therapy;  
KW growth regulation; developmental process; immunotherapy; zcyto20; PCR;  
KW primer; ss.

XX OS Homo sapiens.

XX PN WO200286087-A2.

XX PD 31-OCT-2002.

XX PF 19-APR-2002; 2002WO-US012887.

XX PR 20-APR-2001; 2001US-0285408P.

XX PR 20-APR-2001; 2001US-0285424P.

XX PR 25-APR-2001; 2001US-0286482P.

XX PR 23-JUN-2001; 2001US-00895834.

XX PR 22-OCT-2001; 2001US-0341050P.

XX PR 22-OCT-2001; 2001US-0341105P.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Sheppard PO, Fox BA, Klucher KM, Taft DW, Kindsvogel WR;

XX DR WPI; 2003-093122/08.

XX PS New zcyto20, zcyto21, zcyto22, zcyto24 and zcyto25 polypeptides and

XX PT polynucleotides useful for treating leukemia, carcinoma, malignant  
XX PT melanoma, AIDS-related Kaposi's sarcoma, myeloma, non-Hodgkin's lymphoma,  
XX PT hepatitis and infections.  
XX PS Example 6; Page 135; 160pp; English.  
XX CC The invention relates to zcyto20, zcyto21, zcyto22, zcyto24 and zcyto25  
XX CC polypeptides and polynucleotides. Sequences of the invention are useful  
XX CC for treating hairy cell leukaemia, renal cell or basal cell carcinoma,  
XX CC malignant melanoma, AIDS-related Kaposi's sarcoma, multiple myeloma, non-  
XX CC Hodgkin's lymphoma, hepatitis B, C or D, infections (e.g. bacterial,  
XX CC fungal or protozoal) or myocarditis. The invention is useful for growth  
XX CC regulation in the liver, blood vessel formation and other developmental  
XX CC processes. The invention is also useful in immunotherapy and gene  
XX CC therapy. The present sequence is a PCR primer used to amplify human  
XX CC zcyto20 DNA

XX SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x AAD50482 (1-18)

Qy 32 ValVallyysArgArg 36  
Db 2 GTTGTAAACGACGG 16

RESULT 179

ADA49993  
ID ADR49993 standard; DNA; 18 BP.

XX AC ADR49993;

XX DT 20-NOV-2003 (first entry)

XX DE Human mitochondrial COX gene primer #41.

XX KW Alzheimer's disease; AD; human; mitochondrial cytochrome c oxidase; COX;  
KW segregation; nontropic; neuroprotective; primer; ss.

XX OS Homo sapiens.

XX PN US2003087858-A1.

XX PD 08-MAY-2003.

XX PF 15-OCT-2001; 2001US-00978600.

XX PR 30-MAR-1994; 94US-00219842.

XX PR 30-MAR-1995; 95US-00413740.

XX PR 23-NOV-1999; 99US-00448312.

XX PA (MITO-) MITOKOR.

XX PI Herrnstadt C, Ghosh SS;

XX DR WPI; 2003-597110/56.

XX PT Compositions and methods for the treatment and diagnosis of Alzheimer's

XX PT disease using nucleic acids related in sequence to (mutants of) the

XX PS cytochrome c oxidase gene.

XX PS Example 2; Page 25; 93pp; English.

XX CC The present invention relates to compositions and method for the  
XX CC treatment and diagnosis of Alzheimer's disease (AD). The method comprises  
XX CC the use of genetic mutations in the human mitochondrial cytochrome c  
XX CC oxidase (COX) gene and their segregation with AD. Also disclosed are  
XX CC antisense sequences specific to mutant human cytochrome c oxidase genes  
XX CC that are designed to bind and inhibit transcription or translation of the  
XX CC target mutant COX genes without inhibiting transcription or translation  
XX CC of wild-type cytochrome c oxidase genes. Also disclosed are probes for  
XX CC detecting a disease state associated with one or more mutations in the  
XX CC mitochondrial COX genes, and a kit comprising a probe for detection of an  
XX CC Alzheimer's disease genotype which is complementary to the sense or  
XX CC antisense strands of a mitochondrial COX gene. Definitive diagnosis of  
XX CC Alzheimer's disease can currently only be accomplished by pathological  
XX CC examination at autopsy, the new method provides a non-invasive diagnostic  
XX CC that is reliable at or before the earliest manifestations of AD symptoms.  
XX CC There is at present no effective therapy for AD other than certain  
XX CC palliative treatments. The new therapeutic compositions and methods  
XX CC provide an effective therapy that addresses the primary cause of AD. The  
XX CC present sequence represents a primer for the human mitochondrial COX  
XX CC gene.

XX SQ Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8.57e+03 Length: 18

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x ADA49993 (1-18)

QY 125 GlyLeuArgArgLeu 129  
DB 2 GGTCTACGAGGCTC 16

RESULT 180

ACAG2736  
ID ACAG2736 standard; cDNA; 18 BP.

XX AC AGA2736;

DT 21-AUG-2003 (first entry)

DE Human transposable element primer ZC976.

XX KW Primer; ss; PCR; VCAM-1 inhibition; bacmid; inflammation; wound;  
KW vascular cell adhesion molecule 1; energy balance; cellular metabolism;  
KW adipogenesis; glucogenesis; glycogenolysis; glucose uptake; blood flow;  
KW protein synthesis; thermogenesis; oxygen use; neurotransmitter; trauma;  
KW acute vascular injury; angioplasty; coronary artery bypass graft; stroke;  
KW aneurysm; obesity; diabetes; lipogenesis; transposable element.

XX OS Unidentified.

XX PN US6521233-B1.

XX PD 18-FEB-2003.

XX PF 19-APR-2000; 2000US-00552225.

XX PR 20-APR-1999; 99US-0130199P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Piddington CS, Bishop PD;

XX DR WPI; 2003-478795/45.

XX PT New adipocyte complement related protein (zacr3) bearing a collagen-like  
PT domain and a C1q domain, useful for modulating energy, modulating fat  
PT formation and storage, particularly for treating e.g. obesity, diabetes  
PT or wounds.

XX PS Example 2; Col 65-66; 37pp; English.

XX CC The invention relates to an isolated polypeptide (designated zacrp3)  
CC which inhibits the expression of vascular cell adhesion molecule 1 (VCAM-  
CC 1). The zacrp3 polypeptide or the fusion protein is useful for modulating  
CC energy balance in mammals by modulating cellular metabolic reaction, e.g.  
CC adipogenesis, glucogenesis, glycogenolysis, lipogenesis, glucose uptake,  
CC protein synthesis, thermogenesis, or oxygen use. The polypeptide is  
CC particularly useful for modulating the formation and storage of fat in  
CC mammals. The zacrp3 polypeptide is also useful for protecting endothelial  
CC cells from injury, as neurotransmitters, or as modulators of  
CC neurotransmission. The zacrp3 polypeptide is also useful for promoting  
CC blood flow within the vasculature of a mammal, or for treating acute  
CC vascular injury due to e.g. angioplasty, coronary artery bypass graft,  
CC trauma, stroke or aneurysm. In particular, the zacrp3 polypeptide is  
CC useful for treating or preventing obesity, diabetes, wounds,  
CC inflammations, etc. The present sequence represents the bacmid  
CC transposable element primer ZC976

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores: 8.57e+03 Length: 18  
Pred. No.: 8.57e+03

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x ACA62736 (1-18)

QY 32 ValVallyArgArg 36  
DB 2 GTTGTAAACGACGG 16

RESULT 181

AA47867  
ID AAD47867 standard; DNA; 18 BP.

XX AC AAD47867;

DT 27-AUG-2003 (first entry)

DE Human interleukin-21 DNA amplifying primer ZC976.

XX KW Interleukin-21; antagonist; cancer; inflammatory; autoimmune disorder;  
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;  
KW myasthenia gravis; diabetes; human; IL-21; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO2003040313-A2.

XX PD 15-MAY-2003.

XX PF 28-OCT-2002; 2002WO-US034502.

XX PR 05-NOV-2001; 2001US-0337586P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Presnell SR, West JW, Novak JE;

XX DR WPI; 2003-441547/41.

XX PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing  
PT and treating disorders with aberrant expression or activity of the IL-21  
PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and  
PT diabetes.

XX PS Example 5; Page 69; 71pp; English.

XX CC The invention relates to polynucleotides and polypeptides of interleukin-  
CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50  
CC that is not detectable in receptor binding studies. The antagonists of  
CC the invention have mutations in the D helix of the IL-21 molecule, and  
CC can be used to inhibit the activity of IL-21 with its cognate receptor.  
CC The IL-21 antagonists are useful for diagnosing and treating disorders  
CC involving the aberrant expression or activity of the IL-21 polypeptide,  
CC such as cancer, inflammatory and autoimmune disorders, including  
CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
CC myasthenia gravis and diabetes. The polypeptides can also be used to  
CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,  
CC and for enhancing in vivo killing of target tissues. The present sequence  
CC is a PCR primer used in an exemplification of the invention to screen  
CC baculovirus clones with the correct insert of human IL-21 DNA

SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores: 8.57e+03 Length: 18  
Pred. No.: 8.57e+03

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 8 Gaps: 0



US-09-966-880A-8 (1-198) x AAD47867 (1-18)

QY 32 ValVallylsArgArg 36  
DB 2 GTTGTAAACGACGG 16

RESULT 182

AAD58385  
ID AAD58385 standard; DNA; 18 BP.

AC AAD58385;

DT 20-NOV-2003 (first entry)

XX PCR primer zc976 used in the exemplification of the invention.

XX Platelet-derived growth factor-D; PDGF-D; bone graft; osteopathic;  
KW radiation-induced osteonecrosis; periodontal disease; protein therapy;  
KW joint injury; osteoporosis; bone loss; fracture; bone healing; PCR;  
KW primer; ss.

XX Unidentified.

OS WO2003068802-A2.

PN 21-AUG-2003.

PD 11-FEB-2003; 2003WO-US004213.

PF 11-FEB-2002; 2002US-035882P.

PR (ZYMO ) ZYMOGENETICS INC.

PS Fox BA, Moore MD, Swiderek KM, Birks CW;

PI WPI; 2003-646473/61.

PT New fusion protein comprising a first platelet-derived growth factor-D  
(PDGF-D) domain, a linker, and a second PDGF-D domain polypeptides,  
useful for stimulating the production of bone and/or connective tissue.

XX Example 1; Page 44; 50pp; English.

XX The invention relates to a fusion protein comprising, from amino to  
CC carboxyl terminus, a first platelet-derived growth factor-D (PDGF-D)  
CC domain polypeptide, a linker polypeptide, and a second PDGF-D domain  
CC polypeptide. The fusion proteins are useful for stimulating the  
CC production of bone and/or connective tissue in both human and non-human  
CC animals. The fusion proteins are specifically useful in non-union  
CC fractures and fractures in patients with compromised healing, bone  
CC grafts, bone healing following radiation-induced osteonecrosis, implants,  
CC or treatment of periodontal disease, joint injuries, osteoporosis or  
CC other conditions characterised by increased bone loss or decreased bone  
CC formation. The invention is useful in protein therapy. The present  
CC sequence is a PCR primer used in the exemplification of the invention.  
CC PDGF-D is known as zveg4

XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 8 Gaps: 0

US-09-966-880A-8 (1-198) x AAD58385 (1-18)

QY 32 ValVallylsArgArg 36  
DB 2 GTTGTAAACGACGG 16

RESULT 183

ADB80425  
ID ADB80425 standard; DNA; 18 BP.

AC ADB80425;

DT 04-DEC-2003 (first entry)

DE Rat CLCA1 gene PCR primer #11.

XX ss; primer; antiinflammatory; antiasthmatic; antiallergic; CLCA1;  
KW calcium activated chloride channel protein; chest disorder;  
KW airway disorder; chronic obstructive lung disease; chronic bronchitis;  
KW bronchial asthma; rhinitis; hay fever; pneumonia.

OS Rattus sp.

XX WO2003037927-A1.

PN 08-MAY-2003.

PD 01-NOV-2002; 2002WO-JF011417.

PF 02-NOV-2001; 2001JP-00337864.

PR 13-DEC-2001; 2001JP-00380099.

PS 18-JAN-2002; 2002JP-00010035.

PA (TAKE ) TAKEDA CHEM IND LTD.

XX Nakanishi A, Morita S;

XX WPI; 2003-430500/40.

PT Rat CLCA1 gene and protein encoded by it useful for screening inhibitors  
of its activity and expression and as chronic obstructive lung disease  
PT and bronchial asthma remedies.

XX Example 3; Page 98; 115pp; Japanese.

XX The invention relates to proteins and their salts and partial peptides  
CC which are the expression product of the rat CLCA1 gene or are related  
CC proteins with similar activity. CLCA1 is a calcium activated chloride  
CC channel protein. The proteins are useful for the treatment, prevention  
CC and diagnosis of chest and airway disorders including chronic obstructive  
CC lung disease, chronic bronchitis, bronchial asthma, chronic rhinitis,  
CC acute rhinitis, allergic rhinitis, hay fever and pneumonia. This sequence  
CC corresponds to a PCR primer used to isolate and clone the rat CLCA1 gene  
CC (ADB80434).

XX Sequence 18 BP; 3 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADB80425 (1-18)

QY 126 LeuArgArgLeuHis 130  
DB 4 CTTCCGAGATTGCAT 18

RESULT 184

ADB80414/c  
ID ADB80414 standard; DNA; 18 BP.

AC ADB80414;

DT 04-DEC-2003 (first entry)

```

XX DE Rat CLCA1 gene PCR primer #1.
XX ss; primer; antiinflammatory; antiasthmatic; antiallergic; CLCA1;
KW calcium activated chloride channel protein; chest disorder;
KW airway disorder; chronic obstructive lung disease; chronic bronchitis;
KW bronchial asthma; rhinitis; hay fever; pneumonia.
XX Rattus sp.
XX WO2003037927-A1.
XX 08-MAY-2003.
XX 01-NOV-2002; 2002WO-JF011417.
XX 02-NOV-2001; 2001JP-00337864.
XX 13-DEC-2001; 2001JP-00380099.
XX 18-JAN-2002; 2002JP-00010035.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX PA
XX Nakanishi A, Morita S;
XX WPI; 2003-430500/40.
XX Rat CLCA1 gene and protein encoded by it useful for screening inhibitors
XX of its activity and expression and as chronic obstructive lung disease
XX and bronchial asthma remedies.
XX Example 1; Page 94; 115pp; Japanese.
XX The invention relates to proteins and their salts and partial peptides
XX which are the expression product of the rat CLCA1 gene or are related
XX proteins with similar activity. CLCA1 is a calcium activated chloride
XX channel protein. The proteins are useful for the treatment, prevention
XX and diagnosis of chest and airway disorders including chronic obstructive
XX lung disease, chronic bronchitis, bronchial asthma, chronic rhinitis,
XX acute rhinitis, allergic rhinitis, hay fever and pneumonia. This sequence
XX corresponds to a PCR primer used to isolate and clone the rat CLCA1 gene
XX (ADB80434).
XX Sequence 18 BP; 6 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 9 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x ADB80414 (1-18)
XX
XX QY 126 LeuArgArgLeuHis 130
XX DB 15 CTTGGAGATTGCAT 1
XX
XX RESULT 185
XX AAD60481
XX ID AAD60481 standard; DNA; 18 BP.
XX AC AAD60481;
XX 18-DEC-2003 (first entry)
XX Human c-IAP-2 antisense oligonucleotide #ISIS #23454.
XX Human; antisense; cellular inhibitor of apoptosis-2; c-IAP-2; cancer;
KW hyperproliferative condition; apoptosis inhibitor 2; autoimmune disease;
KW API-1; hIAP-1; MIRC; gene therapy; phosphorothioate; ss.
XX Homo sapiens.
OS

```

```

OS Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..18
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone; All cytidine residues
XX are 5-methylcytidines"
XX modified_base 1..4
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX modified_base 15..18
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX US2003083300-A1.
XX 01-MAY-2003.
XX 16-JUL-2002; 2002US-00197290.
XX 23-SEP-1999; 99WO-US022083.
XX 04-OCT-2001; 2001US-00857299.
XX (BENN/) BENNETT C F.
XX (ACKE/) ACKERMANN E J.
XX (COWS/) COWSERT L M.
XX Bennett CF, Ackermann EJ, Cowsert LM;
XX WPI; 2003-755119/71.
XX New antisense compound, preferably an oligonucleotide, for inhibiting
XX expression of human Cellular Inhibitor of Apoptosis-2 in human cells or
XX tissues, and for treating diseases, such as cancer or an autoimmune
XX disease.
XX Claim 3; Page 22; 34pp; English.
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding human cellular inhibitor of apoptosis-2 (also known as c-IAP-2,
XX apoptosis inhibitor 2, API-1, hIAP-1 and MIRC) to inhibit its expression.
XX Antisense compounds of the invention are used to induce apoptosis in
XX human cells or tissues to treat diseases or conditions associated with
XX insufficient apoptosis. They are used to treat diseases or conditions
XX associated with c-IAP-2 such as hyperproliferative conditions especially
XX cancer or autoimmune diseases. The invention is also useful in antisense
XX gene therapy. The present sequence is an antisense oligonucleotide
XX targetted to human c-IAP-2 DNA
XX Sequence 18 BP; 4 A; 3 C; 2 G; 9 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 8.57e+03 Length: 18
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 9 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAD60481 (1-18)
XX
XX QY 59 LeuLeuPheLeuArg 63
XX DB 4 CTTTATTCTTAGA 18
XX
XX RESULT 186
XX AAD60513
XX ID AAD60513 standard; DNA; 18 BP.
XX AC AAD60513;

```

XX 18-DEC-2003 (first entry)  
 XX Human c-IAP-2 antisense oligonucleotide #ISIS #23486.  
 XX Human; antisense; cellular inhibitor of apoptosis-2; c-IAP-2; cancer;  
 XX hyperproliferative condition; apoptosis inhibitor 2; autoimmune disease;  
 KW API-1; hIAP-1; MHC; gene therapy; phosphorothioate; ss.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FT modified\_base 1..18  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone; All cytidine residues  
 FT are 5-methylcytidines"  
 FT modified\_base 1..4  
 FT /tag= b  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
 FT modified\_base 15..18  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
 XX US2003083300-A1.  
 XX 01-MAY-2003.  
 XX 16-JUL-2002; 2002US-00197290.  
 XX 23-SEP-1999; 99WO-US022083.  
 XX 04-OCT-2001; 2001US-00857299.  
 XX (BEN/) BENNETT C F.  
 XX (ACK/) ACKERMANN E J.  
 XX (COWS/) COWSERT L M.  
 XX Bennett CF, Ackermann EJ, Cowsert LM;  
 XX WPI; 2003-755119/71.  
 XX New antisense compound, preferably an oligonucleotide, for inhibiting  
 FT expression of human Cellular Inhibitor of Apoptosis-2 in human cells or  
 FT tissues, and for treating diseases, such as cancer or an autoimmune  
 FT disease.  
 XX Claim 3; Page 22; 34pp; English.  
 XX The invention relates to antisense compounds targetted to a nucleic acid  
 CC encoding human cellular inhibitor of apoptosis-2 (also known as c-IAP-2,  
 CC apoptosis inhibitor 2, API-1, hIAP-1 and MHC) to inhibit its expression.  
 CC Antisense compounds of the invention are used to induce apoptosis in  
 CC human cells or tissues to treat diseases or conditions associated with  
 CC insufficient apoptosis. They are used to treat diseases or conditions  
 CC associated with c-IAP-2 such as hyperproliferative conditions especially  
 CC cancer or autoimmune diseases. The invention is also useful in antisense  
 CC gene therapy. The present sequence is an antisense oligonucleotide  
 CC targetted to human c-IAP-2 DNA  
 XX Sequence 18 BP; 2 A; 4 C; 3 G; 9 T; 0 U; 0 Other;  
 SQ Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAD60513 (1-18)

QY 38 SerAlaThrSerPhe 42  
 Db |||||  
 4 AGTGTACCTCTTTT 18  
 RESULT 187  
 ID ADD24810/C  
 XX ADD24810 standard; DNA; 18 BP.  
 XX AC ADD24810;  
 XX 15-JAN-2004 (first entry)  
 XX Human CYP3A4 mutant A392G probe H193.  
 XX diagnostic; pharmaceutical tolerance; side effect; drug; human;  
 KW allelic variability; polymorphism; phase I; phase II;  
 KW detoxification mechanism; PCR; primer; probe; NAT2; CYP2D6; CYP1A2;  
 KW CYP3A4; MEH; TPMT; MTHFR; paraoxonase; CYP2C9; CYP2C19; CYP2E1; DPD; ss.  
 XX Homo sapiens.  
 OS WO2003018837-A2.  
 XX 06-MAR-2003.  
 XX 22-AUG-2002; 2002WO-EP009386.  
 XX 24-AUG-2001; 2001DE-01040651.  
 XX 30-APR-2002; 2002DE-01019373.  
 XX (ADNA-) ADNAGEN AG.  
 XX Waschuetza S, Schnakenberg E, Lustig M;  
 XX WPI; 2003-290079/28.  
 XX Diagnostic kit, useful for assessing a subject's tolerance of drugs,  
 FT comprises reagents for determining alleles of genes encoding  
 FT detoxification enzymes.  
 XX Claim 6; Page 39; 156pp; German.  
 XX This invention describes a novel diagnostic kit for determining tolerance  
 CC of pharmaceuticals in humans by determining allelic variability of at  
 CC least two polymorphisms of a human enzyme involved in phase I and/or II  
 CC of the detoxification mechanism in a blood, tissue or other human sample,  
 CC where tolerance is determined from presence or absence of alleles. The  
 CC kit comprises two pairs of oligonucleotide primers, in which each pair  
 CC amplifies by PCR, part of a gene for a human detoxification mechanism-  
 CC associated enzyme. The kit may also contain two further pairs of  
 CC oligonucleotides, serving as probes for detection of amplified DNA  
 CC segments, especially where the probes are complementary to a single  
 CC strand of one allele of the target gene. The probes are labelled with  
 CC fluorophores (LC-Red640 or LC-Red705 for 5'-labelling or fluorescein for  
 CC 3'-labelling) which generate a different signal in the hybridized and non  
 CC hybridized condition. The enzymes detected include NAT2, CYP2D6, CYP1A2,  
 CC CYP3A4, MEH, TPMT, MTHFR, paraoxonase, CYP2C9, CYP2C19, CYP2E1 or DPD.  
 CC The kit is used to determine an individual's tolerance of a particular  
 CC drug, to establish a suitable dose and/or to predict if a subject will  
 CC show side-effects to a drug. The kit provides minimally invasive, safe  
 CC and reliable determination of the metabolic capacity of phase I and/or II  
 CC enzymes at the molecular level. This sequence represents a probe used in  
 CC the kit of the invention.  
 XX Sequence 18 BP; 0 A; 9 C; 2 G; 7 T; 0 U; 0 Other;  
 SQ Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0

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DB:          9          Gaps:          0
US-09-966-880A-8 (1-198) x ADD24810 (1-18)
QY      22 LysGlyArgArgGlu 26
Db      16 AAGGCGAGGAGAG 2

RESULT 188
AAD61885
ID AAD61885 standard; DNA; 18 BP.
XX
AC AAD61885;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human Zalphall cDNA clone sequencing primer, ZC 976.
XX
KW Cytokine receptor; Zalphall; cell proliferation; cell development;
KW splenic disorder; blood disorder; bone disorder; immune disorder;
KW haematopoietic; lymphoid; inflammatory; therapy; human; primer; ss.
XX
OS Homo sapiens.
XX
PN US6576744-B1.
XX
PD 10-JUN-2003.
XX
PF 23-SEP-1999; 99US-00404641.
XX
PR 23-SEP-1998; 98US-0100896P.
PR 09-MAR-1999; 99US-0123546P.
PR 06-JUL-1999; 99US-0142574P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Presnell SR, Conklin DC, Novak JE, Hammond AK;
XX
DR WPI; 2003-799829/75.
XX
PT Novel cytokine receptor Zalphall useful for treating lymphoid, immune,
PT inflammatory, splenic, blood or bone disorders.
XX
PS Example 1; Col 85; Opp; English.
XX
CC The invention relates to a cytokine receptor designated Zalphall and its
CC nucleic acid sequence. Zalphall protein is useful for detecting ligands
CC that stimulate the proliferation and/or development of haematopoietic,
CC lymphoid and myeloid cells in vitro and in vivo. Zalphall DNA is useful
CC in identifying a region of the genome associated with human disease
CC states. Zalphall protein is useful for treating lymphoid, immune,
CC inflammatory, splenic, blood or bone disorders. The present sequence is
CC a primer used for sequencing human Zalphall cDNA clone
XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8.57e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     2.53%          Indels:      0
DB:              9              Gaps:          0

US-09-966-880A-8 (1-198) x AAD61885 (1-18)
QY      32 valvallysArgArg 36
Db      2 GTTGTAAACGACG 16

RESULT 189
ADD36973/C
ID ADD36973 standard; DNA; 18 BP.

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XX
AC ADD36973;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human papillomavirus E6 gene-specific PCR primer/probe Seq ID86.
XX
KW cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervical cancer;
KW cervical cell; cervix; PCR; primer; probe; ss.
XX
OS Human papillomavirus.
XX
PN WO2003057914-A2.
XX
PD 17-JUL-2003.
XX
PF 07-JAN-2003; 2003WO-GB0000034.
XX
PR 07-JAN-2002; 2002GB-00000239.
PR 19-JUN-2002; 2002GB-00014124.
XX
PA (NORC-) NORCHIP AS.
PA (ALLA) ALLARD S J.
XX
PI Karlsen F;
XX
DR WPI; 2003-587136/55.
XX
PT An in vitro method of screening human subjects to assess their risk of
PT developing cervical carcinoma, comprises screening the subject for
PT expression of mRNA transcripts from the L1 gene and the E6 gene of human
PT papillomavirus.
XX
PS Disclosure; SEQ ID NO 86; 102pp; English.
XX
CC This invention relates to a novel method for the detection of human
CC papillomavirus mRNA for use in the screening of human female subjects to
CC assess their risk of developing cervical carcinoma. The invention
CC comprises screening the subject for expression of mRNA transcripts from
CC the L1 gene and the E6 gene of human papillomavirus, where subjects
CC positive for expression of L1 and/or E6 mRNA are scored as being at risk
CC of developing cervical carcinoma. The presence of the human
CC papillomavirus (in particular HPV16 and HPV18) has been associated with
CC cervical cancer in numerous epidemiological studies. The methods of the
CC invention are useful for screening human subjects to assess their risk of
CC developing cervical carcinoma, or for identifying human subjects having
CC abnormal cell changes in the cervix. The present sequence is that of a
CC PCR primer (which may also be suitable as a probe) which may be used to
CC amplify the E6 gene of human papillomavirus in the method of the
CC invention.
XX
SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      8.57e+03      Length:      18
Score:          5.00          Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     2.53%          Indels:      0
DB:              9              Gaps:          0

US-09-966-880A-8 (1-198) x ADD36973 (1-18)
QY      174 ArgGlnLeuArgArg 178
Db      18 AGACAGCTCAGAGA 4

RESULT 190
ADD36831/C
ID ADD36831 standard; DNA; 18 BP.
XX
AC ADD36831;
XX

```

DT 15-JAN-2004 (first entry)  
XX Human papillomavirus PCR primer 14.  
DE  
XX  
XX cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervical cancer;  
KW cervical cell; cervix; PCR; primer; ss.  
XX  
XX Human papillomavirus.  
OS  
XX  
XX WO2003057914-A2.  
XX  
XX  
XX 17-JUL-2003.  
XX  
XX  
XX 07-JAN-2003; 2003WO-GB0000034.  
XX  
XX  
XX 07-JAN-2002; 2002GB-00000239.  
PR  
XX 19-JUN-2002; 2002GB-00014124.  
XX  
XX (NORC-) NORCHIP AS.  
PA (ALLA/) ALLARD S J.  
XX  
XX  
XX Karlisen F;  
XX  
XX WPI; 2003-587136/55.  
XX  
XX  
XX An in vitro method of screening human subjects to assess their risk of  
PT developing cervical carcinoma, comprises screening the subject for  
PT expression of mRNA transcripts from the L1 gene and the E6 gene of human  
PT papillomavirus.  
XX  
XX Example 1; Page 63; 102pp; English.  
XX  
XX This invention relates to a novel method for the detection of human  
CC papillomavirus mRNA for use in the screening of human female subjects to  
CC assess their risk of developing cervical carcinoma. The invention  
CC comprises screening the subject for expression of mRNA transcripts from  
CC the L1 gene and the E6 gene of human papillomavirus, where subjects  
CC positive for expression of L1 and/or E6 mRNA are scored as being at risk  
CC of developing cervical carcinoma. The presence of the human  
CC papillomavirus (in particular HPV16 and HPV18) has been associated with  
CC cervical cancer in numerous epidemiological studies. The methods of the  
CC invention are useful for screening human subjects to assess their risk of  
CC developing cervical carcinoma, or for identifying human subjects having  
CC abnormal cell changes in the cervix. The present sequence is that of a  
CC PCR primer which was used to amplify sequence of the human papillomavirus  
CC in the exemplification of the invention.  
XX  
SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

KW cervical carcinoma; L1 gene; E6 gene; HPV16; HPV18; HPV; cervical cancer;  
XX cervical cell; cervix; PCR; primer; ss.  
XX  
OS Human papillomavirus.  
XX  
XX WO2003057914-A2.  
XX  
XX  
XX 17-JUL-2003.  
XX  
XX  
XX 07-JAN-2003; 2003WO-GB0000034.  
XX  
XX  
XX 07-JAN-2002; 2002GB-00000239.  
PR  
XX 19-JUN-2002; 2002GB-00014124.  
XX  
XX (NORC-) NORCHIP AS.  
PA (ALLA/) ALLARD S J.  
XX  
XX  
XX Karlisen F;  
XX  
XX WPI; 2003-587136/55.  
XX  
XX  
XX An in vitro method of screening human subjects to assess their risk of  
PT developing cervical carcinoma, comprises screening the subject for  
PT expression of mRNA transcripts from the L1 gene and the E6 gene of human  
PT papillomavirus.  
XX  
XX Disclosure; Page 54; 102pp; English.  
XX  
XX This invention relates to a novel method for the detection of human  
CC papillomavirus mRNA for use in the screening of human female subjects to  
CC assess their risk of developing cervical carcinoma. The invention  
CC comprises screening the subject for expression of mRNA transcripts from  
CC the L1 gene and the E6 gene of human papillomavirus, where subjects  
CC positive for expression of L1 and/or E6 mRNA are scored as being at risk  
CC of developing cervical carcinoma. The presence of the human  
CC papillomavirus (in particular HPV16 and HPV18) has been associated with  
CC cervical cancer in numerous epidemiological studies. The methods of the  
CC invention are useful for screening human subjects to assess their risk of  
CC developing cervical carcinoma, or for identifying human subjects having  
CC abnormal cell changes in the cervix. The present sequence is that of a  
CC PCR primer which was used to amplify the E6 gene of human  
CC papillomavirus in the method of the invention.  
XX  
SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8.57e+03 Length: 18  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD36741 (1-18)  
QY 174 ArgGlnLeuArgArg 178  
DB 18 AGACAGCTCAGAAGA 4

RESULT 192  
ADD36741/c  
ID ADD22030 standard; DNA; 18 BP.  
XX  
XX ADD22030;  
XX  
XX 15-JAN-2004 (first entry)  
XX  
XX HPV E6 gene transcribed mRNA detecting oligonucleotide, SEQ ID No 69.  
XX E6; human papillomavirus; HPV; NASBA; primer; PCR; ss.  
XX  
XX Human papillomavirus.  
XX

PN WO2003057927-A2.  
 XX 17-JUL-2003.  
 PD  
 XX  
 XX  
 PF 07-JAN-2003; 2003WO-GB000030.  
 XX  
 XX 07-JAN-2002; 2002GB-00000258.  
 PR  
 XX (NORC-) NORCHIP AS.  
 XX (ALLA/) ALLARD S J.  
 XX  
 XX Karlisen F;  
 PI  
 XX WPI; 2003-587141/55.  
 DR  
 XX  
 XX New oligonucleotide primer and probe for detecting the presence of mRNA  
 PT transcripts from the E6 gene of a human papillomavirus in clinical  
 PT samples.  
 XX  
 XX Claim 1; SEQ ID NO 69; 28pp; English.  
 PS  
 XX  
 XX The invention relates to a novel oligonucleotide molecule used for  
 CC detecting mRNA transcribed from the E6 gene of a human papillomavirus  
 CC (HPV). The oligonucleotide comprises any of the 133 fully defined  
 CC sequences having 17-26 bp given in the specification. The invention  
 CC further provides the detection of HPV mRNA in a test sample suspected of  
 CC containing HPV, comprising performing an amplification reaction on a  
 CC preparation of a nucleic acid isolated from the test sample to amplify a  
 CC portion of the mRNA transcribed from the E6 gene of HPV, where the  
 CC amplification reaction is performed using the primer-pair of  
 CC oligonucleotide cited above. The invention also provides: a reagent kit  
 CC for use in the detection of HPV by NASBA, comprising an oligonucleotide  
 CC primer-pair and, optionally, an enzyme mixture comprising an RNA directed  
 CC DNA polymerase, a ribonuclease that hydrolyzes the RNA strand of an RNA-  
 CC DNA hybrid without hydrolyzing single or double stranded RNA or DNA, and  
 CC an RNA polymerase that recognises the promoter sequence present in at  
 CC least one NASBA P1 primer oligonucleotide included in the reagent kit.  
 CC The oligonucleotide of the invention is useful in detecting mRNA  
 CC transcripts from the E6 gene of HPV in clinical samples. This  
 CC polynucleotide sequence represents one of the 133 oligonucleotides used  
 CC for detecting mRNA transcribed from the E6 gene of a human papillomavirus  
 CC (HPV) of the invention.  
 XX  
 XX SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD22030 (1-18)

QY 174 ArgGlnLeuArgArg 178  
 Db 18 AGACAGCTCAGAGA 4

RESULT 193  
 ADD22316/c  
 ID ADD22316 standard; DNA; 18 BP.

XX  
 XX ADD22316;

XX 15-JAN-2004 (first entry)

XX HPV E6 gene transcribed mRNA detecting RT-PCR primer #48.  
 XX E6; human papillomavirus; HPV; NASBA; primer; RT-PCR; ss.  
 XX Human papillomavirus.  
 OS

PN WO2003057927-A2.  
 XX 17-JUL-2003.  
 PD  
 XX  
 XX  
 PF 07-JAN-2003; 2003WO-GB000030.  
 XX  
 XX 07-JAN-2002; 2002GB-00000258.  
 PR  
 XX (NORC-) NORCHIP AS.  
 XX (ALLA/) ALLARD S J.  
 XX  
 XX Karlisen F;  
 PI  
 XX WPI; 2003-587141/55.  
 DR  
 XX  
 XX New oligonucleotide primer and probe for detecting the presence of mRNA  
 PT transcripts from the E6 gene of a human papillomavirus in clinical  
 PT samples.  
 XX  
 XX Disclosure; Page 25; 28pp; English.  
 PS  
 XX  
 XX The invention relates to a novel oligonucleotide molecule used for  
 CC detecting mRNA transcribed from the E6 gene of a human papillomavirus  
 CC (HPV). The oligonucleotide comprises any of the 133 fully defined  
 CC sequences having 17-26 bp given in the specification. The invention  
 CC further provides the detection of HPV mRNA in a test sample suspected of  
 CC containing HPV, comprising performing an amplification reaction on a  
 CC preparation of a nucleic acid isolated from the test sample to amplify a  
 CC portion of the mRNA transcribed from the E6 gene of HPV, where the  
 CC amplification reaction is performed using the primer-pair of  
 CC oligonucleotide cited above. The invention also provides: a reagent kit  
 CC for use in the detection of HPV by NASBA, comprising an oligonucleotide  
 CC primer-pair and, optionally, an enzyme mixture comprising an RNA directed  
 CC DNA polymerase, a ribonuclease that hydrolyzes the RNA strand of an RNA-  
 CC DNA hybrid without hydrolyzing single or double stranded RNA or DNA, and  
 CC an RNA polymerase that recognises the promoter sequence present in at  
 CC least one NASBA P1 primer oligonucleotide included in the reagent kit.  
 CC The oligonucleotide of the invention is useful in detecting mRNA  
 CC transcripts from the E6 gene of HPV in clinical samples. This  
 CC polynucleotide sequence represents an oligonucleotide used for detecting  
 CC mRNA transcribed from the E6 gene of a human papillomavirus (HPV) of the  
 CC invention.  
 XX  
 XX SQ Sequence 18 BP; 2 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.57e+03 Length: 18  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x ADD22316 (1-18)

QY 174 ArgGlnLeuArgArg 178  
 Db 18 AGACAGCTCAGAGA 4

RESULT 194  
 AAN92708/c  
 ID AAN92708 standard; DNA; 19 BP.

XX  
 XX AAN92708;

XX 31-OCT-2002 (revised)

XX 14-MAY-1990 (first entry)  
 XX Probe GH89 for DQalpha A1.2, A1.3 and A1.4 alleles.  
 XX DQalpha; GH89; ss.  
 XX Synthetic.  
 OS

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XX PN WO8911548-A.
XX PD 30-NOV-1989.
XX PF 18-MAY-1989; 89WO-US0002170.
XX PR 20-MAY-1988; 88US-00197000.
XX PR 04-MAY-1989; 89US-00347495.
XX PA (CETU ) CETUS CORP.
XX PI Saiki RK, Brlich HA;
XX PR WPI; 1989-370739/50.
XX DR
XX PT Assay reagent contg. oligo-nucleotide probe attached via spacer - each
XX PT probe having hybridisation region complementary to specific analyte
XX PT sequence, e.g. for diagnosis of genetic disease.
XX PS Example; Page 29; 47pp; English.
XX CC
XX CC Probe fixed to a filter allows simultaneous non radioactive detection of
XX CC 50 or more specific nucleotide sequences in a single test sample.
XX CC (Updated on 31-OCT-2002 to add missing OS field.)
XX SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 1 Gaps: 0

US-09-966-880A-8 (1-198) x AAN92708 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 195
AAQ38565/C
ID AAQ38565 standard; DNA; 19 BP.
XX AC AAQ38565;
XX DT 25-MAR-2003 (revised)
XX DT 15-APR-1993 (first entry)
XX DE Negative control site.
XX KW Probe; binding site; Giardia; genome; giardin; Hexamitidae; conserved;
XX KW region; hypervariable; detection assay; primer; PCR;
XX KW nucleic acid hybridisation; genus; subgroup; species; water; faecal;
XX KW human; pathogenic; internal positive control sequence; heat-induced;
XX KW mRNA; ss.
XX OS Synthetic.
XX PN EP517154-A1.
XX PD 09-DEC-1992.
XX PF 02-JUN-1992; 92EP-00109271.
XX PR 06-JUN-1991; 91US-00712904.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Atlas RM, Bej AK, Mahbubani MH;
XX PT

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DR WPI; 1992-408636/50.
XX Detection of Giardia species in water and faecal samples - by detecting
XX PT hybridisation of a probe to a complementary portion of giardin gene.
XX PS Disclosure; Page 9; 34pp; English.
XX CC
XX CC The sequences given in AAQ31855, AAQ31856 and AAQ38565 are used as
XX CC internal control regions in a method to identify the giardin gene within
XX CC the Giardia genome. Giardia species are members of the Hexamitidae, and
XX CC all contain within their genomes the giardin gene. The giardin gene has
XX CC several conserved regions, esp. between 78-190 bp, 267-385 bp and 639-809
XX CC bp. The gene also has hypervariable regions, esp. between 405-62 bp. The
XX CC conserved and hypervariable regions can be used as targets for detection
XX CC assays based upon nucleic acid hybridisation. Probes which bind
XX CC substantially to the conserved regions will permit detection of all
XX CC members of the genus. Probes which bind substantially to the
XX CC hypervariable regions will permit detection of subgroups within the genus
XX CC or to specific species. This internal negative control sequence can be
XX CC used in detection of Giardia in water samples or in faecal samples from a
XX CC patient suspected of being infected with Giardia. Identification of the
XX CC hypervariable regions of the giardin gene allows differentiation between
XX CC human pathogenic Giardia and harmless species. By detecting the presence
XX CC or absence of heat-induced mRNA, living organisms can be distinguished
XX CC from dead organisms. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ38565 (1-19)
QY 56 HisValGluLeuLeu 60
DB 18 CACGTAGAACTGCTC 4

RESULT 196
AAQ25996/C
ID AAQ25996 standard; DNA; 19 BP.
XX AC AAQ25996;
XX DT 25-MAR-2003 (revised)
XX DT 15-JAN-1993 (first entry)
XX DE Negative control-DQ alpha1.2, 1.3, 4.
XX KW Internal positive control sequence; PCR; amplification; Legionella.
XX OS Synthetic.
XX PN WO9211273-A1.
XX PD 09-JUL-1992.
XX PF 19-DEC-1991; 91WO-US009688.
XX PR 20-DEC-1990; 90US-00630899.
XX PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX PI Picone TKH, McCallum T, Zoccoli MA;
XX PR WPI; 1992-250019/30.
XX PT Nucleic acid primers for the amplification of Legionella DNA - amplify
XX PT select target regions and enable detection of pathogenic and non-

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PT pathogenic forms with shorter, simpler testing.  
 PS Disclosure; Page 31; 73pp; English.  
 XX  
 XX The sequence DQalpha1.2, 1.3, 4 is a negative control sequence for  
 CC Legionella. The positive control sequence is used in the co-  
 CC amplification of DNA from Legionella species using polymerase primers.  
 CC These primers allow for amplification of select target regions of the  
 CC genome of the genus Legionella. Detection of pathogenic and non-  
 CC pathogenic species and discrimination within the genus are possible using  
 CC less test sample and less time. See also AAQ25981-26000, 26376-26379.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores: Length: 19  
 Pred. No.: 9e+03 Matches: 5  
 Score: 5.00 Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 2  
 US-09-966-880A-8 (1-198) x AAQ25996 (1-19)  
 QY 56 HisValGluLeuLeu 60  
 DB 18 CACGTAGAACTGTC 4  
 RESULT 197  
 AAQ48922/c  
 ID AAQ48922 standard; DNA; 19 BP.  
 XX  
 AC AAQ48922;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 16-MAR-1994 (first entry)  
 XX  
 DE Cross-linking oligonucleotide 18.  
 XX  
 KW Crosslink; ON; oligonucleotide; hairpin loop; stem loop; interior loop;  
 KW bridge; fixation; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_binding 9  
 FT /tag= c  
 FT /note= "crosslinked to base 9 of (AAQ48910) via an oxime  
 FT linkage as in example 13b; The ONs also bind by  
 FT hybridisation"  
 FT modified\_base 9  
 FT /tag= a  
 FT /mod\_base= 2'-O-[propion-3-al\_bis(o-nitrobenzyl)  
 FT acetal] uridine  
 FT /note= "ref: example 4-A"  
 FT modified\_base 17  
 FT /tag= b  
 FT /mod\_base= 2'-O-[propion-3-al\_bis(o-nitrobenzyl)  
 FT acetal] uridine  
 FT /note= "ref: example 4-A"  
 FT misc\_binding 18  
 FT /tag= d  
 FT /note= "crosslinked to base 18 of (AAQ48910) via an oxime  
 FT linkage as in example 13b; The ONs also bind by  
 FT hybridisation"  
 XX  
 XX WO9318052-A1.  
 XX  
 PD 16-SEP-1993.  
 XX  
 PF 05-MAR-1993; 93WO-US002059.  
 XX

PR 05-MAR-1992; 92US-00846376.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Cook PD, Manoharan M, Bruce T;  
 XX  
 DR WPI; 1993-303395/38.  
 XX  
 XX New covalently crosslinked oligo-nucleotide(s) - used to fix duplex  
 PT structures or hairpin loop, stem loop, interior loop, bulge or other  
 PT structures.  
 XX  
 PS Disclosure; Page 71; 145pp; English.  
 XX  
 CC Sequences (AAQ48905-28) consist of novel crosslinked oligo-nucleotides. A  
 CC number of crosslinking methods are claimed, which are used to fix  
 CC separate ON strands in duplex structures or to fix a single ON strand in  
 CC a hairpin loop, stem loop, interior loop, bulge or other similar higher-  
 CC order structures. Fixing a strand or strands in a duplex structure also  
 CC can disrupt the normal function of a single stranded nucleic acid-binding  
 CC protein by forming nuclease resistant mimics of the protein binding  
 CC receptors. The ONs have diagnostic, therapeutic and prophylactic  
 CC applications as well as being used as research agents. (Updated on 25-MAR-  
 CC -2003 to correct PN field.)  
 XX  
 SQ Sequence 19 BP; 8 A; 1 C; 8 G; 0 T; 2 U; 0 Other;  
 Alignment Scores: Length: 19  
 Pred. No.: 9e+03 Matches: 5  
 Score: 5.00 Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 2  
 US-09-966-880A-8 (1-198) x AAQ48922 (1-19)  
 QY 179 IleLeuLeuProLeu 183  
 DB 17 ATTCTCTACCTCTG 3  
 RESULT 198  
 AAQ34454/c  
 ID AAQ34454 standard; DNA; 19 BP.  
 XX  
 AC AAQ34454;  
 XX  
 DT 17-DEC-2001 (revised)  
 DT 12-MAY-1993 (first entry)  
 XX  
 DE DQAl probe AG9.2, for alleles 0102, 0103 and 0501.  
 XX  
 KW Amplification; conformation polymorphism; SSCP; DQ-alpha; DQ-beta;  
 KW cystic fibrosis; neurofibromatosis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN USN7751892-N.  
 XX  
 PD 01-DEC-1992.  
 XX  
 PF 29-AUG-1991; 91US-00751892.  
 XX  
 PR 29-AUG-1991; 91US-00751892.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
 XX  
 PI Mann D, Dean M, Carrington M, White MB;  
 XX  
 DR WPI; 1993-017809/02.  
 XX  
 PT Distinguishing multiple alleles and identifying new alleles - by single-  
 PT strand conformation polymorphism technique using specific gel



PT electrophoresis conditions.  
 XX Disclosure; Page 19; 36pp; English.  
 PS  
 XX The oligomer AG9.2 represents a probe for DQA1 alleles 0501, 0102 and 0103 and is used to distinguish multiple alleles of a gene of the immunoglobulin supergene family. The DNA encoding the gene of interest in a sample is amplified and then denatured. The amplified DNA is then separated on a non-denaturing polyacrylamide gel consisting of 5 percent bis-acrylamide with 0-10 percent glycerol, and the presence or absence of DNA bands showing hybridisation is detected. Before amplification of the gene, the alleles may be divided into subsets by oligonucleotide hybridisation. Using single stranded conformation polymorphism (SSCP) multiple alleles in complex genetic systems can be distinguished e.g. DQ-alpha and DQ-beta and new alleles identified. The method may be used in studying genetic associations with disease, in forensic analyses and typing tissues for transplantation. The SSCP method has been used for detection of mutant alleles which correlate with the presence of disorders such as cystic fibrosis and neurofibromatosis. See also AAQ34443-73. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)  
 XX  
 SQ Sequence 19 BP; 5 A; 3 C; 6 G; 5 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAQ34454 (1-19)  
 QY 56 HisvalgluLeu 60  
 Db |||||  
 19 CACGTAGAACTGTC 5  
 RESULT 199  
 AAQ52889  
 ID AAQ52889 standard; RNA; 19 BP.  
 AC AAQ52889;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-MAY-1994 (first entry)  
 XX  
 DE Cytomegalovirus target sequence 66.  
 XX  
 KW RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HbRNA;  
 KW picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;  
 KW papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;  
 KW T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;  
 KW influenza virus; HSV; herpes simplex virus; vector; immune response;  
 KW antibody; ribozyme; viral RNA; treatment; ss.  
 XX  
 OS Synthetic.  
 XX  
 FN WO9323569-A1.  
 XX  
 PD 25-NOV-1993.  
 XX  
 XX 29-APR-1993; 93WO-US004020.  
 XX  
 PR 11-MAY-1992; 92US-00882689.  
 PR 14-MAY-1992; 92US-00882712.  
 PR 14-MAY-1992; 92US-00882713.  
 PR 14-MAY-1992; 92US-00882714.  
 PR 14-MAY-1992; 92US-00882823.  
 PR 14-MAY-1992; 92US-00882824.  
 PR 14-MAY-1992; 92US-00882886.

PR 14-MAY-1992; 92US-00882888.  
 PR 14-MAY-1992; 92US-00882889.  
 PR 14-MAY-1992; 92US-00882921.  
 PR 14-MAY-1992; 92US-00882922.  
 PR 14-MAY-1992; 92US-00883823.  
 PR 14-MAY-1992; 92US-00883849.  
 PR 14-MAY-1992; 92US-00884073.  
 PR 14-MAY-1992; 92US-00884074.  
 PR 14-MAY-1992; 92US-00884333.  
 PR 14-MAY-1992; 92US-00884422.  
 PR 14-MAY-1992; 92US-00884431.  
 PR 14-MAY-1992; 92US-00884436.  
 PR 14-MAY-1992; 92US-00884521.  
 PR 31-JUL-1992; 92US-00923738.  
 PR 26-AUG-1992; 92US-00935854.  
 PR 26-AUG-1992; 92US-00936086.  
 PR 18-SEP-1992; 92US-00948359.  
 PR 15-OCT-1992; 92US-00963322.  
 PR 07-DEC-1992; 92US-00987129.  
 PR 07-DEC-1992; 92US-00987130.  
 PR 07-DEC-1992; 92US-00987133.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecsek JU;  
 PI Mamone JA;  
 XX  
 DR WPI; 1993-386599/48.  
 XX  
 XX Enzymatic RNA molecules - used to inhibit viral replication, infection  
 PT and gene expression.  
 PT  
 PS Claim 5; Fig 13; 287pp; English.  
 XX  
 CC The sequences (AAQ52824-Q52890) are pref. Cytomegalovirus target  
 CC sequences for enzymatic RNA molecules. The RNA molecules are  
 CC complementary to a substrate binding region in the specified gene target.  
 CC They also have enzymatic activity, in that they specifically cleave RNA  
 CC in the target. The ERMs interfere with viral replication and therefore  
 CC have anti-viral properties. They can be used to attenuate viruses to be  
 CC used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated  
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct  
 CC PI field.)  
 XX  
 SQ Sequence 19 BP; 3 A; 5 C; 9 G; 0 T; 2 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAQ52889 (1-19)  
 QY 124 GluGlyLeuArgArg 128  
 Db |||||  
 1 GAGGCCUACGCCGU 15  
 RESULT 200  
 AAQ90410  
 ID AAQ90410 standard; DNA; 19 BP.  
 XX  
 AC AAQ90410;  
 XX  
 DT 08-JAN-1996 (first entry)  
 XX  
 DE RC-A5 (synthetic DNA probe with 5' amino terminal #9).  
 XX  
 KW RC-A5; HLA; dQa; self-addressable electronic device; SAED; hybridisation;  
 KW ss.  
 XX

```

OS Synthetic.
XX FH Key
XX misc_feature 1
XX Location/Qualifiers
FT FT /tag= a
FT FT /note= "3' aminolink2 Thymine; allows binding to any
FT FT amine"
XX
XX WO9512808-A1.
XX
XX 11-MAY-1995.
XX
XX 26-OCT-1994; 94WO-US012270.
XX
XX 01-NOV-1993; 93US-00146504.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E;
XX
XX WPI; 1995-185870/24.
XX
XX New self-addressable electronic devices - used for multi-step and
XX multiplex reactions such as DNA hybridisation(s), clinical diagnostics
XX and bio:polymer synthesis.
XX
XX Example 1; Page 41; 86pp; English.
XX
XX The sequences represented by, AAQ90402-15 are synthetic DNA probes
XX containing 5' amino termini. The sequences shown in AAQ90390-401 are
XX synthetic DNA probes with 3' ribonucleoside termini. These sequences were
XX specific for the polymorphisms of HLA gene dga. The sequences were used
XX in the device of the invention. This is a self-addressable electronic
XX device (SAED) that can be used to carry out multi-step and multiplex
XX reactions, such as nucleic acid hybridisations. The advantages of this
XX method are that these reactions can be carried out with complete and
XX precise electronic control, and that the rate, specificity and
XX sensitivity of these reactions are greatly improved at micro-locations
XX
XX Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
SQ

```

Alignment Scores:

Pred. No.:	9e+03	Length:	19
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x AAQ90410 (1-19)

QY 56 HisValGluLeuLeu 60  
 |||||  
 2 CACGTAGAACTGCTC 16

Db

RESULT 201  
 AAT10762  
 ID AAT10762 standard; RNA; 19 BP.  
 XX  
 AC AAT10762;  
 XX  
 XX 09-SEP-1996 (first entry)  
 DT  
 DE Oligonucleotide probe, RC-A5.  
 XX  
 XX Electronically self-addressable device; ED: electrode; current source;  
 KW attachment layer; permeable; counterion; genetic typing; probe;  
 KW detection; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX Key modified\_base 1  
 XX Location/Qualifiers  
 FT

```

FT FT /tag= a
FT FT /note= "5'-amino terminus"
XX
XX WO9601836-A1.
XX
XX 25-JAN-1996.
XX
XX 05-JUL-1995; 95WO-US008570.
XX
XX 07-JUL-1994; 94US-00271882.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX
XX WPI; 1996-097582/10.
XX
XX Electronically self-addressable device - used for electronic control of,
XX e.g. nucleic acid hybridisation.
XX
XX Example 1; Page 61; 155pp; English.
XX
XX The sequences given in AAT10742-67 are synthetic oligonucleotides which
XX are used in the construction of the electronically self-addressable
XX device (ED) of the invention. The ED comprises a substrate, an electrode
XX or opt. a number of electrodes supported by the substrate, a current
XX source operatively connected to the electrode and an attachment layer
XX adjacent to the electrode which is permeable to a counterion but not
XX permeable to a molecule capable of insulating or binding to the
XX electrode. The attachment layer is capable of attaching a macromolecule.
XX The ED is used for genetic typing and comprises a number of
XX electronically addressable locations each comprising an electrode, and a
XX binding entity, such as one of these probes, attached to each of the
XX locations capable of detecting the presence of a genetic sequence
XX
XX Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
SQ

```

Alignment Scores:

Pred. No.:	9e+03	Length:	19
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x AAT10762 (1-19)

QY 56 HisValGluLeuLeu 60  
 |||||  
 2 CACGTAGAACTGCTC 16

Db

RESULT 202  
 AAT7746  
 ID AAT7746 standard; DNA; 19 BP.  
 XX  
 AC AAT7746;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 26-SEP-1997 (first entry)  
 XX  
 DE Primer GP125 used in production of protein C transgene.  
 XX  
 XX Human; lactoferrin; transgenic bovine; ovum; bovine; ovary; zygote;  
 KW transgene; pre-implantation stage embryo; milk; milk protein;  
 KW serum protein; industrial enzyme; alpha-S1 casein; protein C; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US5633076-A.  
 PN  
 XX 27-MAY-1997.  
 PD  
 XX 16-NOV-1993; 93US-00154019.  
 PF

XX 01-DEC-1989; 89US-00444745.  
PR 27-NOV-1990; 90US-00619131.  
PR 15-JUN-1992; 92US-00898956.  
PR 15-JUN-1993; 93US-00077788.  
PA (PHAR-) PHARMING BV.  
XX  
XX Heyneker HL, Deboer HA, Krimpenfort PJA, Lee SH, Platenburg G;  
PI Pieper F, Strijker R;  
XX WPI; 1997-297339/27.  
XX  
XX Production of transgenic bovine embryo - by introducing trans:gene into  
PT fertilised ovum in vitro.  
XX  
XX Example 17; Col 46; 91pp; English.  
XX  
XX The sequences given in AAT77746-47 are primers which were used in the  
CC production of a protein C transgene which was used in the method of the  
CC invention to produce a transgenic bovine. The method of the invention  
CC comprises obtaining an ovum from bovine ovaries, maturing it in vitro,  
CC fertilising the mature ovum in vitro to form a zygote, introducing a  
CC transgene into the zygote in vitro where the transgene integrates into  
CC the genome of the zygote to form a transgenic embryo, maturing the zygote  
CC to a preimplantation stage embryo in vitro, and transplanting the embryo  
CC into a recipient female bovine, who gestates the embryo to produce a  
CC transgenic bovine. The method may also be used to generate transgenic  
CC bovine embryo's. The transgenic cows produced by the method of the  
CC invention secrete recombinant proteins in their milk, especially human  
CC milk proteins, human serum proteins and industrial enzymes. The milk from  
CC the transgenic cows containing the recombinant polypeptides may be used  
CC in food formulations in liquid or dried form. The food formulations will  
CC be supplemented with one or more recombinant polypeptides from the  
CC transgenic milk. The production of transgenic bovine milk containing one  
CC or more recombinant polypeptides is desirable since it provides a matrix  
CC wherein little or no purification is necessary for human consumption.  
CC (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT77746 (1-19)  
Qy 32 ValVallysArgArg 36  
Db 5 GTTGTAACACGCG 19  
|||  
RESULT 203  
AAT46986  
ID AAT46986 standard; DNA; 19 BP.  
XX  
AC AAT46986;  
XX  
DT 01-DEC-1997 (first entry)  
XX  
DE 19-mer probe for use with APX chip.  
XX  
XX apparatus; enhanced detection; biological reaction; biochip;  
KW fluid system; diagnosis; analysis; multistep; multiplex reaction;  
KW synthesis; biopolymer; automated DNA analysis system; self-addressable;  
KW self-assembling; electronic; target probe; denaturation; APX chip; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 9

FT modified\_base 1  
FT /\*tag= a  
FT /note= "5'-Bodipy Texas Red labelled C"  
XX  
XX W09712030-A1.  
XX  
XX 03-APR-1997.  
XX  
XX 06-SEP-1996; 96WO-US014353.  
XX  
XX 27-SEP-1995; 95US-00534454.  
XX  
XX (NANO-) NANOGEN INC.  
XX  
XX Heller MJ, Oconnell JP, Juncosa RD, Sosnowski RG, Jackson TR;  
PI  
XX WPI; 1997-212892/19.  
XX  
XX Self-addressable and self-assembling system for biological reactions -  
PT comprises array of specific binding regions on biochip, also new  
PT fluorescence detection system and stringency control device.  
XX  
XX Disclosure; Page 39; 69pp; English.  
XX  
XX The invention concerns an apparatus for enhanced detection of a  
CC biological reaction between a sample and an active area of a biochip,  
CC comprises the biochip and a fluidic system designed to pass the sample  
CC over the active area. The apparatus can be used for diagnosis, analysis  
CC and multistep/multiplex reactions (including synthesis of biopolymers),  
CC especially those involving nucleic acid hybridisation (but also antigen-  
CC antibody reactions). Use of a flow system improves diagnostic efficiency,  
CC allows more complete sampling and the detection device provides imaging  
CC of very small volumes. Together these elements provide a highly automated  
CC DNA analysis system from self-addressable and self-assembling electronic  
CC components. AAT46985-86 are 5'-labelled bodipy Texas Red target probes  
CC used to determine the results of electronic denaturation experiments  
CC run on an APX chip having 25 test microlocations with 80 micron diameter  
CC utilising platinum electrodes  
XX  
SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT46986 (1-19)  
Qy 56 HisValGluLeuLeu 60  
Db 2 CACGTAGAACTGCTC 16  
|||  
RESULT 204  
AAT06677/C  
ID AAT06677 standard; RNA; 19 BP.  
XX  
AC AAT06677;  
XX  
DT 25-MAR-2003 (revised)  
XX  
DT 21-MAY-1998 (first entry)  
XX  
DE Modified oligonucleotide in covalently cross-linked nucleic acid.  
XX  
XX Covalent cross-link; modified oligonucleotide; abasic site;  
KW space spanning group; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH modified\_base 9

FT FT /\*tag= a  
 FT /note= "nucleotide is a 2'-O- [propion-3-al bis(o-  
 FT nitrobenzyl)acetal] group"  
 FT 17  
 FT modified\_base  
 FT /\*tag= b  
 FT /note= "nucleotide is a 2'-O- [propion-3-al bis(o-  
 FT nitrobenzyl)acetal] group"  
 XX XX  
 PN US5719271-A.  
 XX  
 XX 17-FEB-1998.  
 PD  
 PD 30-AUG-1994; 94US-00295743.  
 XX  
 XX 05-MAR-1992; 92US-00846376.  
 PR  
 PR 05-MAR-1993; 93WO-US002059.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX Manoharan M, Bruice T, Cook PD;  
 PI  
 PI WPI; 1998-158831/14.  
 DR  
 DR Covalently cross-linked nucleic acids - in which 2'- or 3'-hydroxy groups  
 PT on sugar moieties of nucleotide(s), on one or more oligonucleotide  
 PT strands, are linked by a non-phosphorus linkage.  
 PT  
 XX Example 12; Col 42; 36pp; English.  
 PS  
 CC This sequence represents an oligonucleotide shown in the patent. The  
 CC invention relates to a cross-linked nucleic acid, which comprises: (a) a  
 CC first nucleotide located on a first oligonucleotide strand having a first  
 CC bond site located on either a 2'- or 3'-OH of the sugar moiety; (b) a  
 CC second nucleotide located on a second oligonucleotide strand having a  
 CC second bond site located on either a 2'- or 3'-OH of the sugar moiety.  
 CC The first strand is linked to the second strand via a non-phosphorus  
 CC covalent cross-linkage between the first and second bond sites, where not  
 CC both sites may be on a 3'-OH or a terminal nucleotide. The cross-linked  
 CC nucleic acids include materials in which oligonucleotide strands are  
 CC covalently cross-linked to themselves or to other strands. Such materials  
 CC can be used, e.g., as RNA mimics which are fixed in specific spatial  
 CC conformations. These materials may be used as therapeutic agents,  
 CC research reagents and diagnostic agents. (Updated on 25-MAR-2003 to  
 CC correct PR field.)  
 XX  
 SQ Sequence 19 BP; 8 A; 1 C; 8 G; 0 T; 2 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAV06677 (1-19)  
 QY 179 IleLeuLeuProLeu 183  
 DB 17 ATTCTCTACTCTCTG 3  
 RESULT 205  
 AAV06469/C  
 ID AAV06469 standard; DNA; 19 BP.  
 AC AAV06469;  
 XX  
 XX 06-MAY-1998 (first entry)  
 DT  
 DE Avian sex determination using Tsex sequence based primer Tsex JH-2.  
 XX Avian; sex determination; Tsex; probe; Z chromosome; W chromosome;  
 KW hybridisation; bird; PCR primer; ss.

XX Synthetic.  
 OS Meleagris gallopavo.  
 XX  
 PN US5707809-A.  
 XX  
 PD 13-JAN-1998.  
 XX  
 XX 12-APR-1996; 96US-00634331.  
 XX  
 XX 21-SEP-1990; 90US-00585915.  
 PR  
 PR 17-SEP-1992; 92US-00947100.  
 PR  
 PR 09-FEB-1994; 94US-00194131.  
 XX  
 XX (PEKE ) PERKIN-ELMER CORP.  
 PA  
 XX Halverson J, Dvorak J;  
 PI  
 PI WPI; 1998-109344/10.  
 DR  
 DR Avian nucleic acid amplification primers and probes - hybridise to Z  
 PT and/or W chromosomes; used for sex determination.  
 PT  
 XX Claim 6; Col 35-36; 20pp; English.  
 PS  
 CC This primer is based on a Tsex sequence obtained from a turkey cDNA  
 CC library. The Tsex sequence or its complementary sequence or a sequence of  
 CC at least eighteen contiguous nucleotides of one of these sequences can be  
 CC used for the identification of sex in avian species. These sequences can  
 CC be used for the production of a variety of nucleic acid hybridisation  
 CC probes and amplification primers. The primers and probes can hybridise to  
 CC both Z and W sex chromosomes allowing for differentiation between the two  
 CC chromosomes based on length polymorphisms. Alternatively, they may  
 CC hybridise to one of the chromosomes, permitting gender identification on  
 CC the basis of sex-specific hybridisation intensity. The combinations of  
 CC primers from different sequences allows amplification of fragments from a  
 CC specific chromosome. The primers/probes are used to determine the sex of  
 CC birds (e.g. poultry or emus) before development of obvious external  
 CC sexual differences  
 XX  
 SQ Sequence 19 BP; 1 A; 7 C; 6 G; 5 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAV06469 (1-19)  
 QY 82 ThrSerTirpSexPro 86  
 DB 17 ACAGCTGGAGCCCA 3  
 RESULT 206  
 AAV23570  
 ID AAV23570 standard; DNA; 19 BP.  
 XX  
 XX AAV23570;  
 AC  
 XX  
 DT 14-JUL-1998 (first entry)  
 XX  
 DE Primer for alphaS1-casein transgene.  
 XX Transgenic bovine; mammary gland specific promoter; milk protein; human;  
 KW mammary secretory cell; lactoferrin; serum protein lysozyme; cow;  
 KW PCR primer; alphaS1-casein; ss.  
 XX Synthetic.  
 OS Bos sp.  
 XX

PN US5741957-A.  
 XX  
 PD 21-APR-1998.  
 XX  
 PF 05-JUN-1995; 95US-00461333.  
 XX  
 PR 01-DEC-1989; 89US-00444745.  
 PR 27-NOV-1990; 90US-00619131.  
 PR 15-JUN-1992; 92US-00898956.  
 PR 15-JUN-1993; 93US-00077788.  
 PR 16-NOV-1993; 93US-00154019.  
 XX  
 PA (PHAR-) PHARMING BV.  
 XX  
 XX Heyneker HL, Krimpenfort PJA, Deboer HA, Platenburg G, Lee SH;  
 PI Pieper F, Strijker R;  
 XX  
 DR WPI; 1998-260573/23.  
 XX  
 XX Transgenic bovine useful for the production of heterologous proteins in  
 PT its milk - contains a transgene linked to bovine secretory signal and is  
 PT under the control of a mammary gland specific promoter and enhancer.  
 XX  
 XX Example 16; Col 45; 92pp; English.  
 PS  
 CC This sequence represents a primer for the bovine alphaS1-casein gene. The  
 CC amplified sequence can be used in the transgenic bovine of the invention.  
 CC The bovine contains in its somatic and germ cells contain a transgene  
 CC comprising: (a) a mammary gland specific promoter and enhancer; (b) a DNA  
 CC sequence encoding a signal sequence functional in bovine mammary gland  
 CC secretory cells; and (c) a DNA sequence comprising a heterologous  
 CC polypeptide of interest. Where the transgenic bovine or a female  
 CC descendant of it expresses the transgene in mammary secretory cells so  
 CC that the polypeptide is detectable in milk produced by the transgenic  
 CC bovine or its descendant. The transgenic bovine is useful for the  
 CC recombinant production of the human milk protein lactoferrin and the  
 CC human serum protein lysozyme in its milk for use in pharmaceuticals and  
 CC in infant formulae. The levels of transgenic protein secreted by the  
 CC transgenic bovine in its milk are higher than that produced by transgenic  
 CC sheep and mice. As the proteins are produced in the milk of the cow, they  
 CC require little or no purification for human consumption  
 XX  
 SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAV23570 (1-19)  
 QY 32 Valvallysargarg 36  
 DB 5 GTTGTAAACGACGG 19  
 RESULT 207  
 AAX81321  
 ID AAX81321 standard; DNA; 19 BP.  
 XX  
 AC AAX81321;  
 XX  
 DT 20-AUG-1999 (first entry)  
 XX  
 XX 5' amino oligonucleotide probe RC-A5.  
 DE  
 XX Microelectronic device; multi-step reaction; microscopic format;  
 KW ion-permeable permeation layer; electrode; electrical control; transport;  
 KW attachment; binding; DNA/RNA hybrid; probe; ss.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 misc\_feature 1  
 /\*tag= a  
 /note= "amino group attached at 5' terminal"  
 WO9929711-A1.  
 17-JUN-1999.  
 01-DEC-1998; 98WO-US025475.  
 05-DEC-1997; 97US-00986065.  
 (NANO-) NANOGEN INC.  
 Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;  
 WPI; 1999-385567/32.  
 New microelectronic device designed to carry out and control multi-step  
 and multiplex molecular biological reactions in microscopic format.  
 Example 1; Page 90; 179pp; English.  
 The specification describes a self-addressable, self-assembling  
 microelectronic device which is designed to actively carry out and  
 control multi-step and multiplex molecular biological reactions in  
 microscopic formats. A key aspect of this invention is played by the ion  
 -permeable permeation layer which overlies the electrode. This permeation  
 layer allows attachment of nucleic acids to permit immobilization but  
 also separates the attached oligonucleotides and hybridized target DNA  
 sequences from the highly reactive electrochemical environment generated  
 immediately at the electrode surface. The microelectronic device is  
 designed and fabricated to actively carry out and control reactions such  
 as nucleic acid hybridizations, antibody/antigen reactions, sample  
 preparation, diagnostics and biopolymer synthesis. The device can  
 electronically control the transport and attachment of specific binding  
 entities, such as nucleic acids and polypeptides, to specific micro-  
 locations. The device can subsequently control the transport and reaction  
 of analytes or reactants at the addressed specific micro-locations. The  
 device is able to concentrate analytes and reactants, remove non-  
 specifically bound molecules, provide stringency control for DNA  
 hybridization reactions and improve the detection of analytes. The  
 present sequence represents a probe used to exemplify the invention  
 SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAX81321 (1-19)  
 QY 56 HisValGluLeuLeu 60  
 DB 2 CACGTAGACTGCTC 16  
 RESULT 208  
 AAX81343/c  
 ID AAX81343 standard; DNA; 19 BP.  
 XX  
 AC AAX81343;  
 XX  
 DT 20-AUG-1999 (first entry)  
 XX  
 DE Biotinylated capture oligonucleotide ATAS.  
 XX  
 KW Microelectronic device; multi-step reaction; microscopic format;



```

XX AAZ21065;
XX AC
XX DT
XX 15-NOV-1999 (first entry)
XX DE Nitrosomonas europaea thiamine synthetase PCR primer Lacr295.
XX KW Nitrosomonas europaea; thiamine synthetase; tryptophan synthetase; thix;
XX trpX; mutant; ammonia-oxidizing microbe; limited growth; PCR primer; ss.
XX OS Synthetic.
XX OS Nitrosomonas europaea.
XX PN JP11235188-A.
XX PD 31-AUG-1999.
XX PF 08-DEC-1998; 98JP-00349146.
XX PR 08-DEC-1997; 97JP-00337547.
XX PA (KURK ) KURITA WATER IND LTD.
XX DR WPI; 1999-544006/46.
XX PT Preparation of mutant of an ammonia-oxidizing microbe - comprising
XX limited growth in natural environment.
XX PS Example 4; Page 7; 17pp; Japanese.
XX CC The present invention describes the preparation of a mutant of an ammonia
XX -oxidizing microbe of limited growth in natural environment in which the
XX function of a gene participating to the limitation of growth derived from
XX an ammonia-oxidizing microbe is artificially inactivated and the gene of
XX inactivated function is exchanged with a corresponding gene on the
XX chromosome by a homologous recombination. The method is useful for the
XX preparation of a mutant of an ammonia-oxidizing microbe of limited growth
XX in natural environment easily. The present sequence represents a PCR
XX primer for Nitrosomonas europaea thiamine synthetase (thix), which is
XX used in the exemplification of the present invention
XX SQ Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ21065 (1-19)
QY 32 ValVallysArgArg 36
Db 15 GTTGTAAACGACG 1

RESULT 211
AAZ28287
ID AAZ28287 standard; DNA; 19 BP.
XX AC
XX AAZ28287;
XX 17-JUN-1999 (first entry)
XX DE Human CYP3A4 gene polymorphism #1.
XX KW CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;
XX CYP3A4 substrate; drug-drug interaction identification; toxin exposure;
XX Genetic linkage detection; phenotypic variation; ss.
XX OS Homo sapiens.
XX PN
XX WO9851819-A1.

XX WO9913106-A1.
XX 18-MAR-1999.
XX PF 02-SEP-1998; 98WO-US018158.
XX PR 10-SEP-1997; 97US-0058612P.
XX PA (AXYS-) AXYS PHARM INC.
XX PI Lichter JB, Guida M;
XX DR WPI; 1999-215070/18.
XX FT New isolated CYP3A4 polymorphic sequences.
XX PS Claim 2; Page 35; 40pp; English.
XX CC This sequence represents a CYP3A4 sequence polymorphism of the invention,
XX which is part of a non-naturally occurring chromosome. Nucleic acids
XX comprising the CYP3A4 polymorphic sequences can be used to screen
XX patients for altered metabolism for CYP3A4 substrates, potential drug-
XX drug interactions, and adverse/side effects as well as diseases that
XX result from environmental or occupational exposure to toxins. They can
XX also be used to establish animal, cell culture and in vitro cell-free
XX models for drug metabolism. Polymorphic CYP3A4 gene sequences can be used
XX for expression studies to determine the effect of promoter and/or intron
XX sequence variations on mRNA expression and stability. The polymorphisms
XX are also used as single nucleotide polymorphisms to detect genetic
XX linkage to phenotypic variation in activity and expression of CYP3A4. The
XX nucleic acids can also be used to generate genetically modified non-human
XX animals or site specific gene modifications in cell lines
XX SQ Sequence 19 BP; 7 A; 3 C; 9 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX28287 (1-19)
QY 22 LysGlyArgArgGlu 26
Db 3 AAGGGCAGGAGAG 17

RESULT 212
AAV72008/C
ID AAV72008 standard; DNA; 19 BP.
XX AC
XX AAV72008;
XX 29-MAR-1999 (first entry)
XX DE Electronic perturbation catalysis oligonucleotide probe HLA 241.
XX KW Electronic perturbation analysis; hybridisation analysis; match hybrid;
XX mismatch hybrid; detection; clinical assay; optoelectronic device;
XX optical memory; nanofabrication; synthesis; self-assembly; denaturation;
XX self-organising; fluorescence; dehybridisation; probe; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 19
XX FT /*tag= a
XX FT /note= "3'-end modified by presence of Biotin"
XX PN
XX WO9851819-A1.

```

```

PD 19-NOV-1998.
XX
XX 07-MAY-1998; 98WO-US009357.
XX
XX 14-MAY-1997; 97US-00855058.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
XX
XX WPI; 1999-059702/05.
XX
XX Hybridisation analysis using electronic stringency control device based
XX on changes in fluorescence - when an electric field is applied to the
XX hybrid, used e.g. for sequencing or for detecting single mismatch
XX mutations, also electronic perturbation catalysis.
XX
XX Example 1; Page 28; 56pp; English.
XX
XX This sequence represents a probe used in a method for studying
XX hybridisation analysis by detecting electronic denaturation using
XX electronic perturbation analysis. The method is particularly used for
XX sequencing and to discriminate between match and mismatch hybrids,
XX particularly to detect point mutations, deletions, inserts, repeat
XX regions, single nucleotide polymorphisms, translocations, intron/exon
XX junctions, etc. The same principle may be used for most molecular
XX biological processes, e.g. antibody-antigen reactions, cell typing and
XX separation, enzymatic and other clinical assays, also in optoelectronic
XX devices and optical memory materials. The method is applicable to any
XX type of reaction, e.g. nanofabrication or other self-assembling or self-
XX organising processes, synthesis of nucleic acids, peptides, polymers etc.
XX The method relies on the observation that perturbation of a fluorescence
XX signal (particularly a peak) occurs at the electric power level which
XX causes denaturation or dehybridisation. The method is very rapid, e.g.
XX match/mismatch hybrids can be distinguished in less than a minute, e.g. 5
XX sec. It permits use of long probes (over 20 bases) and probe specificity
XX is determined by the position of the label. Since analysis does not
XX require removal of mismatched probes, the sample can be analysed
XX repeatedly to improve assay statistics
XX
XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72008 (1-19)

QY 56 HisValGlutLeuLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 213
AAV72007
ID AAV72007 standard; DNA; 19 BP.
XX
XX AAV72007;
XX
XX 29-MAR-1999 (first entry)
XX
XX Electronic perturbation catalysis oligonucleotide probe HLA 253.
XX
XX Electronic perturbation analysis; hybridisation analysis; match hybrid;
XX mismatch hybrid; detection; clinical assay; optoelectronic device;
XX optical memory; nanofabrication; synthesis; self-assembly; denaturation;
XX self-organising; fluorescence; dehybridisation; probe; ss.
XX
XX Synthetic.
XX

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FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "5'-end modified by presence of Bodipy Texas Red"
XX
XX WO9851819-A1.
XX
XX 19-NOV-1998.
XX
XX 07-MAY-1998; 98WO-US009357.
XX
XX 14-MAY-1997; 97US-00855058.
XX
XX (NANO-) NANOGEN INC.
XX
XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;
XX
XX WPI; 1999-059702/05.
XX
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XX on changes in fluorescence - when an electric field is applied to the
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XX mutations, also electronic perturbation catalysis.
XX
XX Example 1; Page 28; 56pp; English.
XX
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XX hybridisation analysis by detecting electronic denaturation using
XX electronic perturbation analysis. The method is particularly used for
XX sequencing and to discriminate between match and mismatch hybrids,
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XX regions, single nucleotide polymorphisms, translocations, intron/exon
XX junctions, etc. The same principle may be used for most molecular
XX biological processes, e.g. antibody-antigen reactions, cell typing and
XX separation, enzymatic and other clinical assays, also in optoelectronic
XX devices and optical memory materials. The method is applicable to any
XX type of reaction, e.g. nanofabrication or other self-assembling or self-
XX organising processes, synthesis of nucleic acids, peptides, polymers etc.
XX The method relies on the observation that perturbation of a fluorescence
XX signal (particularly a peak) occurs at the electric power level which
XX causes denaturation or dehybridisation. The method is very rapid, e.g.
XX match/mismatch hybrids can be distinguished in less than a minute, e.g. 5
XX sec. It permits use of long probes (over 20 bases) and probe specificity
XX is determined by the position of the label. Since analysis does not
XX require removal of mismatched probes, the sample can be analysed
XX repeatedly to improve assay statistics
XX
XX Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72007 (1-19)

QY 56 HisValGlutLeuLeu 60
Db 2 CACGTAGAACTGCTC 16

RESULT 214
AAV72011/C
ID AAV72011 standard; DNA; 19 BP.
XX
XX AAV72011;
XX
XX 29-MAR-1999 (first entry)
XX
XX Electronic perturbation catalysis oligonucleotide probe HLA 376.
XX

```



KW Electronic perturbation analysis; hybridisation analysis; match hybrid;  
KW mismatch hybrid; detection; clinical assay; optoelectronic device;  
KW optical memory; nanofabrication; synthesis; self-assembly; denaturation;  
KW self-organising; fluorescence; dehybridisation; probe; ss.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT modified\_base 19  
FT /\*tag= a  
FT /note= "3'-end modified by presence of Biotin"  
XX  
XX WO9851819-A1.  
XX  
XX 19-NOV-1998.  
XX  
XX PF 07-MAY-1998; 98WO-US009357.  
XX  
XX PR 14-MAY-1997; 97US-00855058.  
XX  
XX PA (NANO-) NANOGEN INC.  
XX  
XX PI Heller MJ, Tu E, Sosnowski RG, Oconnell JP;  
XX WPI; 1999-059702/05.  
XX  
XX Hybridisation analysis using electronic stringency control device based  
PT on changes in fluorescence - when an electric field is applied to the  
PT hybrid, used e.g. for sequencing or for detecting single mismatch  
PT mutations, also electronic perturbation catalysis.  
XX  
XX Example 1; Page 28; 56pp; English.  
XX  
XX This sequence represents a probe used in a method for studying  
CC hybridisation analysis by detecting electronic denaturation using  
CC electronic perturbation analysis. The method is particularly used for  
CC sequencing and to discriminate between match and mismatch hybrids,  
CC particularly to detect point mutations, deletions, inserts, repeat  
CC regions, single nucleotide polymorphisms, translocations, intron/exon  
CC junctions, etc. The same principle may be used for most molecular  
CC biological processes, e.g. antibody-antigen reactions, cell typing and  
CC separation, enzymatic and other clinical assays, also in optoelectronic  
CC devices and optical memory materials. The method is applicable to any  
CC type of reaction, e.g. nanofabrication or other self-assembling or self-  
CC organising processes, synthesis of nucleic acids, peptides, polymers etc.  
CC The method relies on the observation that perturbation of a fluorescence  
CC signal (particularly a peak) occurs at the electric power level which  
CC causes denaturation or dehybridisation. The method is very rapid, e.g.  
CC match/mismatch hybrids can be distinguished in less than a minute, e.g. 5  
CC sec. It permits use of long probes (over 20 bases) and probe specificity  
CC is determined by the position of the label. Since analysis does not  
CC require removal of mismatched probes, the sample can be analysed  
CC repeatedly to improve assay statistics  
XX  
SQ Sequence 19 BP; 4 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72011 (1-19)

Qy 56 HisValGluLeuLeu 60  
Db 18 CACGTAGACTGCTC 4

RESULT 215  
AAV72009/C  
ID AAV72009 standard; DNA; 19 BP.

XX  
AC AAV72009;  
XX  
DT 29-MAR-1999 (first entry)  
XX  
DE Electronic perturbation catalysis oligonucleotide probe HLA 378.  
XX  
XX Electronic perturbation analysis; hybridisation analysis; match hybrid;  
KW mismatch hybrid; detection; clinical assay; optoelectronic device;  
KW optical memory; nanofabrication; synthesis; self-assembly; denaturation;  
KW self-organising; fluorescence; dehybridisation; probe; ss.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT modified\_base 19  
FT /\*tag= a  
FT /note= "3'-end modified by presence of Biotin"  
XX  
XX WO9851819-A1.  
XX  
XX 19-NOV-1998.  
XX  
XX PF 07-MAY-1998; 98WO-US009357.  
XX  
XX PR 14-MAY-1997; 97US-00855058.  
XX  
XX PA (NANO-) NANOGEN INC.  
XX  
XX PI Heller MJ, Tu E, Sosnowski RG, Oconnell JP;  
XX WPI; 1999-059702/05.  
XX  
XX Hybridisation analysis using electronic stringency control device based  
PT on changes in fluorescence - when an electric field is applied to the  
PT hybrid, used e.g. for sequencing or for detecting single mismatch  
PT mutations, also electronic perturbation catalysis.  
XX  
XX Example 1; Page 28; 56pp; English.  
XX  
XX This sequence represents a probe used in a method for studying  
CC hybridisation analysis by detecting electronic denaturation using  
CC electronic perturbation analysis. The method is particularly used for  
CC sequencing and to discriminate between match and mismatch hybrids,  
CC particularly to detect point mutations, deletions, inserts, repeat  
CC regions, single nucleotide polymorphisms, translocations, intron/exon  
CC junctions, etc. The same principle may be used for most molecular  
CC biological processes, e.g. antibody-antigen reactions, cell typing and  
CC separation, enzymatic and other clinical assays, also in optoelectronic  
CC devices and optical memory materials. The method is applicable to any  
CC type of reaction, e.g. nanofabrication or other self-assembling or self-  
CC organising processes, synthesis of nucleic acids, peptides, polymers etc.  
CC The method relies on the observation that perturbation of a fluorescence  
CC signal (particularly a peak) occurs at the electric power level which  
CC causes denaturation or dehybridisation. The method is very rapid, e.g.  
CC match/mismatch hybrids can be distinguished in less than a minute, e.g. 5  
CC sec. It permits use of long probes (over 20 bases) and probe specificity  
CC is determined by the position of the label. Since analysis does not  
CC require removal of mismatched probes, the sample can be analysed  
CC repeatedly to improve assay statistics  
XX  
SQ Sequence 19 BP; 4 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72009 (1-19)

QY 56 HisValGluLeuLeu 60  
 Db 18 CACGTAGACTGCTC 4

RESULT 216  
 AAV72012/c  
 ID AAV72012 standard; DNA; 19 BP.  
 AC AAV72012;  
 XX  
 DT 29-MAR-1999 (first entry)  
 XX  
 DE Electronic perturbation catalysis oligonucleotide probe HLA 401.  
 XX  
 KW Electronic perturbation analysis; hybridisation analysis; match hybrid;  
 KW mismatch hybrid; detection; clinical assay; optoelectronic device;  
 KW optical memory; nanofabrication; synthesis; self-assembly; denaturation;  
 KW self-organising; fluorescence; dehybridisation; probe; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /note= "5'-end modified by presence of Biotin"  
 XX  
 PN WO9851819-A1.  
 XX  
 XX 19-NOV-1998.  
 XX  
 XX 07-MAY-1998; 98WO-US009357.  
 XX  
 XX 14-MAY-1997; 97US-00855058.  
 XX  
 XX (NANO-) NANOGEN INC.  
 XX  
 XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;  
 XX WPI; 1999-059702/05.  
 XX  
 XX Hybridisation analysis using electronic stringency control device based  
 XX on changes in fluorescence - when an electric field is applied to the  
 XX hybrid, used e.g. for sequencing or for detecting single mismatch  
 XX mutations, also electronic perturbation catalysis.  
 XX  
 XX Example 1; Page 28; 56pp; English.  
 XX  
 XX This sequence represents a probe used in a method for studying  
 XX hybridisation analysis by detecting electronic denaturation using  
 XX electronic perturbation analysis. The method is particularly used for  
 XX sequencing and to discriminate between match and mismatch hybrids,  
 XX particularly to detect point mutations, deletions, insertions, repeat  
 XX regions, single nucleotide polymorphisms, translocations, intron/exon  
 XX junctions, etc. The same principle may be used for most molecular  
 XX biological processes, e.g. antibody-antigen reactions, cell typing and  
 XX separation, enzymatic and other clinical assays, also in optoelectronic  
 XX devices and optical memory materials. The method is applicable to any  
 XX type of reaction, e.g. nanofabrication or other self-assembling or self-  
 XX organising processes, synthesis of nucleic acids, peptides, polymers etc.  
 XX The method relies on the observation that perturbation of a fluorescence  
 XX signal (particularly a peak) occurs at the electric power level which  
 XX causes denaturation or dehybridisation. The method is very rapid, e.g.  
 XX match/mismatch hybrids can be distinguished in less than a minute, e.g. 5  
 XX sec. It permits use of long probes (over 20 bases) and probe specificity  
 XX is determined by the position of the label. Since analysis does not  
 XX require removal of mismatched probes, the sample can be analysed  
 XX repeatedly to improve assay statistics  
 XX  
 XX SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
 XX

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 Db: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72012 (1-19)

QY 56 HisValGluLeuLeu 60  
 Db 18 CACGTAGACTGCTC 4

RESULT 217  
 AAV72003  
 ID AAV72003 standard; DNA; 19 BP.  
 AC AAV72003;  
 XX  
 DT 29-MAR-1999 (first entry)  
 XX  
 DE Electronic denaturation experiment 19-mer DNA probe.  
 XX  
 KW Electronic denaturation; hybridisation analysis; match hybrid;  
 KW mismatch hybrid; detection; clinical assay; optoelectronic device;  
 KW optical memory; nanofabrication; synthesis; self-assembly; perturbation;  
 KW self-organising; fluorescence; dehybridisation; probe; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /note= "nucleotide is modified by the presence of Bodipy  
 Texas Red"  
 XX  
 PN WO9851819-A1.  
 XX  
 XX 19-NOV-1998.  
 XX  
 XX 07-MAY-1998; 98WO-US009357.  
 XX  
 XX 14-MAY-1997; 97US-00855058.  
 XX  
 XX (NANO-) NANOGEN INC.  
 XX  
 XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;  
 XX WPI; 1999-059702/05.  
 XX  
 XX Hybridisation analysis using electronic stringency control device based  
 XX on changes in fluorescence - when an electric field is applied to the  
 XX hybrid, used e.g. for sequencing or for detecting single mismatch  
 XX mutations, also electronic perturbation catalysis.  
 XX  
 XX Disclosure; Page 12; 56pp; English.  
 XX  
 XX This sequence represents a probe used in a method for studying  
 XX hybridisation analysis by detecting electronic denaturation. The method  
 XX is particularly used for sequencing and to discriminate between match and  
 XX mismatch hybrids, particularly to detect point mutations, deletions,  
 XX insertions, repeat regions, single nucleotide polymorphisms, translocations,  
 XX intron/exon junctions, etc. The same principle may be used for most  
 XX molecular biological processes, e.g. antibody-antigen reactions, cell  
 XX typing and separation, enzymatic and other clinical assays, also in  
 XX optoelectronic devices and optical memory materials. The method is  
 XX applicable to any type of reaction, e.g. nanofabrication or other self-  
 XX assembling/self-organising processes, synthesis of nucleic acids,  
 XX peptides, polymers etc. The method relies on the observation that  
 XX perturbation of a fluorescence signal (particularly a peak) occurs at the  
 XX electric power level which causes denaturation or dehybridisation. The  
 XX method is very rapid, e.g. 5 sec. It permits use of long probes (over 20  
 XX bases) and probe specificity is determined by the position of the label.  
 XX Since analysis does not require removal of mismatched probes, the sample

Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5

CC can be analysed repeatedly to improve assay statistics  
 XX  
 SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Alignment Scores: 9e+03 Length: 19  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72003 (1-19)

QY 56 HisValGluLeuLeu 60  
 DB 2 CACGTAGACTGCTC 16

RESULT 218  
 AAV72010/c  
 ID AAV72010 standard; DNA; 19 BP.

XX AAV72010;

XX 29-MAR-1999 (first entry)

XX Electronic perturbation catalysis oligonucleotide probe HLA 375.

XX Electronic perturbation analysis; hybridisation analysis; match hybrid;  
 KW mismatch hybrid; detection; clinical assay; optoelectronic device;  
 KW optical memory; nanofabrication; synthesis; self-assembly; denaturation;  
 KW self-organising; fluorescence; denaturation; probe; ss.

XX Synthetic.

XX Key Location/Qualifiers  
 FH modified\_base 19  
 FT /\*tag= a  
 FT /note= "3'-end modified by presence of Biotin"

XX W09851819-A1.

XX 19-NOV-1998.

XX 07-MAY-1998; 98WO-USO09357.

XX 14-MAY-1997; 97US-00855058.

XX (NANO-) NANOGEN INC.

XX Heller MJ, Tu E, Sosnowski RG, Oconnell JP;

XX WPI; 1998-059702/05.

XX Hybridisation analysis using electronic stringency control device based  
 on changes in fluorescence - when an electric field is applied to the  
 hybrid, used e.g. for sequencing or for detecting single mismatch  
 mutations, also electronic perturbation catalysis.

XX Example 1; Page 28; 56pp; English.

XX This sequence represents a probe used in a method for studying  
 hybridisation analysis by detecting electronic denaturation using  
 electronic perturbation analysis. The method is particularly used for  
 sequencing and to discriminate between match and mismatch hybrids,  
 particularly to detect point mutations, deletions, insertions, repeat  
 regions, single nucleotide polymorphisms, translocations, intron/exon  
 junctions, etc. The same principle may be used for most molecular  
 biological processes, e.g. antibody-antigen reactions, cell typing and  
 separation, enzymatic and other clinical assays, also in optoelectronic  
 devices and optical memory materials. The method is applicable to any  
 type of reaction, e.g. nanofabrication or other self-assembly or self-  
 organising processes, synthesis of nucleic acids, peptides, polymers etc.

CC The method relies on the observation that perturbation of a fluorescence  
 signal (particularly a peak) occurs at the electric power level which  
 causes denaturation or dehybridisation. The method is very rapid, e.g.  
 CC match/mismatch hybrids can be distinguished in less than a minute, e.g. 5  
 sec. It permits use of long probes (over 20 bases) and probe specificity  
 is determined by the position of the label. Since analysis does not  
 CC require removal of mismatched probes, the sample can be analysed  
 CC repeatedly to improve assay statistics

XX Sequence 19 BP; 4 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV72010 (1-19)

QY 56 HisValGluLeuLeu 60

DB 18 CACGTAGACTGCTC 4

RESULT 219

AAA88263/c

ID AAA88263 standard; DNA; 19 BP.

XX AAA88263;

XX 06-AUG-2003 (revised)

DT 15-DEC-2000 (first entry)

DE Nitrosomonas europaea IF014298 tryptophan synthase PCR primer #3.

XX Nitrosomonas europaea; nitrification; inhibition; waste water; sludge;  
 KW ammonia oxidising microbe; bioluminescence; tryptophan synthase;  
 KW PCR primer; ss.

XX Nitrosomonas europaea.

XX JP2000184898-A.

XX 04-JUL-2000.

XX 21-DEC-1998; 98JP-00362680.

XX 21-DEC-1998; 98JP-00362680.

XX (KURK ) KURITA WATER IND LTD.

XX WPI; 2000-494007/44.

XX Evaluation of nitrification inhibiting activity of waste water against  
 active sludge.

XX Example 4; Page 10; 16pp; Japanese.

XX The present invention describes a method for the evaluation of  
 nitrification inhibiting activity of waste water against active sludge in  
 CC which an ammonia oxidising microbe recombinant body which has  
 CC bioluminescence activity and growth of which is restricted in natural  
 CC environment is mixed with waste water and the luminescence of the mixture  
 CC is used as the index. The method can be used for the rapid and easy  
 CC measurement of the extent of nitrification inhibiting activity of waste  
 CC water against active sludge. The present sequence represents a PCR primer  
 CC for Nitrosomonas europaea IF014298 tryptophan synthase, which is used in  
 CC an example from the present invention. (Updated on 06-AUG-2003 to correct  
 CC OS field.)

XX Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA88263 (1-19)

Qy 32 ValVallyeArgArg 36  
 Db 15 GTTGTAAACGACG 1

RESULT 220

AAA82679  
 ID AAA82679 standard; DNA; 19 BP.

XX AAA82679;

XX 04-DEC-2000 (first entry)

XX cdk2 ribozyme binding site #116.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX Mammalia.

XX WO200032765-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US028772.

XX 04-DEC-1998; 98US-0110954P.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.

XX Disclosure; Page 50; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment

XX Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA82679 (1-19)

Qy 193 PheArgThrLeuGly 197

Db 1 TTTCCGACTCTGGGG 15

RESULT 221

AAA84087  
 ID AAA84087 standard; DNA; 19 BP.

XX AAA84087;

XX 04-DEC-2000 (first entry)

XX Cyclin C ribozyme binding site #59.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX Mammalia.

XX WO200032765-A2.

XX 08-JUN-2000.

XX 06-DEC-1999; 99WO-US028772.

XX 04-DEC-1998; 98US-0110954P.

XX (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1.

XX Disclosure; Page 71; 109pp; English.

XX The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1. Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment

XX Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAA84087 (1-19)

Qy 62 LeuArgTyrIleSer 66

Db 1 CTACGGTATATTCA 15

RESULT 222

AAA84086  
 ID AAA84086 standard; DNA; 19 BP.

XX AAA84086;

XX 04-DEC-2000 (first entry)

XX Cyclin C ribozyme binding site #58.

XX Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

XX Mammalia.

PN WO200032765-A2.  
XX  
PD  
XX  
XX 08-JUN-2000.  
XX 06-DEC-1999; 99WO-US028772.  
XX  
XX 04-DEC-1998; 98US-0110954P.  
XX  
XX (IMMU-) IMMUSOL INC.  
XX  
XX Tritz R, Welch PJ, Barber JR, Robbins JM;  
XX  
XX WPI; 2000-412314/35.  
XX  
XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
PT PCNA and Cyclin B1.  
XX  
XX Disclosure; Page 71; 109pp; English.  
XX  
XX The present invention relates to a hairpin or hammerhead ribozyme,  
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
CC Representative examples of ribozyme recognition sites are given in  
CC AA82415 to AA86787. The ribozyme of the invention is useful for  
CC inhibiting restenosis by introduction of the ribozyme into cells. The  
CC ribozyme is resistant to endonuclease activity and hence is efficient in  
CC restenosis treatment  
XX  
SQ Sequence 19 BP; 5 A; 3 C; 4 G; 7 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAA84086 (1-19)  
  
QY 62 LeuArgTyrlleSer 66  
DB 3 CTACGGTATATTCA 17  
  
RESULT 223  
AAZ87624  
ID AAZ87624 standard; DNA; 19 BP.  
XX  
AC AAZ87624;  
XX  
DT 04-MAY-2000 (first entry)  
XX  
XX Bovine alphaS1 casein gene specific primer.  
XX  
XX Transgenic bovine; transgene; milk; serum protein; industrial enzyme;  
KW infant formulation; lactoferrin; intestinal tract infection; lysozyme;  
KW iron absorption; albumin; antibacterial; iron sequestration; PCR primer;  
KW alphaS1 casein; ss.  
XX  
OS Bos sp.  
XX  
XX US6013857-A.  
XX  
XX 11-JAN-2000.  
XX  
XX 05-JUN-1995; 95US-00464167.  
XX  
XX 01-DEC-1989; 89US-00444745.  
XX 27-NOV-1990; 90US-00619131.  
XX 15-JUN-1992; 92US-00898956.  
XX 15-JUN-1993; 93US-00077788.  
XX 16-NOV-1993; 93US-00154019.

XX  
PA (PHAR-) PHARMING BV.  
XX  
XX Deboer HA, Heyneker HL, Platenburg G, Krimpenfort PJA, Lee SH;  
PI Pieper F, Strijker R;  
XX  
XX WPI; 2000-146563/13.  
XX  
XX Transgenic cattle containing transgene controlled by mammary-specific  
PT regulator, for expressing proteins in the milk, particularly human  
PT lactoferrin for infant feeding formulations.  
XX  
XX Example 16; Col 45; 92pp; English.  
XX  
XX The invention provides a transgenic bovine in which the somatic and germ  
CC cells contain a transgene comprising a regulatory sequence from a gene  
CC expressed in mammary glands, DNA encoding a signal sequence and DNA  
CC encoding a naturally occurring heterologous polypeptide. The transgenic  
CC bovine, or its descendants, produce milk containing the heterologous  
CC polypeptide. The transgenic bovines are used to express human milk and  
CC serum proteins or industrial enzymes, specifically for infant  
CC formulations that contain human lactoferrin for control of intestinal  
CC tract infections and to improve iron absorption, particularly when  
CC potentiated by human lysozyme. The polypeptide expressed may also be  
CC human albumin, used as a plasma extender. The polypeptide expressed in  
CC milk of the transgenic bovine requires little if any purification before  
CC human consumption and is expressed at significantly higher levels than in  
CC transgenic mice or sheep. Large polypeptides that are difficult to  
CC express in other systems can also be expressed. Sequences AAZ87624-25  
CC represent primers for amplifying bovine alphaS1 casein gene fragments  
XX  
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAZ87624 (1-19)  
  
QY 32 ValVallysArgArg 36  
DB 5 GTTGTAAACGACGG 19  
  
RESULT 224  
AAZ88066/c  
ID AAZ88066 standard; DNA; 19 BP.  
XX  
AC AAZ88066;  
XX  
XX 20-APR-2000 (first entry)  
XX  
XX MLV proviral long terminal repeat DNA PCR primer #4.  
DE Lentiviral vector; packaging; gag; pol; gene therapy; infection;  
KW gene expression; PCR primer; ss.  
XX  
XX Murine leukemia virus.  
XX  
XX WO200000600-A2.  
XX  
XX 06-JAN-2000.  
XX  
XX 26-MAY-1999; 99WO-US011516.  
XX  
XX 26-MAY-1998; 98US-0086635P.  
XX (CHAN/) CHANG L.  
XX  
XX Chang L;  
PI

XX WPI; 2000-137067/12.  
XX  
XX New packaging vector comprising a nucleotide sequence encoding Gag and  
PT Pol proteins of a reference lentivirus useful for the delivery of non-  
PT lentiviral genes to target cells.  
XX  
XX Example; Page 132; 311pp; English.  
XX  
XX The present invention describes a packaging vector (PV) comprising a  
CC nucleotide sequence encoding Gag and Pol proteins of a reference  
CC lentivirus that differs from the reference lentivirus at least in that:  
CC (a) its major splice donor site is either deleted or is sufficiently  
CC different from the reference lentivirus so that it is not a potential  
CC site for homologous recombination; and (b) it lacks a functional major  
CC packaging signal so that the introduced vector causes the host cell to  
CC produce packaging vector particles comprising functional Gag and Pol  
CC proteins. The vectors are useful for transforming (eukaryotic) cells to  
CC express specific genes at high levels, e.g. for gene therapy. The  
CC improved vectors are safer, yet permit increased efficiency of packaging.  
CC The recombinant viral genome and increased long-term gene expression.  
CC These properties are required for gene therapy as a means of treating  
CC infectious and non-infectious diseases. Unlike other retroviruses, the  
CC lentiviruses are able to infect non-dividing cells. The present sequence  
CC represents an HIV proviral long terminal repeat DNA PCR primer which is  
CC used in the exemplification of the present invention  
XX  
SQ Sequence 19 BP; 8 A; 5 C; 4 G; 2 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAZ88066 (1-19)  
  
Qy 169 SerValArgLeuSer 173  
Db 18 TCTGTCGATGTCT 4  
  
RESULT 225  
AAA49122  
ID AAA49122 standard; DNA; 19 BP.  
XX  
XX AAA49122;  
XX  
XX 16-NOV-2000 (first entry)  
XX  
XX pMOS-R primer used in the construction of piece for HIV vaccine.  
XX  
XX HIV; human immunodeficiency virus; vaccine; AIDS; PCR primer; snut;  
XX silent nucleotide substitution; ss.  
XX Synthetic.  
XX  
XX WO200029561-A2.  
XX  
XX 25-MAY-2000.  
XX  
XX 27-MAR-2000; 2000WO-DK000144.  
XX  
XX 29-MAR-1999; 99DX-00000427.  
XX  
XX 09-APR-1999; 99US-0128558P.  
XX  
XX (STAT-) STATENS SERUM INST.  
XX  
XX Fomsgaard A;  
XX  
XX WPI; 2000-387778/33.  
XX  
XX

PT Producing nucleotide sequence construct with optimized codons for human  
PT immunodeficiency virus (HIV) genetic vaccine involves obtaining a first  
PT nucleotide sequence from a HIV patient, redesigning and assembling it  
PT with snuts.  
XX  
XX Example 4; Page 33; 150pp; English.  
XX  
XX The present invention relates to a nucleotide construct with optimised  
CC codons for use as a human immunodeficiency virus (HIV) DNA vaccine. The  
CC construct uses codons from highly expressed mammalian proteins to code  
CC for each derivative of an early, primary HIV envelope gene. The first  
CC stage in the production of the construct was the cloning of an HIV  
CC envelope gene. A nucleotide sequence encoding this gene was then created  
CC using codons from highly expressed mammalian genes. The next stage was  
CC the creation of snuts (AAA49060-A49079) by redesigning this nucleotide  
CC construct so that restriction enzyme sites surrounded functional regions  
CC of the sequence. The snuts were then assembled into pieces (AAA49080-  
CC A49092). The present sequence is a PCR primer that was used in the  
CC assembly of the pieces. Each derivative of the envelope gene (AAA49093-  
CC A49097) was then built using the pieces. The HIV DNA vaccine may be used  
CC as a prophylactic vaccine and as a therapeutic vaccine in HIV infected  
CC patients  
XX  
SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAA49122 (1-19)  
  
Qy 32 ValVallysArgArg 36  
Db 1 GTTGTAAACGACGG 15  
  
RESULT 226  
AAC70391  
ID AAC70391 standard; DNA; 19 BP.  
XX  
XX AAC70391;  
XX  
XX 09-FEB-2001 (first entry)  
XX  
XX Single nucleotide polymorphism PCR primer #148.  
XX  
XX Single nucleotide polymorphism; SNP; human; genetic disease;  
XX disease susceptibility; cardiovascular system; endocrine system;  
XX neurological system; forensic testing; paternity testing; PCR primer; ss.  
XX Homo sapiens.  
XX  
XX WO200058519-A2.  
XX  
XX 05-OCT-2000.  
XX  
XX 30-MAR-2000; 2000WO-US008440.  
XX  
XX 31-MAR-1999; 99US-0127248P.  
XX  
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
XX (AFFY-) AFFYMETRIX INC.  
XX  
XX Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;  
XX Lipshutz R, Patil N, Sklar P;  
XX  
XX WPI; 2000-611722/58.  
XX  
XX Nucleic acid selected from one of 106 genes comprising single nucleotide  
PT polymorphisms, allele-specific oligonucleotides to the genes are useful  
PT

PT for phenotypic correlations, forensics, paternity testing, medicine and  
PT genetic analysis.  
XX Claim 8; Fig 5; 214pp; English.  
XX The present invention is concerned with a number of human single  
XX nucleotide polymorphisms (SNPs) which the inventors identified in human  
XX genes. These SNPs can be used in disease diagnosis and prediction of an  
XX individual's susceptibility to disease, in forensic and paternity testing  
XX and in genetic mapping. In particular, the SNPs of the invention can be  
XX used to diagnose susceptibility to diseases of the cardiovascular,  
XX endocrine and neurological systems, such as coronary artery disease,  
XX schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's  
XX diseases  
SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x AAC70391 (1-19)  
QY 101 AsnProAsnLeuSer 105  
Db 2 AACCCCAACCTTCT 16  
RESULT 227  
AAC70385  
ID AAC70385 standard; DNA; 19 BP.  
AC AAC70385;  
XX 09-FEB-2001 (first entry)  
DT  
DE Single nucleotide polymorphism PCR primer #144.  
XX Single nucleotide polymorphism; SNP; human; genetic disease;  
KW disease susceptibility; cardiovascular system; endocrine system;  
KW neurological system; forensic testing; paternity testing; PCR primer; ss.  
XX Homo sapiens.  
XX WO200058519-A2.  
PN 05-OCT-2000.  
PD 30-MAR-2000; 2000WO-US008440.  
XX 31-MAR-1999; 99US-0127248P.  
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (AFFY-) AFFYMETRIX INC.  
XX Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;  
PI Lipshutz RJ, Patil N, Sklar P;  
XX WPI; 2000-611722/58.  
XX Nucleic acid selected from one of 106 genes comprising single nucleotide  
XX polymorphisms, allele-specific oligonucleotides to the genes are useful  
XX for phenotypic correlations, forensics, paternity testing, medicine and  
XX genetic analysis.  
XX Claim 8; Fig 5; 214pp; English.  
XX The present invention is concerned with a number of human single  
XX nucleotide polymorphisms (SNPs) which the inventors identified in human  
XX genes. These SNPs can be used in disease diagnosis and prediction of an

CC individual's susceptibility to disease, in forensic and paternity testing  
CC and in genetic mapping. In particular, the SNPs of the invention can be  
CC used to diagnose susceptibility to diseases of the cardiovascular,  
CC endocrine and neurological systems, such as coronary artery disease,  
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's  
CC diseases  
SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 3 Gaps: 0  
US-09-966-880A-8 (1-198) x AAC70385 (1-19)  
QY 101 AsnProAsnLeuSer 105  
Db 2 AACCCCAACCTTCT 16  
RESULT 228  
AAC70388  
ID AAC70388 standard; DNA; 19 BP.  
XX AC AAC70388;  
XX 09-FEB-2001 (first entry)  
DT  
DE Single nucleotide polymorphism PCR primer #146.  
XX Single nucleotide polymorphism; SNP; human; genetic disease;  
KW disease susceptibility; cardiovascular system; endocrine system;  
KW neurological system; forensic testing; paternity testing; PCR primer; ss.  
XX Homo sapiens.  
XX WO200058519-A2.  
PN 05-OCT-2000.  
PD 30-MAR-2000; 2000WO-US008440.  
XX 31-MAR-1999; 99US-0127248P.  
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (AFFY-) AFFYMETRIX INC.  
XX Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;  
PI Lipshutz RJ, Patil N, Sklar P;  
XX WPI; 2000-611722/58.  
XX Nucleic acid selected from one of 106 genes comprising single nucleotide  
XX polymorphisms, allele-specific oligonucleotides to the genes are useful  
XX for phenotypic correlations, forensics, paternity testing, medicine and  
XX genetic analysis.  
XX Claim 8; Fig 5; 214pp; English.  
XX The present invention is concerned with a number of human single  
XX nucleotide polymorphisms (SNPs) which the inventors identified in human  
XX genes. These SNPs can be used in disease diagnosis and prediction of an  
XX individual's susceptibility to disease, in forensic and paternity testing  
XX and in genetic mapping. In particular, the SNPs of the invention can be  
XX used to diagnose susceptibility to diseases of the cardiovascular,  
XX endocrine and neurological systems, such as coronary artery disease,  
XX schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's  
XX diseases  
SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

CC construction of a hLF transgene cassette

XX Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores: 9e+03 Length: 19  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 3

US-09-966-880A-8 (1-198) x AAA59922 (1-19)

Qy 32 Valvallysarg 36  
 |||||  
 Db 5 GTTGTAACGACGG 19

RESULT 230  
 AAC64682/C  
 ID AAC64682 standard; DNA; 19 BP.  
 XX AC AAC64682;  
 XX 27-FEB-2001 (first entry)  
 XX Nitrosomonas europaea trpX PCR primer SEQ ID NO:5.  
 XX Nitrosomonas europaea; trpX; TRPA-1; TRPA-2; frozen microbe body;  
 KW ammonia-oxidising microbe; inhibition; nitrification; luciferase;  
 KW PCR primer; ss.  
 XX Nitrosomonas europaea.  
 OS JP2000262285-A.  
 PN 26-SEP-2000.  
 XX 15-MAR-1999; 99JP-00067954.  
 XX 15-MAR-1999; 99JP-00067954.  
 XX (KURK ) KURITA WATER IND LTD.  
 XX WPI; 2000-675515/66.  
 XX Preparation of the frozen microbe body of an ammonia-oxidizing microbe  
 PT and a frozen microbe body useful for measurement of the inhibiting rate  
 PT on nitrification activity.  
 XX Example 1; Page 10; 21pp; Japanese.  
 PS The present invention describes a method for the preparation of the  
 CC frozen microbe body of an ammonia-oxidising microbe in which a protective  
 CC agent containing a protein which protects the bioluminescence activity of  
 CC an ammonia-oxidising microbe having luciferase gene and protects the  
 CC response ability to a nitrification-inhibiting substance is made to co-  
 CC exist when the ammonia-oxidising microbe is frozen. Also described is a  
 CC frozen microbe body of an ammonia-oxidising microbe prepared by freezing  
 CC an ammonia-oxidising microbe having luciferase gene in the co-existence  
 CC of the above protective agent. The frozen microbe body can be used for  
 CC the measurement of the inhibiting rate on nitrification activity. The  
 CC present sequence represents a PCR primer, which is used in an example  
 CC from the present invention  
 XX Sequence 19 BP; 3 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores: 9e+03 Length: 19  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53%

Alignment Scores: 9e+03 Length: 19  
 Pred. No.: 5.00 Matches: 5  
 Score: 100.00% Conservative: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 2.53% Gaps: 0  
 DB: 3

US-09-966-880A-8 (1-198) x AAC70388 (1-19)

Qy 101 AsnProAsnLeuSer 105  
 |||||  
 Db 2 AACCCACGCTTCT 16

RESULT 229  
 AAA59922  
 ID AAA59922 standard; DNA; 19 BP.  
 XX AC AAA59922;  
 XX 16-OCT-2000 (first entry)  
 XX PCR primer used in hLF transgene expression cassette construction.  
 XX Lactoferrin; transgenic bovine species; milk; infant formula;  
 KW alphaS1-casein expression regulatory sequence; PCR primer; ss.  
 XX Bos sp.  
 OS US6066725-A.  
 PN 23-MAY-2000.  
 XX 21-SEP-1998; 98US-00158313.  
 XX 01-DEC-1989; 89US-00444745.  
 PR 27-NOV-1990; 90US-00619131.  
 PR 15-JUN-1992; 92US-00898956.  
 PR 15-JUN-1993; 93US-00077788.  
 PR 16-NOV-1993; 93US-00154019.  
 PR 07-JUN-1995; 95US-00476798.  
 XX (PHAR-) PHARMING BV.  
 XX Deboer HA, Heyneker HL, Lee SH, Krimpenfort PJA, Platenburg G;  
 PI Pieper F, Strijker R;  
 XX WPI; 2000-450654/39.  
 XX New isolated cDNA sequence encoding the mature human lactoferrin protein,  
 PT useful for generating higher amounts of lactoferrin in bovine milk, which  
 PT are beneficial and safe for human consumption.  
 XX Example 16; Col 45; 89pp; English.  
 PS This invention relates to a cDNA sequence encoding the mature human  
 CC lactoferrin (hLF) protein. Lactoferrin is the major iron binding protein  
 CC in human milk, and may play a role in the absorption of iron by the small  
 CC intestine. The invention concerns the expression of hLF in bovine milk.  
 CC Included in the invention are methods for the production of transgenic  
 CC bovine species, which produce milk with high lactoferrin levels. The hLF  
 CC coding sequence is placed under the control of bovine alphaS1-casein  
 CC expression regulation sequences. The transgenic milk may be either used  
 CC as normal milk, or further treated to purify the recombinant polypeptide.  
 CC Purified hLF obtained from the transgenic cows may be used in food  
 CC formulations such as infant formula. The methods contained in the  
 CC invention may be used to obtain milk from transgenic cows which has  
 CC nutritional or other beneficial value. The advantage of the production of  
 CC transgenic bovine milk using the isolated lactoferrin cDNA sequence, is  
 CC that it provides a matrix where little or no purification is necessary  
 CC prior to human consumption. The present sequence represents a PCR primer  
 CC used to amplify the alphaS1-casein DNA sequence for use in the



DB: 3 Gaps: 0

US-09-966-880A-8 (1-198) x AAC64682 (1-19)

Qy 32 ValVallyeArgArg 36  
 |||||

Db 15 GTTGTAAACGACGG 1

RESULT 231  
 AAC68319  
 ID AAC68319 standard; DNA; 19 BP.  
 XX  
 AC AAC68319;  
 XX  
 DT 20-FEB-2001 (first entry)  
 XX  
 DE Primer 1 used in construction of transgene cassette.  
 XX  
 KW Lactoferrin; mammary; milk; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US6140552-A.  
 XX  
 PD 31-OCT-2000.  
 XX  
 PF 07-JUN-1995; 95US-00476798.  
 XX  
 PR 01-DEC-1989; 89US-00444745.  
 PR 27-NOV-1990; 90US-00619131.  
 PR 15-JUN-1992; 92US-00898956.  
 PR 15-JUN-1993; 93US-00077788.  
 PR 16-NOV-1993; 93US-00154019.  
 XX  
 PA (PHAR-) PHARMING BV.  
 XX  
 PI Strijker R, Heynaker HL, Platenburg G, Pieper F, Krimpenfort PUA;  
 PI Lee SH, Deboer HA;  
 XX  
 DR WPI; 2001-040323/05.  
 XX  
 PT New transgenic bovine whose mammary gland cells contain DNA encoding a  
 PT signal sequence, and a polypeptide of interest and an expression  
 PT regulatory sequence, for producing polypeptides in bovine milk.  
 XX  
 PS Example; Col 44; 88pp; English.  
 XX  
 CC The present invention relates to a transgenic or chimeric bovine whose  
 CC mammary gland cells contain a construct encoding a signal sequence, a  
 CC polypeptide of interest and a regulatory sequence that promotes  
 CC expression of the DNA sequence. The transgenic or chimeric bovine is  
 CC useful for producing recombinant polypeptides in milk of female  
 CC transgenic mammals. The recombinant polypeptide may be used in food  
 CC formulations, particularly in infant formula having either nutritional or  
 CC beneficial value. An infant formula containing human lactoferrin from the  
 CC transgenic bovine milk provides bacteriostatic effect, which aids in  
 CC controlling diarrhoea in newborn. Recombinant polypeptides may also be  
 CC used to supplement common diet formulations

Qy 32 ValVallyeArgArg 36  
 |||||

US-09-966-880A-8 (1-198) x AAC68319 (1-19)

Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAC68319 (1-19)

Qy 32 ValVallyeArgArg 36  
 |||||

Db 5 GTTGTAAACGACGG 19

RESULT 232  
 AAH44505  
 ID AAH44505 standard; DNA; 19 BP.  
 XX  
 AC AAH44505;  
 XX  
 DT 25-OCT-2001 (first entry)  
 XX  
 DE Human glutaredoxin-Bio36 PCR primer 2.  
 XX  
 KW Human; glutaredoxin-Bio36; hGRX-Bio36; genital system disease;  
 KW cardiovascular system disease; cerebral ischaemia; PCR primer;  
 KW cerebral nerve cell damage; immunological disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN CN1297897-A.  
 XX  
 PD 06-JUN-2001.  
 XX  
 PF 24-NOV-1999; 99CN-00124106.  
 XX  
 PR 24-NOV-1999; 99CN-00124106.  
 XX  
 PA (SHAN-) SHANGHAI SHENGYUAN GENE DEV CO LTD.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2001-489646/54.  
 XX  
 PT New human oxyglutelinoid and its code sequence.  
 XX  
 PS Example 3; Page 13 (Disclosure); 25pp; Chinese.  
 XX  
 CC The present invention describes the human glutaredoxin-Bio36 (hGRX-Bio36)  
 CC protein. The present invention also discloses a method of applying the  
 CC protein in treating various diseases, such as genital system disease,  
 CC cardiovascular system disease, cerebral ischaemia and cerebral nerve cell  
 CC damage and immunological diseases. The present sequence represents a PCR  
 CC primer for hGRX-Bio36, which is used in an example from the present  
 CC invention

Qy 108 IlePheThrAlaArg 112  
 |||||

Db 3 ATCTTCACGGCTCGC 17

US-09-966-880A-8 (1-198) x AAH44505 (1-19)

Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0

US-09-966-880A-8 (1-198) x AAH44505 (1-19)

Qy 108 IlePheThrAlaArg 112  
 |||||

Db 3 ATCTTCACGGCTCGC 17

RESULT 233  
 AAH44651/C  
 ID AAH44651 standard; DNA; 19 BP.  
 XX  
 AC AAH44651;  
 XX  
 DT 09-NOV-2001 (first entry)  
 XX  
 DE Hydrazide 19-mer oligonucleotide.  
 XX  
 KW Hydrazide; multiple attachment moiety; binding; biomolecule;  
 KW phenyl boronic acid; microarray; solid-phase synthesis; diagnostic;  
 KW analytical technique; immobilised reagent; hybridisation;

KW gene sequence identification; ss.  
 XX Synthetic.  
 XX WO200151689-A1.  
 XX 19-JUL-2001.  
 XX 11-AUG-2000; 2000WO-US022205.  
 XX 11-JAN-2000; 2000US-0175550P.  
 XX (NANO-) NANOGEN INC.  
 XX Schweitzer M, Windhab N, Havens JR, Onofrey TJ, Greef CH, Wang D;  
 XX WPI; 2001-557493/C2.  
 XX Binding biomolecules to substrate by contacting with branched linking  
 XX group to form branched linking structure, and contacting linking  
 XX structure with binding group in substrate.  
 XX Example 2; Page 28; 90pp; English.  
 XX The present invention describes biomolecules which are bound to a  
 CC substrate by contacting with a branched linking group to form a branched  
 CC linking structure, and contacting the linking structure with a binding  
 CC group contained within the substrate to form a coupled substrate binding  
 CC structure. Also described are: (1) the use of branched and unbranched  
 CC phenyl boronic acid containing molecules to bind biomolecules to a  
 CC substrate; and (2) a microarray with binding groups coupled to  
 CC biomolecules. The biomolecules can be used for solid-phase synthesis  
 CC and/or synthesis of small molecule libraries e.g. deoxyribonucleic acid,  
 CC ribonucleic acid, pyranosyl-ribonucleic acid, and peptides, and for  
 CC analytical techniques that require immobilised reagents e.g.  
 CC hybridisation based assays, diagnostics, and gene sequences.  
 CC identification. The present sequence represents a hydrazide 19-mer  
 CC oligonucleotide which is used in an example from the present invention  
 XX  
 SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAH44651 (1-19)  
 Qy 56 HisValGluLeuLeu 60  
 Db 18 CACGTAGACTGCTC 4  
 RESULT 234  
 AAH49500/C  
 ID AAH49500 standard; DNA; 19 BP.  
 XX  
 AC AAH49500;  
 XX  
 DT 21-DEC-2001 (first entry)  
 XX  
 DE Oligonucleotide containing acetyl/aldehyde modification.  
 XX  
 KW Acetyl group-containing reactive monomer; phosphoramidite;  
 KW nucleotide synthesis; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1/\*tag= a

FT  
 FT /mod\_base= OTHER  
 FT /note= "5' end is modified by presence of an acetyl or  
 XX aldehyde group"  
 XX WO200170751-A1.  
 XX 27-SEP-2001.  
 XX 19-FEB-2001; 2001WO-EP001799.  
 XX 18-MAR-2000; 2000DE-01013600.  
 XX (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.  
 XX Schweitzer M;  
 XX WPI; 2001-616397/71.  
 XX New stable, acetal group-containing reactive monomers, useful as  
 PT intermediates in the synthesis of oligo- or polynucleotides containing  
 PT reactive aldehyde groups for conjugation with modifying agents.  
 XX  
 PS Disclosure; Fig 4; 48pp; German.  
 XX  
 CC This invention describes novel acetyl group-containing reactive monomers  
 CC (I) for oligo- or polynucleotide synthesis. The use of the monomers (I)  
 CC or the mono-, oligo- or polynucleotides (A) is claimed in oligo- or  
 CC polynucleotide synthesis or replication, especially by the  
 CC phosphoramidite method or PCR; and the use of the mono-, oligo- or  
 CC polynucleotides (B) is claimed for conjugation reactions via the aldehyde  
 CC groups. A wide range of modified oligo- or polynucleotides can be  
 CC prepared by incorporating an acetal group using (I), converting the  
 CC acetal group into aldehyde and coupling with further reactants (e.g.  
 CC drugs, reporter groups, radioisotopes, antibodies or enzymes)  
 CC reactive aldehyde group. (I) are storage-stable (unlike the corresponding  
 CC free aldehydes, which oxidize spontaneously in air) and easily handled,  
 CC prepared and incorporated in oligo- or polynucleotides. (I) are stable  
 CC under the conditions of standard oligo- or polynucleotide synthesis or  
 CC replication methods (e.g. the phosphoramidite method or PCR) and  
 CC deprotection reactions. The acetal groups in the oligo- or polynucleotide  
 CC products are easily converted into aldehyde. This sequence represents an  
 CC oligonucleotide used to illustrate the method of the invention  
 XX  
 SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 4 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAH49500 (1-19)  
 Qy 56 HisValGluLeuLeu 60  
 Db 18 CACGTAGACTGCTC 4  
 RESULT 235  
 AAH57841  
 ID AAH57841 standard; DNA; 19 BP.  
 XX  
 AC AAH57841;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX  
 DE Cell-cycle dependent kinase cdk2 ribozyme binding site SEQ ID NO:265.  
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
 KW recognition site; target; ribozyme binding site; eye disease; vulvular;  
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; WMP;

KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;  
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;  
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;  
KW sickle cell retinopathy; ss.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200130362-A2.  
PN 03-MAY-2001.  
XX 26-OCT-2000; 2000WO-US029500.  
XX 26-OCT-1999; 99US-0161532P.  
PR (IMMU-) IMMUSOL INC.  
XX Robbins JM, Tritz R;  
PI WPI; 2001-300427/31.  
XX Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
XX Example 1; Page 91; 408pp; English.  
XX The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (II) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (i). (i) can have antipsoriatic,  
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,  
CC ophthalmological, vulnary, keratolytic and virucide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (i) can be used  
CC in gene therapy. (i) and (ii) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAH57841 (1-19)

QY 193 PheArgThrLeuGly 197  
Db 1 TTTCGGACTCTGGGG 15

RESULT 236  
AAH59249  
ID AAH59249 standard; DNA; 19 BP.  
XX  
AC AAH59249;  
XX  
DT 10-SEP-2001 (first entry)

Cyclin C ribozyme binding site SEQ ID NO:1673.  
Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
recognition site; target; ribozyme binding site; eye disease; vulnary;  
proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;  
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;  
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;  
KW sickle cell retinopathy; ss.  
XX Homo sapiens.  
OS Synthetic.  
XX WO200130362-A2.  
PN 03-MAY-2001.  
XX 26-OCT-2000; 2000WO-US029500.  
XX 26-OCT-1999; 99US-0161532P.  
PR (IMMU-) IMMUSOL INC.  
XX Robbins JM, Tritz R;  
PI WPI; 2001-300427/31.  
XX Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
XX Example 1; Page 193; 408pp; English.  
XX The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (i) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (ii) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (i). (i) can have antipsoriatic,  
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,  
CC ophthalmological, vulnary, keratolytic and virucide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (i) can be used  
CC in gene therapy. (i) and (ii) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 19 BP; 6 A; 3 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AAH59249 (1-19)

QY 62 LeuArgThrLeuSer 66  
Db 1 CTACGGTATATTCA 15

RESULT 237  
AAH59248  
ID AAH59248 standard; DNA; 19 BP.  
XX  
AC AAH59248;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Cyclin C ribozyme binding site SEQ ID NO:1672.  
XX  
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
KW recognition site; target; ribozyme binding site; eye disease; vulnary;  
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
KW antiproliferative; antiseborrheic; antidiabetic; virucide;  
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;  
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;  
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;  
KW sickle cell retinopathy; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200130362-A2.  
XX  
PD 03-MAY-2001.  
XX  
PF 26-OCT-2000; 2000WO-US029500.  
XX  
PR 26-OCT-1999; 99US-0161532P.  
XX  
PA (IMMU-) IMMUSOL INC.  
XX  
PI Robbins JM, Tritz R;  
XX  
DR WPI; 2001-300427/31.  
XX  
PT Treating proliferative skin or eye diseases and scarring, using ribozymes  
PT that cleave RNA encoding cytokines involved in inflammation, matrix  
PT metalloproteinases, growth factors and cell-cycle dependent kinases.  
XX  
PS Example 1; Page 193; 408pp; English.  
XX  
CC The present invention describes a method for treating a proliferative  
CC skin or eye disease and scarring. The method involves administering a  
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in  
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
CC dependent kinase, growth factor or a reductase, or administering a  
CC nucleic acid molecule (II) comprising a promoter operably linked to a  
CC nucleic acid segment encoding (I). (I) can have antiproliferative,  
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,  
CC ophthalmological, vulnary, keratolytic and virucide activities, and  
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
CC in gene therapy. (I) and (II) are useful for treating proliferative skin  
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,  
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can  
CC also be used for treating proliferative eye diseases such as diabetic  
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
CC prematurity and retinal detachment, and for treating and preventing  
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn  
CC scar. AAH57577 to AAH62099 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 19 BP; 5 A; 3 C; 4 G; 7 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAH59248 (1-19)

QY 62 LeuAtgTyrIleSer 66

Db 3 CTACGGTATATTCA 17

RESULT 238

AAH26909/c

ID AAH26909 standard; DNA; 19 BP.

XX AAH26909;

AC AAH26909;

DT 21-DEC-2001 (first entry)

XX Biotinylated DNA capture probe C2(ATA5) for electron hybridisation.

DE Capture probe; hybridisation; electronics; photonics; nanotechnology; ss.

XX Synthetic.

XX Key Location/Qualifiers

FN modified\_base 19

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "biotinylation"

XX WO200153799-A1.

XX 26-JUL-2001.

XX 12-JAN-2001; 2001WO-US000926.

XX 24-JAN-2000; 2000US-00489855.

XX (NANO-) NANOGEN INC.

XX Edman CF, Heller MJ, Gurtner C, Formosa R;

XX WPI; 2001-607116/69.

XX Device for photoelectric transport of charged materials in liquid

XX environment for micro- and opto- electronic devices, has a substrate

XX generating light induced current, conductor, permeation layer and light

XX source to illuminate substrate.

XX Disclosure; Page 60; 119pp; English.

XX The present sequence is that of biotinylated capture probe C2(ATA5).

XX which was used to demonstrate an electron hybridisation method of the

XX invention. Mn203 stabilised n-type silicon photoelectrodes coated with a

XX streptavidin-agarose permeation layer were shown to constitute a simple

XX platform for rapid manipulation of DNA oligonucleotides by electron

XX hybridisation. In this process, a set of unlabelled oligonucleotides

XX (capture strands) are first targeted to specific locations and anchored.

XX A second set of fluorescently labeled oligonucleotides (target strands) is

XX then targeted to the same locations and actively hybridised to the

XX capture strands. In the example provided, 2 sets of biotinylated capture

XX probes, C1 (see AAH26908) and C2 (present sequence), were successively

XX transported and anchored to 4 different locations on a streptavidin-

XX agarose and Mn203 coated amorphous silicon substrate. 2 Fluorescence

XX labeled target sequences, T1 (see AAH26910) and T2 (see AAH26911), were

XX then transported to a location with complementary capture probes and a

XX location with non-complementary capture probes. This step produced 2

XX clearly detectable fluorescence signals at the 2 locations with matching

XX sequences. The ratio between signal and non-specific background was

XX better than 4. The method allows for detection of DNA oligonucleotides in

XX an extremely short time. The invention generally provides systems and

XX devices for photoelectroretrotranspore transport and hybridisation of

XX oligonucleotides. The techniques of the invention have wide use in

XX manufacture of micro electronic and opto electronic devices. Self-

XX assembly fabrication techniques based on DNA polymers enables micron, sub

XX -micron or nanoscale devices to be fabricated

XX SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAH26909 (1-19)

Qy 56 HisValGluLeuLeu 60  
 |||||  
 Db 18 CACGTAGACTGCTC 4

RESULT 239  
 AAS43497  
 ID AAS43497 standard; DNA; 19 BP.  
 AC AAS43497;  
 DT 18-DEC-2001 (first entry)  
 DE Corneodesmosin PCR primer #6.  
 KW Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;  
 KW antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.  
 OS Homo sapiens.  
 XX WO200162788-A2.  
 XX 30-AUG-2001.  
 PF 23-FEB-2001; 2001WO-GB000795.  
 XX 23-FEB-2000; 2000GB-00004312.  
 XX (OXAG-) OXAGEN LTD.  
 PA Olaveson M, Lench N, Allen M, Tazi-Ahnni R;  
 PI WPI; 2001-570627/64.  
 DR Corneodesmosin protein and polynucleotide encoding it, having one or more  
 PT polymorphisms useful in treating, diagnosing or determining  
 PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory  
 PT diseases.  
 XX Disclosure; Page 25; 60pp; English.

CC The invention relates to corneodesmosin protein (I) and nucleic acid (II)  
 CC encoding the corneodesmosin gene, where the gene comprises a base  
 CC substitution, deletion or insertion at one or more positions. (I) and  
 CC (II) are useful for screening for agents for use in prognosis, diagnosis  
 CC and treatment of individuals having or being susceptible to  
 CC corneodesmosin-mediated diseases, by monitoring the reaction between the  
 CC molecules and the agents. The nucleotide and amino acid polymorphisms are  
 CC useful for diagnosing or determining susceptibility to corneodesmosin-  
 CC mediated disease, which facilitates subsequent treatment of the disease  
 CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)  
 CC are useful in diagnostic, prognostic or therapeutic methods and as  
 CC research tools for e.g. in drug screening. (II) is useful as probes or  
 CC primers for detecting an allele of the polymorphism or in the regulation  
 CC of corneodesmosin gene. Antibodies which binds to (I) are useful for  
 CC screening DNA cline libraries for cells secreting the antigen. (II) is  
 CC useful as a model to investigate the role of corneodesmosin in normal  
 CC skin function. AAS43492-AAS43749 represent corneodesmosin coding  
 CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the  
 CC invention

XX SQ Sequence 19 BP; 4 A; 7 C; 5 G; 2 T; 0 U; 1 Other;

Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 5 Gaps: 0

US-09-966-880A-8 (1-198) x AAS43497 (1-19)

Qy 129 LeuHisArgAlaGly 133  
 |||||  
 Db 4 CTCACAGAGCTGGA 18

RESULT 240  
 ABV73311/c  
 ID ABV73311 standard; DNA; 19 BP.  
 XX AC ABV73311;  
 XX 22-JAN-2003 (first entry)  
 DE Troponin T cDNA amplifying primer.  
 KW Replacement cell; primordial stem cell; pluripotent; immunosuppressive;  
 KW cell therapy; nuclear transfer; skeletal; troponin T; PCR; primer; ss.  
 OS Bos taurus.  
 XX WO200273188-A1.  
 XX 19-SEP-2002.  
 PF 13-MAR-2002; 2002WO-US007394.  
 XX 13-MAR-2001; 2001US-0275104P.  
 XX (ADCE-) ADVANCED CELL TECHNOLOGY INC.  
 PA Lanza R;  
 PI WPI; 2002-713528/77.  
 DR Producing replacement cells and/or tissues for treating patients in need  
 PT of replacement cells comprises exposing the pluripotent cells to  
 PT environmental cues in order to encourage development along a certain  
 PT path.  
 XX Example 4; Page 28; 53pp; English.

CC The invention relates to producing replacement cells and/or tissues for a  
 CC mammal. The method involves (a) isolating a primordial stem cell or other  
 CC embryonic pluripotent cell or cells; (b) introducing into the primordial  
 CC stem cell or embryonic pluripotent cells at least one selectable marker  
 CC operatively linked to a cell or tissue specific promoter, enhancer or  
 CC other regulatory genetic element so that the selectable marker is  
 CC expressed in the cell or tissue type of interest; (c) permitting the  
 CC primordial stem cell or embryonic cells to differentiate into  
 CC differentiated cells and tissues; and (d) selecting for cells and tissues  
 CC that express the selectable marker in order to produce replacement cells  
 CC and/or tissues. The method is useful for treating patients in need of  
 CC replacement cells. The method eliminates the need for in vitro isolation  
 CC and differentiation of embryonic stem cells in producing isogenic  
 CC replacement tissues using nuclear transfer. The present sequence  
 CC represents a PCR primer for amplifying troponin T cDNA for creation of  
 CC tissue-engineered cardiac tissue by nuclear transfer in Bos taurus  
 XX SQ Sequence 19 BP; 4 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABV73311 (1-19)

QY 126 LeuArgArgLeuHis 130

Db 17 CTTGGCGGCTACAT 3

RESULT 241

ABK68748

ID ABK68748 standard; DNA; 19 BP.

XX

AC ABK68748;

XX

DT 02-JUL-2002 (first entry)

XX

DE Oligonucleotide #2 for detecting polymorphism in CYP3A4 gene.

XX

KW Human; single nucleotide polymorphism; SNP; cytochrome p450; CYP; CYP3A4;  
KW ss.

XX

OS Homo sapiens.

XX

PN WO200218641-A2.

XX

PD 07-MAR-2002.

XX

PF 30-AUG-2001; 2001WO-1B001580.

XX

PR 30-AUG-2000; 2000GB-00021286.

XX

PA (GEMI-) GEMINI GENOMICS PLC.

XX

PI Risinger C, Andersson MK, Lewander T, Olaisson E;

XX

DR WPI; 2002-351712/38.

XX

PT Novel primer pairs and sequence determination oligonucleotides useful for  
PT amplifying and detecting novel single nucleotide polymorphisms in the 5'  
PT flanking regions of cytochrome p450 (CYP3A4 and CYP2C9 genes  
PT respectively.

XX

PS Disclosure; Page 3; 47pp; English.

XX

CC The present invention relates to PCR primer pairs for amplifying and  
CC sequence determination oligonucleotides for detecting single nucleotide  
CC polymorphisms (SNPs) in the 5'-flanking regions of human cytochrome p450  
CC (CYP) genes encoding CYP3A4 or CYP2C9. The SNPs correspond to position  
CC 461 of a defined 1345 base pair sequence for CYP3A4 or position 957,  
CC 1049, 1164, 1526, 1661 and 1662 of a 2438 base pair sequence for CYP2C9.  
CC The PCR primers are useful for amplifying the CYP sequences and the  
CC oligonucleotides are useful for detecting SNPs in the 5'-flanking regions  
CC of the CYP3A4 or CYP2C9 genes. ABK68747-ABK68750 represent previously  
CC published oligonucleotides for detecting a polymorphism in the CYP3A4  
CC gene

XX

SQ Sequence 19 BP; 7 A; 3 C; 9 G; 0 T; 0 U; 0 Other;

XX

Alignment Scores: 9e+03 Length: 19  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6

US-09-966-880A-8 (1-198) x ABK68748 (1-19)

QY 22 LysGlyArgArgGlu 26

Db 3 AAGCGCAGGAGAG 17

RESULT 242

ABN88432

ID ABN88432 standard; DNA; 19 BP.

XX

AC ABN88432;

XX

DT 19-AUG-2002 (first entry)

XX

DE Mouse genome polymorphic region related PCR primer SEQ ID NO:122.

XX

KW Molecular recognition; solid support assay system; non-standard base;  
KW hybridisation; PCR primer; ss.

XX

OS Mus sp.

OS Synthetic.

XX

PN WO200233126-A2.

XX

PD 25-APR-2002.

XX

PF 15-OCT-2001; 2001WO-US031993.

XX

PR 14-OCT-2000; 2000US-0240397P.

XX

PR 10-APR-2001; 2001US-0282831P.

XX

PR 18-MAY-2001; 2001US-00861292.

XX

PR 22-MAY-2001; 2001US-0293259P.

XX

PA (ERAG-) ERAGEN BIOSCIENCES INC.

XX

PI Grenier JK, Marshall DJ, Prudent JR, Richmond CS, Roesch EB;

XX

PI Scherrer CW, Sherrill CB, Ptacin JL;

XX

DR WPI; 2002-479679/51.

XX

PT Assaying oligonucleotides in sample by using capture oligonucleotide that  
PT is coupled to support, and has molecular recognition sequence including  
PT non-standard base, which is complementary to target oligonucleotide.

XX

PS Example 5; Page 51; 92pp; English.

XX

CC The present invention describes assaying a target oligonucleotide (T),  
CC comprising contacting a capture oligonucleotide (I) having a molecular  
CC recognition sequence (MS) with a non-standard base, under hybridising  
CC conditions, with a sample to hybridise (T) to (I), where (I) is coupled  
CC to a support and (T) has a tagging sequence complementary to MS of (I)  
CC and an analyte-specific sequence (AS) or its complement, and detecting  
CC the hybridisation of (T) to (I). The method can be used for assaying  
CC oligonucleotides. The method can also be used for simultaneously  
CC detecting at least two alleles in a sample comprising genomic DNA. The  
CC method is preferably useful for assaying oligonucleotides including DNA  
CC or RNA fragments. The present sequence represents a PCR primer for a  
CC polymorphic region of the mouse genome, which is used in an example from  
CC the present invention

XX Sequence 19 BP; 3 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

SQ

Alignment Scores: 9e+03 Length: 19  
Pred. No.: 5.00 Matches: 5  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 2.53% Gaps: 0  
DB: 6

US-09-966-880A-8 (1-198) x ABN88432 (1-19)

QY 111 AlaArgLeuTyPhe 115

Db 1 GCAGGGCTCTACTTC 15

```
RESULT 243
AAD38569/C
ID AAD38569 standard; DNA; 19 BP.
XX
AC AAD38569;
XX
DT 10-SEP-2002 (first entry)
XX
DE Bovine leukocyte antigen class I exon 3 specific probe, BoLA-ClEx3B18L.
XX
KW Bovine; immunological rejection; nuclear transfer; NT; immune response;
KW MHC-I; major histocompatibility complex; bovine leukocyte antigen;
KW embryo transfer; BoLA class I exon 3 DNA; probe; ss.
XX
OS Bos sp.
XX
PN WO200229000-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US030925.
XX
PR 03-OCT-2000; 2000US-0237673P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Davies CJ, Schlafer DH, Hall JR;
XX
XX WPI; 2002-444101/47.
XX
PT Minimizing immunological rejection of nuclear transfer fetuses, by
PT transferring the nuclear transfer embryo into an embryo recipient for
PT development of the fetus.
XX
PS Example 1; Page 19; 103pp; English.
XX
CC The present invention relates to a method of minimising immunological
CC rejection of a nuclear transfer (NT) foetus by transferring a nuclear
CC transfer embryo into an embryo recipient under conditions effective for
CC the development of a nuclear transfer foetus with minimal risk of
CC immunological rejection of the foetus due to maternal anti-foetal major
CC histocompatibility complex (MHC)-I immune response. The method is useful
CC for minimising immunological rejection of a NT foetus. It is also useful
CC for performing embryo transfer. The present DNA sequence is a probe
CC specific for bovine leukocyte antigen (BoLA) class I exon 3 DNA. This
CC probe is used in the exemplification of the invention
XX
SQ Sequence 19 BP; 6 A; 2 C; 9 G; 2 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x AAD38569 (1-19)

QY 104 LeuSerLeuArgile 108
Db 17 CTGTCCTCCGCATC 3

RESULT 244
ABL57055/C
ID ABL57055 standard; DNA; 19 BP.
XX
AC ABL57055;
XX
DT 22-JUL-2002 (first entry)
XX
DE Hydrazide phosphoramidite oligonucleotide O10.
XX
```

```
KW Macromolecule; hydrazide; immobilisation; ss.
XX
OS Synthetic.
XX
FH Location/Qualifiers
FT modified_base 1..19
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "6-(2Cyanooethoxy) (diisopropylamino)
FT phosphanyloxy)-N'-tritylhexanohydrazide"
XX
PN WO200214558-A2.
XX
PD 21-FEB-2002.
XX
PF 10-AUG-2001; 2001WO-US041663.
XX
PR 11-AUG-2000; 2000WO-US022205.
XX
PA (NANO-) NANOGEN INC.
XX
PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TU, Greef CH, Wang D;
XX
XX WPI; 2002-404476/43.
XX
PT Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.
XX
PS Example 2; Page 40; 120pp; English.
XX
CC The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC 19-mer, designated oligo O10, which was produced in an example from the
CC invention. The invention describes an improved process for immobilisation
CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC RNA and peptides, especially macromolecules containing multiple reactive
CC sites, to a substrate surface or other conjugation target. It also
CC describes the preparation of oligos containing one or more hydrazides,
CC which can be used for conjugation to surface binding moieties, or for
CC other conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
XX applications
XX
SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9e+03 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 6 Gaps: 0

US-09-966-880A-8 (1-198) x ABL57055 (1-19)

QY 56 HisValGluLeuLeu 60
Db 18 CACGTAGAACTGCTC 4

RESULT 245
ABL57067/C
ID ABL57067 standard; DNA; 19 BP.
XX
AC ABL57067;
XX
DT 22-JUL-2002 (first entry)
XX
DE Phosphoramidite oligonucleotide.
XX
```

KW Macromolecule; hydrazide; immobilisation; ss.  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT modified\_base 1..19  
 FT /tag= a  
 FT /note= "phosphoramidite linkage"  
 FT  
 XX WO200214558-A2.  
 PN  
 XX  
 XX 21-FEB-2002.  
 PD  
 XX  
 XX 10-AUG-2001; 2001WO-US041663.  
 PF  
 XX  
 XX 11-AUG-2000; 2000WO-US022205.  
 PR  
 XX  
 XX (NANO-) NANOGEN INC.  
 PA  
 XX  
 XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;  
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;  
 PI  
 XX  
 XX WPI; 2002-404476/43.  
 DR  
 XX  
 XX Compound for binding macromolecule to substrate surface or conjugation  
 PT targets, contains phosphorous containing reactive group, hydrazide  
 PT protecting group and benzene ring, and has predefined formula.  
 PT  
 XX  
 XX Disclosure; Fig 6; 120pp; English.  
 PS  
 XX  
 XX The present sequence is of an oligonucleotide used to illustrate the  
 CC synthetic steps using phosphoramidites to produce macromolecules with  
 CC multiple reactive sites. These moieties can contain ester groups that are  
 CC converted into hydrazides during the deprotection of the oligonucleotides  
 CC with hydrazine. The invention describes an improved process for  
 CC immobilisation of macromolecules including DNA, RNA, peptide nucleic  
 CC acids, pyranosyl-RNA and peptides, especially macromolecules containing  
 CC multiple reactive sites, to a substrate surface or other conjugation  
 CC target. It also describes the preparation of oligos containing one or  
 CC more hydrazides, which can be used for conjugation to surface binding  
 CC moieties, or for other conjugation reactions. The process is useful e.g.  
 CC in nucleic acid hybridisation based assays, DNA chip technology and  
 CC biosensor applications  
 CC  
 XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-966-880A-8 (1-198) x ABL57067 (1-19)  
 QY 56 HisValGluLeuLeu 60  
 Db 18 CACGTAGACTGCTC 4  
 RESULT 246  
 ABL57058/c  
 ID ABL57058 standard; DNA; 19 BP.  
 XX  
 XX ABL57058;  
 AC  
 XX 22-JUL-2002 (first entry)  
 DT  
 XX Hydrazide precursor phosphoramidite oligonucleotide O11.  
 DE  
 XX Macromolecule; hydrazide; immobilisation; ss.  
 KW  
 XX Synthetic.  
 OS

XX Key Location/Qualifiers  
 FT modified\_base 1..19  
 FT /tag= b  
 FT /note= "phosphoramidite linkage"  
 FT  
 XX modified\_base 1  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Ethyl 6-(2-cyanoethoxy) (diisopropylamino)  
 FT phosphanyloxy) hexanoate"  
 FT 19  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "3' Cy3 dye"  
 FT  
 XX WO200214558-A2.  
 PN  
 XX  
 XX 21-FEB-2002.  
 PD  
 XX  
 XX 10-AUG-2001; 2001WO-US041663.  
 PF  
 XX  
 XX 11-AUG-2000; 2000WO-US022205.  
 PR  
 XX  
 XX (NANO-) NANOGEN INC.  
 PA  
 XX  
 XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;  
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;  
 PI  
 XX  
 XX WPI; 2002-404476/43.  
 DR  
 XX  
 XX Compound for binding macromolecule to substrate surface or conjugation  
 PT targets, contains phosphorous containing reactive group, hydrazide  
 PT protecting group and benzene ring, and has predefined formula.  
 PT  
 XX  
 XX Example 3; Page 42; 120pp; English.  
 PS  
 XX The present sequence is of a hydrazine treated hydrazide precursor  
 CC phosphoramidite 19-met, designated oligo O11, which was produced in an  
 CC example from the invention. The invention describes an improved process  
 CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic  
 CC acids, pyranosyl-RNA and peptides, especially macromolecules containing  
 CC multiple reactive sites, to a substrate surface or other conjugation  
 CC target. It also describes the preparation of oligos containing one or  
 CC more hydrazides, which can be used for conjugation to surface binding  
 CC moieties, or for other conjugation reactions. The process is useful e.g.  
 CC in nucleic acid hybridisation based assays, DNA chip technology and  
 CC biosensor applications  
 CC  
 XX Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-966-880A-8 (1-198) x ABL57058 (1-19)  
 QY 56 HisValGluLeuLeu 60  
 Db 18 CACGTAGACTGCTC 4  
 RESULT 247  
 ABQ77335  
 ID ABQ77335 standard; DNA; 19 BP.  
 XX  
 XX ABQ77335;  
 AC  
 XX 08-MAY-2003 (first entry)  
 DT  
 XX Bovine H-PABP associated primer P2.  
 DE



XX Polymerase chain reaction; PCR; hybridisation; adapter primer;  
 KW extension primer; cell-free protein biosynthesis; amplification; primer;  
 KW bovine; heart; fatty acid binding protein; H-FABP; ss.  
 XX Bos taurus.  
 OS  
 XX WO200290371-A2.  
 PN  
 XX 14-NOV-2002.  
 PD  
 XX 18-MAR-2002; 2002WO-DE001047.  
 PF  
 XX 16-MAR-2001; 2001DE-01013265.  
 PR  
 XX (RINA-) RINA NETZWERK RNA TECHNOLOGIEN GMBH.  
 PA  
 XX Merk H, Erdmann V, Stiege W;  
 PI WPI; 2003-148335/14.  
 DR  
 XX Preparation of long nucleic acids, useful for in vitro, cell-free protein  
 PT synthesis, comprises attaching an adapter and extension primers to a base  
 PT sequence.  
 PT  
 XX Disclosure; Fig 1; 37pp; German.  
 PS  
 XX This invention describes a novel method for preparing long nucleic acids  
 CC by polymerase chain reaction (PCR) which comprises (i) hybridising a base  
 CC sequence (I) to adapter primers (Adp) at both 3' and 5' ends, (ii)  
 CC hybridising the products at both ends with extension primers (EP)  
 CC containing an extension sequence (ES) and (iii) producing an amplified  
 CC nucleic acid extended at both the 3' and 5' ends from the base sequence.  
 CC The invention also describes a nucleic acid for cell-free protein  
 CC biosynthesis, comprising a protein-encoding sequence, a ribosome-binding  
 CC site (RBS) and optionally a promoter, transcription terminator, a  
 CC expression enhancer, stabiliser or affinity tag. The method is useful for  
 CC preparing nucleic acids for the cell-free, in vitro biosynthesis of  
 CC proteins, particularly in prokaryotic systems, or for in vitro  
 CC transcription systems, particularly Escherichia coli D10, for selective  
 CC amplification of a sequence from a nucleic acid library and for  
 CC characterisation of gene sequences, where the protein expressed is  
 CC analysed for structure and/or function. The method makes the large-scale  
 CC preparation of nucleic acids that contain regulatory regions (to improve  
 CC transcriptional and translational efficiency) possible. It eliminates the  
 CC need to prepare long extension primers for each base sequence, since each  
 CC Adp contains a short, base sequence-specific region and a constant region  
 CC that hybridises to the extension sequence (which is universal), so the  
 CC method can be applied to any chosen sequence. This sequence represents a  
 CC primer associated with bovine heart fatty acid binding protein (H-FABP),  
 CC used to illustrate the method described in the disclosure of the  
 CC invention  
 CC  
 SQ Sequence 19 BP; 6 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ABQ77335 (1-19)

Qy 32 ValVallysArgArg 36  
 |||||  
 Db 5 GTTGTAAACGACGG 19  
 |||||

RESULT 248  
 ACF03602/C  
 ID ACF03602 standard; DNA; 19 BP.  
 XX

AC ACF03602;  
 XX  
 DT 15-SEP-2003 (first entry)  
 XX  
 XX Human NOV1 reverse PCR primer SEQ ID NO:172.  
 DE  
 XX Human; NOVX; cytostatic; cardiant; antiinflammatory; immunosuppressive;  
 KW antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;  
 KW anorectic; antiasthmatic; nephrotropic; antiarthritic; hepatotropic;  
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;  
 KW relaxant; anticonvulsant; hypotensive; vasotropic; antiparkinsonian;  
 KW vulnary; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;  
 KW cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;  
 KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;  
 KW acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;  
 KW Alzheimer's disease; Parkinson's disease; Goitre; infection; stroke;  
 KW muscular dystrophy; epilepsy; wasting disorder; PCR primer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Synthetic.  
 OS  
 XX WO200294870-A2.  
 PN  
 XX 28-NOV-2002.  
 PD  
 XX  
 XX 02-NOV-2001; 2001WO-US051580.  
 PF  
 XX 02-NOV-2000; 2000US-0245291P.  
 PR  
 XX 02-NOV-2000; 2000US-0245317P.  
 PR  
 XX 07-NOV-2000; 2000US-0246562P.  
 PR  
 XX 08-NOV-2000; 2000US-0246871P.  
 PR  
 XX 26-JAN-2001; 2001US-0264389P.  
 PR  
 XX 26-JAN-2001; 2001US-0264423P.  
 PR  
 XX 29-JAN-2001; 2001US-0264799P.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Grosse WM, Macdougall JR, Smithson G, Millet I, Stone DJ;  
 PI Gunther E, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;  
 PI Spytek KA, Edinger SR, Gangolli EA, Gorman L, Taupier RJ, Li L;  
 PI Guo X, Fernandes ER, Vernet CAM, Tcherniev VT, Casman SJ, Shenoy S;  
 PI Mishra V, Furtak K, Baumgartner JC, Colman SD;  
 PI  
 XX WPI; 2003-140359/13.  
 DR  
 XX New NOVX polypeptide useful for preventing or treating NOVX-associated  
 PT disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and  
 PT in chromosome mapping, tissue typing or pharmacogenomics.  
 PT  
 XX Example 2; Page 232; 346pp; English.  
 XX  
 XX ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412  
 CC to ABR57435. (I) have cytostatic, cardiant, antiinflammatory, nootropic,  
 CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,  
 CC antiarteriosclerotic, anorectic, antiasthmatic, nephrotropic, virucide,  
 CC antiarthritic, hepatotropic, neuroprotective, antibacterial, relaxant,  
 CC antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,  
 CC vulnary, angiogenic and antiangiogenic activities, and can be used in  
 CC gene therapy and vaccines. The NOVX polypeptides and their antibodies can  
 CC be used to determine the presence or absence of (I) in a sample. The NOVX  
 CC polypeptides, polynucleotides encoding them, and antibodies against them,  
 CC are useful in manufacturing a medicament for treating or preventing a  
 CC syndrome associated with a NOVX-associated disorder such as hypertension,  
 CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,  
 CC autoimmune disorders, allergies, blood disorders, obesity, acquired  
 CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig)A nephropathy,  
 CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, Goitre,  
 CC infections (e.g. bacterial, viral, parasitic), stroke, muscular  
 CC dystrophy, epilepsy, and other wasting disorders associated with chronic  
 CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX  
 CC sequence, which are used in an example from the present invention  
 CC  
 XX Sequence 19 BP; 2 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 9e+03 Length: 19  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACP03602 (1-19)

Qy 122 GluProGluGlyIleu 126

Db 18 GAACCAAGAGGGGTC 4

RESULT 249

AAL50790

ID AAL50790 standard; DNA; 19 BP.

XX AC AAL50790;

XX DT 30-JAN-2003 (first entry)

XX DE Exonuclease degradation stabilised coding sequence-related PCR primer 12.

XX PCR; primer; ss; exonuclease degradation stabilised coding sequence;

XX protein synthesis.

XX Unidentified.

XX WO200274952-A2.

XX PD 26-SEP-2002.

XX PF 18-MAR-2002; 2002WO-DE001048.

XX PR 16-MAR-2001; 2001DE-01013265.

XX PR 16-MAR-2001; 2001DE-01045014.

XX PR 05-OCT-2001; 2001DE-01051071.

XX PA (RINA-) RINA NETZWERK RNA TECHNOLOGIEN GMBH.

XX PI Merk H, Stiege W;

XX DR WPI; 2003-018805/01.

XX PT Nucleic acids stabilized against exonucleases, useful for protein

XX production in cell-free or cellular systems, contains molecules attached

XX to bulky specific binding partners.

XX PS Disclosure; Fig 1; 38pp; German.

XX CC The invention comprises nucleic acid coding sequences which have been

XX stabilised against exonuclease degradation. The nucleic acids of the

XX invention are useful for the preparation of an encoded protein in cell-

XX free or cellular systems - especially for characterisation of gene

XX CC sequences and for analysis of the structure/function of encoded proteins.

XX CC The present DNA sequence represents a PCR primer that was used in the

XX invention

XX SQ Sequence 19 BP; 6 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x AAL50790 (1-19)

Qy 32 ValVallysArgArg 36

Db 5 GTTGTAAACGACGG 19

RESULT 250

ACC79586

ID ACC79586 standard; DNA; 19 BP.

XX AC ACC79586;

XX DT 05-AUG-2003 (first entry)

XX DE Progesterone receptor reverse PCR primer.

XX Gene expression control; regulatory peptide; selectively suppress;

XX cancer; gene therapy; gene expression; regulation; suppression;

XX modulation; progesterone receptor; PCR primer; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO2003033701-A1.

XX PD 24-APR-2003.

XX PF 11-OCT-2002; 2002WO-GB004633.

XX PR 11-OCT-2001; 2001GB-00024391.

XX PA (GENE-) GENE EXPRESSION TECHNOLOGIES LTD.

XX PI Hart S, Ali S, Pufong BT, Porter ACG, Buluwela L, Vainikka S;

XX PI Jenkinson JD, Kanda P;

XX DR WPI; 2003-372329/35.

XX PT Suppressing or modulating the expression of a selected gene in a cell

XX comprises introducing into the cell a molecule comprising a nucleic acid

XX binding portion, and an expression repressor portion or a modifying

XX portion.

XX PS Example 10; Page 70; 98pp; English.

XX CC The present invention describes a method for suppressing or modulating

XX the expression of a selected gene in a cell. The method comprises

XX introducing into the cell a molecule comprising a nucleic acid binding

XX portion which binds to a site at or associated with the selected gene

XX which site is present in a genome, and an expression repressor portion or

XX a modifying portion. The nucleic acid binding portion comprises an

XX oligonucleotide or oligonucleotide mimic or analogue. The repressor

XX also comprises a polypeptide or peptidomimetic that is capable of

XX modulating covalent modification of nucleic acid or chromatin and is not

XX an endonuclease. The method is useful in controlling gene expression

XX using a complex of an oligonucleotide and a regulatory peptide. The

XX ability to selectively suppress the expression of a gene is useful in

XX many areas of biology, such as in methods of treatment where the

XX expression of the gene may be undesirable (e.g. cancer), in preparing

XX models of disease and in modifying the phenotype in order to produce

XX desirable properties. The molecule is useful in manufacturing an agent or

XX a medicament for modulating or suppressing the expression of the selected

XX gene in a patient or in an animal cell. The method is useful in gene

XX therapy. The present sequence represents a PCR primer for a progesterone

XX receptor, which is used in an example from the present invention

XX SQ Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0

DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC79586 (1-19)

QY 178 ArgileLeuLeuPro 182  
 DB 3 CGGATCTGCTTCCT 17

RESULT 251

ID ACC79583 standard; DNA; 19 BP.

XX ACC79583;

DT 05-AUG-2003 (first entry)

DE Human androgen receptor antisense PCR primer.

XX Gene expression control; regulatory peptide; selectively suppress;  
 KW cancer; gene therapy; gene expression; regulation; suppression;  
 KW modulation; androgen receptor; PCR primer; ss.

XX Homo sapiens.

OS Synthetic.

XX WO2003033701-A1.

PN 24-APR-2003.

PD 11-OCT-2002; 2002WO-GB004633.

PF 11-OCT-2001; 2001GB-00024391.

XX (GENE-) GENE EXPRESSION TECHNOLOGIES LTD.

PA Hart S, Ali S, Pufong BT, Porter ACG, Buluwela L, Vainikka S;  
 PI Jenkinson JD, Kanda P;

XX WPI; 2003-372329/35.

XX Suppressing or modulating the expression of a selected gene in a cell  
 PT comprises introducing into the cell a molecule comprising a nucleic acid  
 PT binding portion, and an expression repressor portion or a modifying  
 PT portion.

PS Example 8; Page 57; 98pp; English.

XX The present invention describes a method for suppressing or modulating  
 CC the expression of a selected gene in a cell. The method comprises  
 CC introducing into the cell a molecule comprising a nucleic acid binding  
 CC portion which binds to a site at or associated with the selected gene  
 CC which site is present in a genome, and an expression repressor portion or  
 CC a modifying portion. The nucleic acid binding portion comprises an  
 CC oligonucleotide or oligonucleotide mimic or analogue. The repressor  
 CC portion comprises a polypeptide or peptidomimetic. The modifying portion  
 CC also comprises a polypeptide or peptidomimetic that is capable of  
 CC modulating covalent modification of nucleic acid or chromatin and is not  
 CC an endonuclease. The method is useful in controlling gene expression  
 CC using a complex of an oligonucleotide and a regulatory peptide. The  
 CC ability to selectively suppress the expression of a gene is useful in  
 CC many areas of biology, such as in methods of treatment where the  
 CC expression of the gene may be undesirable (e.g. cancer), in preparing  
 CC models of disease and in modifying the phenotype in order to produce  
 CC desirable properties. The molecule is useful in manufacturing an agent or  
 CC a medicament for modulating or suppressing the expression of the selected  
 CC gene in a patient or in an animal cell. The method is useful in gene  
 CC therapy. The present sequence represents a PCR primer for the human  
 CC androgen receptor, which is used in an example from the present invention

XX Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9e+03 Length: 19  
 Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 7 Gaps: 0

US-09-966-880A-8 (1-198) x ACC79583 (1-19)

QY 178 ArgileLeuLeuPro 182

DB 3 CGGATCTGCTTCCT 17

RESULT 252

ADE27202

ID ADE27202 standard; RNA; 19 BP.

XX AC ADE27202;

XX 29-JAN-2004 (first entry)

DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:146.

XX short interfering nucleic acid; siNA; downregulation; inhibition; SCD;  
 KW stearoyl-CoA desaturase; RNA interference; anorectic; anti-diabetic;  
 KW anti-atherosclerotic; cytoskeletal; virucide; obesity; diabetes;  
 KW atherosclerosis; cancer; viral infection; drug screening;  
 KW genetic engineering; pharmacogenomic; gene mapping; ss.

OS Synthetic.

XX WO2003070885-A2.

PN 28-AUG-2003.

PD 13-FEB-2003; 2003WO-US004317.

PF 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 06-JUN-2002; 2002US-0386782P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 03-SEP-2002; 2002US-0409293P.

PR 20-SEP-2002; 2002US-0412304P.

PR 15-JAN-2003; 2003US-0440129P.

XX (RIBO-) RIBOZYME PHARM INC.

XX McSwiggen J, Beigelman L, Thompson J;

XX WPI; 2003-721687/68.

XX New short interfering nucleic acid, useful e.g. for treatment and  
 PT diagnosis of obesity or diabetes, downregulates expression of the  
 PT stearoyl-CoA desaturase gene.

XX Example 3; SEQ ID NO 146; 139pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)  
 CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene  
 CC by RNA interference. Also described: (1) modulating expression of SCD  
 CC genes in cells, tissue explants or organisms by introduction of siNA; (2)  
 CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or  
 CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting  
 CC siNAs have anorectic, anti-diabetic, anti-atherosclerotic, cytoskeletal and  
 CC virucide activities. The siNAs can be used to modulate expression of SCD  
 CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;  
 CC diabetes (types I and II); atherosclerosis; cancer and viral infections.  
 CC They can also be used for drug screening; diagnosis; target  
 CC identification and validation; genetic engineering; pharmacogenomics;  
 CC studying gene function and gene mapping (e.g. of single-nucleotide  
 CC polymorphisms). The present sequence represents an SCD siNA, which is  
 CC used in the exemplification of the present invention.

XX Sequence 19 BP; 5 A; 2 C; 8 G; 0 T; 4 U; 0 Other;

CC polymorphisms). The present sequence represents an SCD siNA, which is  
CC used in the exemplification of the present invention.  
XX  
SQ Sequence 19 BP; 4 A; 8 C; 2 G; 0 T; 5 U; 0 Other;  
  
Alignment Scores:                      9e+03                      Length:                      19  
Pred. No.:                      5.00                      Matches:                      5  
Score:                      100.00%                      Conservative:                      0  
Percent Similarity:                      100.00%                      Mismatches:                      0  
Best Local Similarity:                      100.00%                      Indels:                      0  
Query Match:                      2.53%                      Gaps:                      0  
DB:                      9  
  
US-09-966-880A-8 (1-198) x ADE27492 (1-19)  
  
Qy                      125 GlyLeuArgArgLeu 129  
Db                      15 GGCTTGAGAGGTTA 1  
  
RESULT 254  
ADE27492/c  
ID ADE27492 standard; RNA; 19 BP.  
XX  
AC ADE27492;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:436.  
XX  
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;  
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;  
KW antiarteriosclerotic; cytosolic; virucide; obesity; diabetes;  
KW atherosclerosis; cancer; viral infection; drug screening;  
KW genetic engineering; pharmacogenomic; gene mapping; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003070885-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 13-FEB-2003; 2003WO-US004317.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 05-JUN-2002; 2002US-0386782P.  
PR 23-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 20-SEP-2002; 2002US-0412304P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Beigelman L, Thompson J;  
XX  
DR WPI; 2003-721687/68.  
XX  
PT New short interfering nucleic acid, useful e.g. for treatment and  
PT diagnosis of obesity or diabetes, downregulates expression of the  
PT stearoyl-CoA desaturase gene.  
XX  
PS Example 3; SEQ ID NO 436; 139pp; English.  
XX  
CC The present invention describes a short interfering nucleic acid (siNA)  
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene  
CC by RNA interference. Also described: (1) modulating expression of SCD  
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)  
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or  
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting  
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and  
CC virucide activities. The siNAs can be used to modulate expression of SCD  
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;  
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.  
CC They can also be used for drug screening; diagnosis; target  
CC identification and validation; genetic engineering; pharmacogenomics;  
CC studying gene function and gene mapping (e.g. of single-nucleotide

Alignment Scores:                      9e+03                      Length:                      19  
Pred. No.:                      5.00                      Matches:                      5  
Score:                      100.00%                      Conservative:                      0  
Percent Similarity:                      100.00%                      Mismatches:                      0  
Best Local Similarity:                      100.00%                      Indels:                      0  
Query Match:                      2.53%                      Gaps:                      0  
DB:                      9  
  
US-09-966-880A-8 (1-198) x ADE27202 (1-19)  
  
Qy                      125 GlyLeuArgArgLeu 129  
Db                      5 GGCUGAGAGGUA 19  
  
RESULT 253  
ADE27492/c  
ID ADE27492 standard; RNA; 19 BP.  
XX  
AC ADE27492;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Stearoyl-CoA desaturase siNA oligonucleotide SEQ ID NO:436.  
XX  
KW short interfering nucleic acid; siNA; downregulation; inhibition; SCD;  
KW stearoyl-CoA desaturase; RNA interference; anorectic; antidiabetic;  
KW antiarteriosclerotic; cytosolic; virucide; obesity; diabetes;  
KW atherosclerosis; cancer; viral infection; drug screening;  
KW genetic engineering; pharmacogenomic; gene mapping; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003070885-A2.  
XX  
PD 28-AUG-2003.  
XX  
PF 13-FEB-2003; 2003WO-US004317.  
XX  
PR 20-FEB-2002; 2002US-0358580P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 05-JUN-2002; 2002US-0386782P.  
PR 23-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 20-SEP-2002; 2002US-0412304P.  
PR 15-JAN-2003; 2003US-0440129P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J, Beigelman L, Thompson J;  
XX  
DR WPI; 2003-721687/68.  
XX  
PT New short interfering nucleic acid, useful e.g. for treatment and  
PT diagnosis of obesity or diabetes, downregulates expression of the  
PT stearoyl-CoA desaturase gene.  
XX  
PS Example 3; SEQ ID NO 436; 139pp; English.  
XX  
CC The present invention describes a short interfering nucleic acid (siNA)  
CC that downregulates expression of the SCD (stearoyl-CoA desaturase) gene  
CC by RNA interference. Also described: (1) modulating expression of SCD  
CC genes in cells, tissue explants or organisms by introduction of siNA; (2)  
CC kits for in vitro or in vivo delivery of siNA; (3) conjugates and/or  
CC complexes of siNA; and (4) vectors that express siNA. SCD inhibiting  
CC siNAs have anorectic, antidiabetic, antiarteriosclerotic, cytostatic and  
CC virucide activities. The siNAs can be used to modulate expression of SCD  
CC genes, in cells, tissue explants or organisms, e.g. for treating obesity;  
CC diabetes (types I and II); atherosclerosis; cancer and viral infections.  
CC They can also be used for drug screening; diagnosis; target  
CC identification and validation; genetic engineering; pharmacogenomics;  
CC studying gene function and gene mapping (e.g. of single-nucleotide

SQ Sequence 19 BP; 6 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9e+03	Length:	19
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x ADE76677 (1-19)

QY 32 ValValLysArgArg 36

DB 5 GTGTAAACGACGG 19

RESULT 255

AAQ05909/c

ID AAQ05909 standard; DNA; 20 BP.

XX AC AAQ05909;

XX 10-JAN-1991 (first entry)

XX HIV mRNA translation inhibiting antisense oligonucleotide (f).

XX Modified antisense oligonucleotide; HIV mRNA translation inhibition;

XX HIV-1; transactivator region; leader sequence; tat gene; probe; ss.

XX Synthetic.

XX EP386563-A.

XX 12-SEP-1990.

XX 25-FEB-1990; 90BP-00103641.

XX 09-MAR-1989; 89DE-03907562.

XX (FARB ) BAYER AG.

XX Stropp U, Baugarten J, Lobberding A, Springer W, Piel N;

PI Kretschmer A, Kolbl H, Frommer W;

XX WPI; 1990-276634/37.

XX Chemically modified antisense oligo-nucleotide(s) - inhibiting translation of HIV RNA.

XX Claim 3(f); Page 8; 15pp; German.

XX The chemically modified sequences are opposed to the HIV-1 transactivator region, leader sequences (nt 21-53, 74-161, 202-279) or exon 2 or 3 of the tat gene (nt 5369-5403, 5421-5548, 5583-5617, 7967-8366, 8385-9183).

XX This sequence comprises nt 5604-5623 and gives 90% inhibition of HIV-1 tat translation in vitro at concns. of 5-25 microm. The sequence is useful for treating HIV infections and their complementary sequences can be used as probes to detect HIV. Chemical modification comprises replacing one or more internit phosphodiester linkages by phosphorothioate or methylphosphonate linkages. See also AAQ05904-11

SQ Sequence 20 BP; 7 A; 2 C; 4 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.44e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x AAQ05909 (1-20)

QY 174 ArgGlnLeuArgArg 178

DB 1 AGACAGCTCAGAGA 15

RESULT 257

AAQ52874

ID AAQ52874 standard; RNA; 20 BP.

XX AC AAQ52874;

XX 25-MAR-2003 (revised)

DT 26-MAY-1994 (first entry)

XX Cytomegalovirus target sequence 51.

XX

QY 10 LysPheLeuTyrGln 14

DB 17 AAGTTTCTCTATCAA 3

RESULT 256

AAQ20407

ID AAQ20407 standard; DNA; 20 BP.

XX AC AAQ20407;

XX 10-APR-1992 (first entry)

XX Capture probe #1 for detecting HPV-6 or HPV-11 E7 gene DNA.

XX Detection probe; sandwich hybridisation assay; human papilloma virus; ss.

XX Synthetic.

XX WO9119812-A.

XX 26-DEC-1991.

XX 11-JUN-1990; 90FR-00007249.

XX 11-JUN-1990; 90FR-00007249.

XX (INMR ) BIO MERIEUX.

XX Cros P, Allibert P, Mallet F, Mabilat C, Mandrand B;

XX WPI; 1992-024428/03.

XX Sandwich hybridisation of single strand nucleic acid - using short immobilised capture probe and detection probe with non-radioactive label, for diagnosing e.g. human papilloma virus or HIV.

XX Claim 31; Page 37; 51pp; French.

XX Target DNA corresponding to the E7 gene of HPV types 6 or 11 is detected using one or both of the capture probes AAQ20407 and AAQ20408 fixed passively to a solid hydrophobic support together with one or both of detection probe(s) AAQ20409 and AAQ20410 labelled with a non-radioactive marker. The capture and detection probes are able to hybridise to non-overlapping segments of the target sequence. See AAQ0389-Q20420 and AAQ20630-Q20663

SQ Sequence 20 BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.44e+03	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.53%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880A-8 (1-198) x AAQ20407 (1-20)

QY 174 ArgGlnLeuArgArg 178

DB 1 AGACAGCTCAGAGA 15

RESULT 257

AAQ52874

ID AAQ52874 standard; RNA; 20 BP.

XX AC AAQ52874;

XX 25-MAR-2003 (revised)

DT 26-MAY-1994 (first entry)

XX Cytomegalovirus target sequence 51.

XX

KW RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; HbRNA;  
 KW picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;  
 KW papilloma virus; HPV; Epstein-Barr virus; EBV; TCV; T-cell  
 KW T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus;  
 KW influenza virus; HSV; herpes simplex virus; vector; immune response;  
 KW antibody; ribozyme; viral RNA; treatment; ss.  
 XX  
 OS Synthetic.

XX WO9323569-A1.

XX 25-NOV-1993.

XX 29-APR-1993; 93WO-US04020.

XX 11-MAY-1992; 92US-00882689.

XX 14-MAY-1992; 92US-00882712.

XX 14-MAY-1992; 92US-00882713.

XX 14-MAY-1992; 92US-00882714.

XX 14-MAY-1992; 92US-00882823.

XX 14-MAY-1992; 92US-00882824.

XX 14-MAY-1992; 92US-00882886.

XX 14-MAY-1992; 92US-00882888.

XX 14-MAY-1992; 92US-00882889.

XX 14-MAY-1992; 92US-00882921.

XX 14-MAY-1992; 92US-00882922.

XX 14-MAY-1992; 92US-00883823.

XX 14-MAY-1992; 92US-00883849.

XX 14-MAY-1992; 92US-00884073.

XX 14-MAY-1992; 92US-00884074.

XX 14-MAY-1992; 92US-00884333.

XX 14-MAY-1992; 92US-00884422.

XX 14-MAY-1992; 92US-00884431.

XX 14-MAY-1992; 92US-00884436.

XX 31-JUL-1992; 92US-00884521.

XX 26-AUG-1992; 92US-00935854.

XX 26-AUG-1992; 92US-00935854.

XX 18-SEP-1992; 92US-00948359.

XX 13-OCT-1992; 92US-00963322.

XX 07-DEC-1992; 92US-00987129.

XX 07-DEC-1992; 92US-00987130.

XX 07-DEC-1992; 92US-00987133.

XX (RIBO-) RIBOZYME PHARM INC.

XX Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecck JJ;

XX Mamone JA;

XX WPI; 1993-386599/48.

XX Enzymatic RNA molecules - used to inhibit viral replication, infection

XX and gene expression.

XX Claim 5; Fig 13; 287pp; English.

XX The sequences (AAQ52824-052890) are pref. Cytomegalovirus target

XX sequences for enzymatic RNA molecules. The RNA molecules are

XX complementary to a substrate binding region in the specified gene target.

XX They also have enzymatic activity, in that they specifically cleave RNA

XX in the target. The ERMs interfere with viral replication and therefore

XX have anti-viral properties. They can be used to attenuate viruses to be

XX used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated

XX on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct

XX PI field.)

XX SQ Sequence 20 BP; 1 A; 9 C; 5 G; 0 T; 5 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 9.44e+03 Length: 20

XX Score: 5.00 Matches: 5

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ52874 (1-20)

QY 74 ArgCysTyrArgVal 78

Db 1 CGGUGCUACCGGUC 15

RESULT 258

AAQ51057/C

ID AAQ51057 standard; DNA; 20 BP.

XX AAQ51057;

XX 25-MAR-2003 (revised)

DT 11-MAY-1994 (first entry)

XX Human glucokinase exon 1a PCR-SSCP analysis downstream primer.

XX Human; glucokinase; short arm; chromosome 7; MODY; insulin secretion;

XX non-insulin dependant diabetes mellitus; NIDDM; glucose-6-phosphate;

XX maturity-onset diabetes of the young; glucose; regulation; mutation;

XX detection; primer; amplify; single-strand conformational polymorphism;

XX adenosine deaminase; ADA; GLUT2; beta-cell glucose transporter;

XX restriction fragment length polymorphism; polymerase chain reaction;

XX RFLP; SSCP; exon; PCR; ss.

XX Synthetic.

XX OS

XX WO9321343-A1.

XX 28-OCT-1993.

XX 14-APR-1993; 93WO-US003560.

XX 22-APR-1992; 92US-00872678.

XX (ARCH-) ARCH DEV CORP.

XX Bell GI, Stoffel M, Takeda J, Vionnet N, Yasuda K, Pilleis SJ;

XX Zouali H, Velho G, Cohen D, Froguel P;

XX WPI; 1993-351752/44.

XX Detection of early onset, non-insulin dependent diabetes mellitus - by

XX detecting a mutation in a glucokinase gene or prod., esp. for maturity

XX onset diabetes of the young.

XX Example 7; Page 31; 60pp; English.

XX The sequences given in AAQ51045-79 are primers which were used in the

XX detection of restriction fragment length polymorphisms (RFLPs) within the

XX human adenosine deaminase gene (ADA), beta-cell glucose transporter gene

XX (GLUT2) and the human glucokinase gene. The glucokinase gene maps to a

XX locus on the short arm of chromosome 7 and mutations within this gene

XX show some correlation with certain forms of non-insulin dependant

XX diabetes mellitus (NIDDM), esp. maturity-onset diabetes of the young

XX (MODY). The polymorphic AluVPA region of ADA cosegregates with one gene

XX responsible for MODY and has been mapped to the long arm of chromosome 6-

XX 20. Glucokinase is an enzyme which catalyses the formation of glucose-6-

XX phosphate from glucose and may be involved in the regulation of insulin

XX secretion and integration of hepatic intermediary metabolism. Nonsense

XX and missense mutations within the glucokinase gene (see also AAQ51038-44)

XX may be identified by the method of the invention. Early onset NIDDM is

XX examined by detecting at least one single nucleotide change in a portion

XX of the gene. The DNA is isolated and a pair of primers are selected which

XX are capable of amplifying an exon of the gene via PCR. The single

XX nucleotide changes are identified in the amplification product. (Updated

XX on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ51057 (1-20)

QY 104 LeuSerLeuArgIle 108  
 DB 18 TTGAGGCTCAGAATC 4

RESULT 259

AAQ52403  
 ID AAQ52403 standard; DNA; 20 BP.

XX AC AAQ52403;

DT 25-MAR-2003 (revised)

DT 13-JUN-1994 (first entry)

XX Sequence used for ligand synthesis in selection process.

XX Ligand; identification; target; selection; amplification; partition;  
 KW detection; binding; affinity; ss.

XX Synthetic.

XX US5270163-A.

XX 14-DEC-1993.

XX 17-AUG-1992; 92US-00931473.

XX 11-JUN-1990; 90US-00536428.

XX 10-JUN-1991; 91US-00714131.

XX (UYRE-) UNIV RES CORP.

XX Tuerk C, Gold L;

XX WPI; 1993-404920/50.

XX Identifying nucleic acids which bind target ligands - by partitioning  
 PT increased affinity nucleic acids from candidate mixt. and amplifying  
 PT these nucleic acids.

XX Example 2; Col 163-164; 129pp; English.

XX A method (SELEX) for identifying nucleic acid ligands which bind target  
 CC ligands comprises, contacting a candidate mixture with the target ligand  
 CC so that nucleic acids with an increased affinity for the target can be  
 CC partitioned from the remainder of the candidate mixture; partitioning the  
 CC increased affinity nucleic acids from the remainder of the candidate  
 CC mixture and amplifying them. Preferably this procedure is repeated  
 CC numerous times to yield a desired level of ligand enrichment. A template  
 CC molecule is used to produce the ligands present in the candidate mixture  
 CC and this oligonucleotide is used as a PCR primer for the production of  
 CC the candidate ligands and as a reverse transcriptase primer for an  
 CC inhibition assay. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ52403 (1-20)

QY 32 ValVallysArgArg 36

DB 4 GTTGTAAACGACGG 18

RESULT 260

AAQ62617  
 ID AAQ62617 standard; DNA; 20 BP.

XX AC AAQ62617;

XX 25-MAR-2003 (revised)

DT 18-JAN-1995 (first entry)

XX Probe to detect nucleic acid hybrids.

XX double helical structure; interactions; detection; probes;  
 KW nucleic acid hybrids; ss.

XX Synthetic.

XX EP599337-A2.

XX 01-JUN-1994.

XX 26-NOV-1993; 93EP-00119103.

XX 27-NOV-1992; 92JP-00318959.

XX 30-NOV-1992; 92JP-00320500.

XX (CANO) CANON KK.

XX Yamamoto N, Okamoto T, Tomida Y, Kawaguchi M, Makino K;  
 PI Murakami A;

XX WPI; 1994-169656/21.

XX Detection of nucleic acid hybrids - using a probe or reagent which causes  
 a detectable change by interaction through a double helical structure.

XX Example 1; Page 10; 22pp; English.

XX The probes (AAQ62617-20) were used in detection of a nucleic acid, in the  
 CC examples the M13mp18DNA (single stranded) is the target sequence. The  
 CC probe is labelled eg, with a spin labeling agent, and added to the sample  
 CC contg. the target nucleic acid. The detection of the target depends on  
 CC the formation of a double helical structure of a hybrid formed between  
 CC the probe and the target. Two or more reagents capable of causing a  
 CC detectable change by interaction through the double helical structure are  
 CC required, and at least one of these is attached to the probe. In this  
 CC example the reagent is 4-aminohexylamino-2,2,6,6-tetramethylpiperidine-N-  
 CC oxyl (TEMPO), and the probe is partially complementary to the target. The  
 CC ESR spectrum was measured and showed that the spin of the TEMPO  
 CC disappeared as the result of the charge transfer from fluorescein to  
 CC TEMPO linked to the probe through the double helix formed from the probe  
 CC and the M13mp18DNA. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ62617 (1-20)

QY 32 ValVallysArgArg 36

DB 1 GTTGTAAACGACGG 15

US-09-966-880A-8 (1-198) x AAQ62619 (1-20)

RESULT 263



```

AAQ82475/c
ID AAQ82475 standard; DNA; 20 BP.
XX
AC AAQ82475;
XX
DT 25-MAR-2003 (revised)
DT 13-SEP-1995 (first entry)
XX
DE Chromosome 11 (locus D11S1222) STS primer cSRL-6b1-tA.
XX
sequence sampled mapping; genomic analysis; complex genome mapping;
KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX
OS Synthetic.
XX
PN WO9429486-A1.
XX
PD 22-DEC-1994.
XX
PF 15-JUN-1994; 94WO-US006810.
XX
PR 15-JUN-1993; 93US-00078471.
PR 07-SEP-1993; 93US-00117952.
XX
(SALK ) SALK INST BIOLOGICAL STUDIES.
PA Evans GA, Smith MW;
XX
PI WPI; 1995-036508/05.
XX
DR Sequencing complex genomes, present as fragments in a cosmid library - by
PT sequencing end-specific nucleotides of each clone then correlating with
PT spatial relationship of cosmid, esp. for mammalian chromosomes.
XX
PS Example 4; Page 83; 128pp; English.
XX
CC Sequences were determined from the ends of chromosome 11-specific cosmids
CC by automated sequencing without intermediate subcloning. A sample of 371
CC DNA sequence fragments were determined and of these, 277 were suitable
CC for STS primer prediction by computer analysis (using the "Primer"
CC program available from E.Lander, MIT). The STSs and cosmids were mapped
CC by in situ hybridisation, somatic cell hybrid analysis or both. Using
CC this method, 370 STSs specific for human chromosome 11 were generated and
CC most of them were regionally mapped. This procedure illustrates a novel
CC method for sequencing complex genomes, designated "sequence sampled
CC mapping". The sequence sampled mapping method is useful for the
CC completion of high density sequence-based maps, and ultimately, for the
CC complete sequencing of genomic DNA directly from cosmid clones. See
CC AAQ82001-Q82706 for STS primers. (Also see AAQ91325-58). (Updated on 25-
CC MAR-2003 to correct FN field.)
XX
SQ Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e-03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ82475 (1-20)

Oy 127 ArgArgLeuHisArg 131
Db 18 AGAAGACTGCACAGA 4

RESULT 264
AAQ99196
ID AAQ99196 standard; DNA; 20 BP.
XX
AC AAQ99196;
XX
DT 07-MAR-1996 (first entry)
XX
DE Phage M13 DNA primer.
XX
KW Artificial male sterility; transgenic plant; barnase; toxin;
XX crop improvement; ribonuclease; DNA primer; ss.
XX
OS Synthetic.
XX
PN WO9520668-A1.
XX
PD 03-AUG-1995.
XX
PF 31-JAN-1995; 95WO-GB000188.
PF 31-JAN-1994; 94GB-00001780.
XX
(NICK-) NICKERSON BIOCHEM LTD.
(GENE-) GENE SHEARS PTY LTD.
XX
Paul W, Scott RJ, Betzner A, Huttner E, Lenee P, Perez P;
WPI; 1995-275453/36.
XX
Prod'n. of plants having a desired phenotypic trait - by crossing first
and second lines which lack the trait, where one of the lines is
transgenic.
XX
Disclosure; Page 45; 78pp; English.
XX
This phage M13 DNA primer and a phage T7 primer were used in a PCR to
obtain a mutant T7 promoter TEV leader Prglu' fragment from pWP178-TEV,
that is cloned into pluescriptII KS- as an XhoI, HindIII fragment,
forming plasmid pWP188-T7mut
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e-03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ99196 (1-20)

Oy 32 ValVallyshArg 36
Db 2 GTTGTAAACGACGG 16

RESULT 265
AAQ99198
ID AAQ99198 standard; DNA; 20 BP.
XX
AC AAQ99198;
XX
DT 07-MAR-1996 (first entry)
XX
DE Phage M13 DNA primer.
XX
KW Artificial male sterility; transgenic plant; barnase; toxin;
XX crop improvement; ribonuclease; DNA primer; ss.
XX
OS Synthetic.
XX
PN WO9520668-A1.
XX
PD 03-AUG-1995.
XX
PF 31-JAN-1995; 95WO-GB000188.
PF 31-JAN-1994; 94GB-00001780.
XX

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XX (NICK-) NICKERSON BIOCHEM LTD.  
PA (GENE-) GENE SHEARS PTY LTD.  
XX PI Paul W, Scott RJ, Betzner A, Huttner E, Lenee P, Perez P;  
XX DR WPI; 1995-275453/36.  
XX Prodn. of plants having a desired phenotypic trait - by crossing first  
PT and second lines which lack the trait, where one of the lines is  
PT transgenic.  
XX PS Disclosure; Page 48; 78pp; English.  
XX CC This phase M13 DNA primer and a phage T7 primer were used in a PCR to  
CC obtain a mutant T7 promoter TEV leader GUS' fragment that is cloned into  
CC pBluescriptII KS- as an XhoI, HindIII fragment, forming plasmid pGUS3  
XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps:  
US-09-966-880A-8 (1-198) x AAQ99198 (1-20)  
QY 32 ValVallysArgArg 36  
DB 2 GTTGTAAACGACGG 16  
RESULT 266  
AAQ99192  
ID AAQ99192 standard; DNA; 20 BP.  
XX AC AAQ99192;  
XX 07-MAR-1996 (first entry)  
XX Phase M13 DNA primer.  
XX Artificial male sterility; transgenic plant; barnase; toxin;  
KW crop improvement; ribonuclease; DNA primer; ss.  
XX Synthetic.  
XX WO9520668-A1.  
XX 03-AUG-1995.  
XX 31-JAN-1995; 95WO-GB000188.  
XX 31-JAN-1994; 94GB-00001780.  
XX (NICK-) NICKERSON BIOCHEM LTD.  
XX (GENE-) GENE SHEARS PTY LTD.  
XX PI Paul W, Scott RJ, Betzner A, Huttner E, Lenee P, Perez P;  
XX DR WPI; 1995-275453/36.  
XX Prodn. of plants having a desired phenotypic trait - by crossing first  
PT and second lines which lack the trait, where one of the lines is  
PT transgenic.  
XX PS Disclosure; Page 44; 78pp; English.  
XX CC This phase M13 DNA primer and a phage T7 primer were used in a PCR to  
CC obtain a T7 promoter TEV leader PRGLU' fragment that is cloned into  
CC pBluescriptII KS- as an XhoI, HindIII fragment, forming plasmid pWP188-

CC TEV  
XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps:  
US-09-966-880A-8 (1-198) x AAQ99192 (1-20)  
QY 32 ValVallysArgArg 36  
DB 2 GTTGTAAACGACGG 16  
RESULT 267  
AAQ90396/C  
ID AAQ90396 standard; DNA; 20 BP.  
XX AC AAQ90396;  
XX 08-JAN-1996 (first entry)  
XX AT-A5 (synthetic DNA probe with 3'ribonucleoside terminal #7).  
XX AT-A5; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;  
KW SAED; hybridisation; ss.  
XX Synthetic.  
XX Key Location/Qualifiers  
FT misc\_feature 20  
FT /\*tag= a  
FT /note= "3' ribonucleoside terminal"  
XX WO9512808-A1.  
XX 11-MAY-1995.  
XX 26-OCT-1994; 94WO-US012270.  
XX 01-NOV-1993; 93US-00146504.  
XX (NANO-) NANOGEN INC.  
XX Heller MJ, Tu B;  
XX WPI; 1995-185870/24.  
XX New self-addressable electronic devices - used for multi-step and  
PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics  
PT and bio-polymer synthesis.  
XX Example 1; Page 40; 86pp; English.  
XX The sequences represented by, AAQ90390-90401 are synthetic DNA probes  
CC containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15  
CC are synthetic DNA probes with 5' amino termini. These sequences were  
CC specific for the polymorphisms of HLA gene dQa. The sequences were used  
CC in the device of the invention. This is a self-addressable electronic  
CC device (SAED) that can be used to carry out multi-step and multiplex  
CC reactions, such as nucleic acid hybridisations. The advantages of this  
CC method are that these reactions can be carried out with complete and  
CC precise electronic control, and that the rate, specificity and  
CC sensitivity of these reactions are greatly improved at micro-locations  
XX SQ Sequence 20 BP; 4 A; 3 C; 7 G; 5 T; 1 U; 0 Other;  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20

Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ90396 (1-20)

QY 56 HisValGluLeuLeu 60  
 DB 18 CACGTAGAACTGTC 4

RESULT 268

AAQ95469

ID AAQ95469 standard; DNA; 20 BP.

XX AC AAQ95469;

XX DT 14-FEB-1996 (first entry)

XX DE Primer A5 (Group 4, set A) for a human chromosomal marker.

XX KW primer; polymerase chain reaction; PCR; linkage study; locus;

XX KW microsatellite marker sequence; automated genotyping; allele;

XX KW polymorphism; detection; Homo sapiens; ss.

XX OS Synthetic.

XX PN WO9515400-A1.

XX PD 08-JUN-1995.

XX PF 05-DEC-1994; 94WO-US013945.

XX PR 03-DEC-1993; 93US-00160837.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Levitt RC;

XX DR WPI; 1995-215278/28.

XX PT Kit for automated genotyping contg. pairs of PCR primers - designed to

XX PT amplify polymorphic nucleotide repeat sequences, arranged in sets each

XX PT with a characteristic fluorescence label, useful e.g. in detection of

XX PT disease related genetic rearrangement.

XX PS Disclosure; Fig 7D-2; 104pp; English.

XX CC The method aims to provide a collection of highly reproducible

XX CC microsatellite marker sequences (WMS) at approx. 10-50 cm intervals

XX CC throughout the human genome which can be detectably labelled. The WMS are

XX CC polymorphic, simple sequence repeats and can be used in automated

XX CC genotyping. esp. fluorescence-based. The primers correspond to the unique

XX CC DNA sequence surrounding each marker, and PCR is used to detect each

XX CC polymorphism. When the WMS show considerable polymorphism (ie. a

XX CC difference in the number of repeats) between individuals, the markers can

XX CC be particularly informative. The WMS can be ideal for linkage studies.

XX CC Kits comprise at least 4 groups, of at least 3 sets, each comprising

XX CC labelled primers for PCR amplification of the DNA. Group 4 primer pairs

XX CC are shown in AAQ95465-480 and AAQ95559-530. The chromosomal markers,

XX CC published size range of the allele and degree of heterozygosity in the

XX CC population for the markers covered by these primer pairs are not given in

XX CC the specification

XX SQ Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAQ95469 (1-20)

QY 172 LeuSerArgGlnLeu 176

DB 2 CTAAGTAGGCAGTTG 16

RESULT 269

AAT07712

ID AAT07712 standard; DNA; 20 BP.

XX AC AAT07712;

XX DT 25-MAR-2003 (revised)

XX DT 16-JUL-1996 (first entry)

XX DE Oligonucleotide 9 used for selection of HIV-1 RT inhibitor.

XX KW DNA polymerase; gp43; ligand; cell sorting; inhibitor; probe; T4; HIV-1;

XX KW systematic evolution of ligands by exponential enrichment; SELEX; primer;

XX KW bacteriophage coat protein; serine protease; mammalian receptor; amplify;

XX KW mammalian hormone; mammalian growth factor; ribosomal protein; T7; PCR;

XX KW viral rev protein; nerve growth factor; HSV; reverse transcriptase;

XX KW polymerase chain reaction; ss.

XX OS Synthetic.

XX PN US5475096-A.

XX PD 12-DEC-1995.

XX PF 10-JUN-1991; 91US-00714131.

XX PR 11-JUN-1990; 90US-00536428.

XX PA (UYRE-) UNIV RES CORP.

XX PI Tuerk C, Gold L;

XX DR WPI; 1996-039557/04.

XX PT Artificial nucleic acid ligands - for selected target proteins.

XX PS Example 2; Col 171-172; 133pp; English.

XX CC AAT07705-T07712 represent oligonucleotides used in the creation of a

XX CC template for a systematic evolution of ligands by exponential enrichment

XX CC (SELEX) reaction on HIV-1 reverse transcriptase (HIV-1 RT). This sequence

XX CC was used as a 3' PCR primer and RT extension primer for the constructed

XX CC sequence. In a SELEX reaction, a target molecule (such as HIV-1 RT) is

XX CC contacted with a mixture of random nucleic acids under conditions

XX CC favourable for binding. Unbound nucleic acids are then separated from

XX CC those bound to the target, and the nucleic acid-target pairs are

XX CC dissociated. The dissociated nucleic acids are amplified to give a ligand

XX CC enriched mixture. These steps are repeated until the specific ligand is

XX CC obtained. This procedure can also be carried out for ligands for

XX CC bacteriophage coat proteins, serine proteases, mammalian receptors,

XX CC mammalian hormones, mammalian growth factors, ribosomal proteins, DNA

XX CC polymerases and viral rev proteins. The ligands identified (such as

XX CC AAT07553-T07660) may be used in assays, diagnostic procedures, or cell

XX CC sorting as an inhibitor of the target molecule function. It may also be

XX CC used as a probe or sequestering agent, and also possess catalytic

XX CC activity. (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT07712 (1-20)

QY 32 ValVallyeArgArg 36  
|||||

Db 4 GTGTAAACGACGG 18

RESULT 270

AAT12093

ID AAT12093 standard; DNA; 20 BP.

XX AAT12093;

XX 10-JUL-1996 (first entry)

XX M. tuberculosis rpoB gene fragment amplification primer P3.

XX Antibiotic; resistance; spectrum; gene; mycobacterium; determination;

XX amplification; tuberculosis; rpoB; fragment; primer; differential;

XX hybridisation; pattern; rifampicin; rifabutin; species identification;

XX ss.

XX Synthetic.

XX WO9533851-A2.

XX 14-DEC-1995.

XX 09-JUN-1995; 95WO-EP002230.

XX 09-JUN-1994; 94EP-00870093.

XX (INNO-) INNOGENETICS NV.

XX De Beenhouwer H, Portaela F, Machtelincx L, Jannes G, Rossau R;

XX WPI; 1996-040250/04.

XX Probes and primers for determ. of antibiotic resistance spectrum of

XX Mycobacterium, opt. coupled with species identification - from different

XX patterns of hybridisation with rpoB gene.

XX Claim 22; Page 39; 69pp; English.

XX The antibiotic resistance spectrum (ARS) of a mycobacterium can be

XX determined by amplifying the relevant part of the antibiotic resistance

XX gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the

XX primer set AAT12091-98, hybridising it with at least 1 rpoB gene probe,

XX detecting the hybrids formed and inferring the ARS, and opt. the spp.,

XX from the differential hybridisation patterns. The method is partic.

XX useful for the detection of rifampicin and/or rifabutin resistance in M.

XX lepreae or M. tuberculosis, and mycobacterial spp. identification. The

XX method is rapid and reliable and provides simultaneous determ. of ARS

XX and spp. identity

XX Sequence 20 BP; 2 A; 4 C; 10 G; 4 T; 0 U; 0 Other;

Alignment Scores: 9.44e+03 Length: 20

Pred. No.: 5.00 Matches: 5

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 2.53% Gaps: 0

DB: 2

US-09-966-880A-8 (1-198) x AAT12093 (1-20)

QY 92 ArchHisValAlaAap 96  
|||||

Db 4 CGCATGTCCGGAT 18

RESULT 271

AAT11459

ID AAT11459 standard; DNA; 20 BP.

XX AAT11459;

XX 10-SEP-1996 (first entry)

XX Retinoblastoma gene, RB1, exon 21 PCR 3' primer.

XX Retinoblastoma; RB; tumour suppressor gene; cancer; diagnosis; screening;

XX mutation; polymerase chain reaction; PCR; ss.

XX Synthetic.

XX WO9601908-A1.

XX 25-JAN-1996.

XX 07-JUL-1995; 95WO-US008604.

XX 08-JUL-1994; 94US-00271942.

XX (VISI-) VISIBLE GENETICS INC.

XX (HSCR-) HSC RES & DEV LP.

XX Gallie BL, Dunn JM, Stevens JK, Hui M;

XX WPI; 1996-097637/10.

XX Identifying mutation(s) in RB1 exons by quantitative amplification - and

XX by comparing length of amplification products and sequencing, for

XX diagnosis and genetic screening of retinoblastoma.

XX Claim 12; Page 23; 48pp; English.

XX AAT11420-T11473 are PCR amplification primers used for the amplification

XX of exons 1 to 27 and the promoter of the human retinoblastoma RB1 gene,

XX used to amplify RB1 exons for use in a method of diagnosing mutations in

XX the RB1 gene. By comparing the lengths of amplification products of RB

XX exons from a suspected RB patient with those of RB wild-type DNA,

XX patients can be diagnosed early which may avoid the need for

XX radiotherapy. Any difference in length of exons between a suspected RB

XX patient and those from wild-type RB1 indicates either a deletion or

XX insertion mutation. Further sequencing of suspect exons can pinpoint the

XX mutation. The method is directed to the diagnosis of and targeted genetic

XX screening for retinoblastoma in family members of a retinoblastoma

XX patient

XX Sequence 20 BP; 4 A; 2 C; 4 G; 10 T; 0 U; 0 Other;

Alignment Scores: 9.44e+03 Length: 20

Pred. No.: 5.00 Matches: 5

Score: 100.00% Conservative: 0

Percent Similarity: 100.00% Mismatches: 0

Best Local Similarity: 100.00% Indels: 0

Query Match: 2.53% Gaps: 0

DB: 2

US-09-966-880A-8 (1-198) x AAT11459 (1-20)

QY 28 TyrLeuCysTyrVal 32  
|||||

Db 2 TACCTATGTTATGTT 16  
|||||

RESULT 272

AA32599

ID AA32599 standard; DNA; 20 BP.

XX AA32599;

XX 30-JUN-1999 (first entry)

XX Target DNA partly complementary to M13mp18 DNA.

XX Nucleic acid detection; pyrylium; virus; microbe; mutation detection;  
 KW infectious disease; diagnosis; target; ss.  
 XX Synthetic.  
 OS  
 XX EP684239-A1.  
 PN  
 XX 29-NOV-1995.  
 PD  
 XX 25-MAY-1995; 95EP-00303567.  
 PF  
 XX 26-MAY-1994; 94JP-00112626.  
 PR  
 XX 07-JUN-1994; 94JP-00125040.  
 PP  
 XX (CANO ) CANON KK.  
 PA  
 XX Yamamoto N, Okamoto T;  
 PI  
 XX WPI; 1996-000982/01.  
 DR  
 XX  
 XX Detection of target substances such as DNA in samples - using at least  
 PT two reagents, one or more of these being a pyrylium cpd., which can  
 PT interact in the presence of the target cpd.  
 PT  
 XX Example 1; Page 70; 87pp; English.  
 PS  
 XX The invention relates to the detection of a target substance in a sample.  
 CC The method comprises: (a) providing at least two reagents (at least one  
 CC of which is a pyrylium cpd. of a specified formula) which can form a  
 CC reaction system for causing changes as a result of an interaction between  
 CC the reagents, the interaction being caused only when the target substance  
 CC is present in the sample; (b) reacting the reagents with the target  
 CC substance; and (c) measuring the resulting changes based on the  
 CC interaction. The methods allow detection of target substances using a  
 CC number of reagents which can form a reaction system causing a change  
 CC based on an interaction which mediates the target substance. They may be  
 CC used e.g. for detection and identification of desired base sequences of  
 CC nucleic acids (DNA or RNA) of viruses, microbes, animals, plants and  
 CC humans and detection of mutation in base sequences; for detection of  
 CC various substances with immune reactions such as immunoassays; and for  
 CC diagnosis of hereditary or infectious diseases. The methods do not  
 CC require B/F separation for detection of hybrid, comprise simple steps and  
 CC are highly sensitive. They allow accurate detection of desired hybrid  
 CC only, even when mismatched hybrid is present  
 CC  
 XX Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAX32599 (1-20)  
 QY 32 ValValValysArgArg 36  
 Db 1 GTTGTAACACGCG 15  
 RESULT 273  
 AAT12858  
 ID AAT12858 standard; DNA; 20 BP.  
 AC AAT12858;  
 XX  
 XX 22-OCT-1996 (first entry)  
 DT  
 XX PCR 3' primer for exon 21 of human RB1 (retinoblastoma-1) gene.  
 DE  
 XX PCR; polymerase chain reaction; retinoblastoma; tumour suppressor;  
 KW

KW cancer; mutation; identification; diagnosis; cystic fibrosis;  
 KW hierarchy assay; method; specificity; ss.  
 XX Homo sapiens.  
 OS  
 XX WO9607761-A2.  
 PN  
 XX 14-MAR-1996.  
 PD  
 XX 07-JUL-1995; 95WO-US008606.  
 PF  
 XX 08-JUL-1994; 94US-00271946.  
 PR  
 XX (VISI-) VISIBLE GENETICS INC.  
 PA  
 XX Dunn JM, Stevens JK, Capatos D, Matthews DE;  
 PI  
 XX WPI; 1996-171632/17.  
 DR  
 XX  
 XX Testing for a disease-associated mutation in a gene - using a hierarchy  
 PT of tests selected to optimise performance while minimising cost.  
 PT  
 XX Example 1; Page 32; 63pp; English.  
 PS  
 XX AAT12839-T12899 (excluding AAT12878) are PCR primers used to amplify  
 CC various regions of the RB-1 genome, including exons 1-27, the promoter  
 CC region and a control sequence unrelated to RB-1 from chromosome 15. The  
 CC primers are used in an example of a method for testing a disease-  
 CC associated mutation in a gene, the gene may not necessarily be a tumour  
 CC suppressor gene like the retinoblastoma gene another example is the  
 CC cystic fibrosis transmembrane conductance regulator (CFTR) gene which may  
 CC be analysed using the same method. The primers are used in various  
 CC groupings to produce a hierarchical assay useful to test a group of  
 CC patients suspected to have a genetic mutation. The method allows the  
 CC optimum (or near optimum) diagnostic algorithm by considering the cost  
 CC and the sensitivity and specificity of each test  
 CC  
 XX Sequence 20 BP; 4 A; 2 C; 4 G; 10 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAT12858 (1-20)  
 QY 28 TyLeuCysTyrVal 32  
 Db 2 TACCTATGTTATGTT 16  
 RESULT 274  
 AAX01439  
 ID AAX01439 standard; DNA; 20 BP.  
 XX  
 XX AAX01439;  
 AC  
 XX 27-AUG-2003 (revised)  
 DT  
 XX 28-APR-1999 (first entry)  
 DT  
 XX PCR primer #4 for M13 template.  
 DE  
 XX PCR primer; chain terminating nucleotide; protected 3'-hydroxyl group;  
 KW nucleic acid sequencing; nucleic acid synthesis; ss.  
 XX Synthetic.  
 OS  
 XX Enterobacteria phage M13.  
 XX  
 XX WO9623807-A1.  
 PN  
 XX 08-AUG-1996.  
 PD

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XX PF 30-JAN-1996; 96WO-SE0000096.
XX PR 31-JAN-1995; 95SE-00000342.
XX PA (KWIA/) KWIATKOWSKI M.
XX PI Kwiatkowski M;
XX DR WPI; 1996-371367/37.
XX PT New nucleotide cpds. with a 3'-acetal function - useful as chain
XX PT terminating nucleotide(s) in the sequencing and synthesis of nucleic
XX PT acids.
XX PS Example 6; Page 17; 32pp; English.
XX CC This sequence represents a labelled PCR primer for a bacteriophage M13
XX CC sequence, the position of the label on this sequence is not specified.
XX CC The invention relates to novel nucleotide compounds, which can be used as
XX CC chain terminating nucleotides which have a protected 3'-hydroxyl group
XX CC which is readily deprotected by acid hydrolysis. As chain terminators
XX CC they can be deprotected to form nucleotides that may be further extended.
XX CC They can be used for sequencing of nucleic acids or for nucleic acid
XX CC synthesis. (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX01439 (1-20)
QY 32 ValVallyeArgArg 36
DB 5 GTTGTAAACGACGG 19

RESULT 275
AAT10748/C
ID AAT10748 standard; RNA; 20 BP.
XX AC AAT10748;
XX DT 09-SEP-1996 (first entry)
XX DE Oligonucleotide probe, At-A5.
XX KW Electronically self-addressable device; ED; electrode; current source;
XX KW attachment layer; permeable; counterion; genetic typing; probe;
XX KW detection; ss.
XX OS Synthetic.
XX PH Key
XX PH modified_base 20
XX FT /*tag= a
XX FT /note= "3'-ribonucleoside terminus"
XX PN WO9601836-A1.
XX PD 25-JAN-1996.
XX PF 05-JUL-1995; 95WO-US008570.
XX PR 07-JUL-1994; 94US-00271882.
XX PA (NANO-) NANOGEN INC.
XX PT

PI Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX WPI; 1996-097582/10.
XX PT Electronically self-addressable device - used for electronic control of,
XX PT e.g. nucleic acid hybridisation.
XX PS Example 1; Page 60; 155pp; English.
XX CC The sequences given in AAT10742-67 are synthetic oligonucleotides which
XX CC are used in the construction of the electronically self-addressable
XX CC device (SD) of the invention. The SD comprises a substrate, an electrode
XX CC or opt. a number of electrodes supported by the substrate, a current
XX CC source operatively connected to the electrode and an attachment layer
XX CC adjacent to the electrode which is permeable to a counterion but not
XX CC permeable to a molecule capable of insulating or binding to the
XX CC electrode. The attachment layer is capable of attaching a macromolecule.
XX CC The SD is used for genetic typing and comprises a number of
XX CC electronically addressable locations each comprising an electrode, and a
XX CC binding entity, such as one of these probes, attached to each of the
XX CC locations capable of detecting the presence of a genetic sequence
XX SQ Sequence 20 BP; 4 A; 3 C; 7 G; 5 T; 1 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAT10748 (1-20)
QY 56 HisValGlutLeuLeu 60
DB 18 CACGTAGACTGCTC 4

RESULT 276
AAT58736
ID AAT58736 standard; cDNA; 20 BP.
XX AC AAT58736;
XX DT 25-MAR-2003 (revised)
XX DT 18-MAR-1997 (first entry)
XX DE Alexandrium LsrDNA reverse primer, D2C.
XX KW Probe; detection; Alexandrium; large-subunit ribosomal RNA gene; LsrDNA;
XX KW marine dinoflagellate; hypervariable domain; D1; D2; A. tamarense;
XX KW A. catenella; A. fundyense; ribotype; North American; Western European;
XX KW Temperate Asian; Tasmanian; Tropical Asian; Affine; Minutum; Andersoni;
XX KW ss.
XX OS Synthetic.
XX PN US5582983-A.
XX PD 10-DEC-1996.
XX PF 14-JUN-1994; 94US-00259745.
XX PR 28-OCT-1992; 92US-00967637.
XX PA (WOOD-) WOODS HOLE OCEANOGRAPHIC INST.
XX PI Scholin CA, Anderson DM;
XX DR WPI; 1997-042301/04.
XX PT Detection of Alexandrium dinoflagellates by nucleic acid hybridisation -
XX PT uses oligo:nucleotide(s) directed to the D2 hyper-variable domain of

```

PT large sub-unit of rRNA gene.  
XX Example 1; Col 7; 49pp; English.  
XX  
CC The sequences given in AAT58735-36 represent primers which were used in  
CC the amplification of the large-subunit ribosomal RNA genes (LSrDNA) from  
CC various strains of the marine dinoflagellates. The primers are targeted  
CC to conserved elements at positions 24-45 (forward primer) and 733-714  
CC (reverse primer) relative to the Procentrum mican LSrRNA. The  
CC amplified fragment contains the evolutionarily variable domains D1 and  
CC D2. Analysis of the LSrDNA has revealed hypervariable domains which  
CC provide highly specific signature sequences useful in identifying and  
CC detecting similar populations of Alexandrium. Analysis of the LSrDNA  
CC sequence lead to the identification of five distinct Alexandrium  
CC tamarensis/catenella/fundense ribotypes which were named with reference  
CC to the geographic origin of the isolates: North American, Western  
CC European and Temperate Asian designations reflect the origins of the  
CC majority of cultures within each cluster. Tasmanian and Tropical Asian  
CC designations reflect the origins of single A. tamarensis cultures.  
CC Alexandrium species designations were used to identify the three  
CC remaining ribotypes. Affine and Minutum were chosen for two of these  
CC since their representatives are the most prominent within their  
CC respective clusters. Andersoni was chosen to delineate the final  
CC ribotype, reflecting both its unique LSrDNA sequence and the isolates  
CC taxonomic classification. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAT58736 (1-20)  
  
QY 170 ValArgLeuSerArg 174  
DB 6 GTCCGCTTTCAAGA 20  
  
RESULT 277  
AAT62432  
ID AAT62432 standard; cDNA; 20 BP.  
XX  
AC AAT62432;  
XX  
DT 08-JUL-1997 (first entry)  
XX  
DE Bovine beta-mannosidosis carrier test sense primer MJ-124.  
XX  
KW Bovine; beta-mannosidase; enzyme; kidney; affinity chromatography;  
KW antibody; primer; probe; PCR; polymerase chain reaction; amplification;  
KW thyroid; hybridisation; detection; point mutation; beta-mannosidosis;  
KW cattle; carrier; Saler breed; ss.  
XX  
OS Synthetic.  
XX  
PN US5605797-A.  
XX  
PD 25-FEB-1997.  
XX  
PF 15-SEP-1994; 94US-00306546.  
XX  
PR 15-SEP-1994; 94US-00306546.  
XX  
PA (UNMS ) UNIV MICHIGAN STATE.  
XX  
PI Cavanagh KT, Chen H, Friderici K, Jones MZ;  
XX  
DR WPI; 1997-153571/14.  
XX

PT Oligo:nucleotide fragments of bovine beta-mannosidase gene - for  
PT detecting mutation associated with beta-mannosidosis.  
XX  
PS Example 2; Col 18; 39pp; English.  
XX  
CC The primers AAT62432-3 were used to detect beta-mannosidosis carriers by  
CC detecting a mutation in the beta-mannosidase gene (AAT62419). The method  
CC of detection is artificial introduction of restriction site (AIRS) which  
CC involves amplifying a 187 bp fragment of the genomic sequence around the  
CC point mutation and selectively introducing a BstNI restriction enzyme  
CC site, especially in the wild type sequence. The mutant sequence will not  
CC contain this site after amplification. Thus upon restriction digestion  
CC with BstNI, wild type and mutant sequences can be separated. This primer  
CC corresponds to bases 2554-2573 of the bovine beta-mannosidase gene  
CC sequence. The assays can be used to identify cattle that are carriers of  
CC beta-mannosidosis, e.g. in the Saler breed  
XX  
SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAT62432 (1-20)  
  
QY 179 IleLeuLeuProLeu 183  
DB 6 ATTCCTTTACCCCTG 20  
  
RESULT 278  
AAV00799  
ID AAV00799 standard; RNA; 20 BP.  
XX  
AC AAV00799;  
XX  
DT 25-MAR-1998 (first entry)  
XX  
DE 3' PCR primer for SELEX ligands to HIV-1 RT.  
XX  
KW Systematic evolution of ligands by exponential enrichment; SELEX; PCR;  
KW binding affinity; diagnosis; inhibitor; probe; catalyst; template; ss;  
KW human immunodeficiency virus type 1; reverse transcriptase; primer;  
KW amplification.  
XX  
OS Synthetic.  
XX  
PN US5670637-A.  
XX  
PD 23-SEP-1997.  
XX  
PF 27-MAR-1995; 95US-00412110.  
XX  
PR 11-JUN-1990; 90US-00536428.  
PR 10-JUN-1991; 91US-00714131.  
XX  
PA (NEXS-) NEXSTAR PHARM INC.  
XX  
PI Tuerk C, Gold L;  
XX  
DR WPI; 1997-479527/44.  
XX  
PT Nucleic acid ligands for binding proteins - obtained by systematic  
PT evolution of ligands by exponential enrichment procedures.  
XX  
PS Example 2; Col 55; 133pp; English.  
XX  
CC This oligonucleotide is used in the generation of a template for the  
CC isolation of nucleic acid ligands which bind the human immunodeficiency  
CC virus type 1 (HIV-1) reverse transcriptase. The ligands are isolated by

CC the systematic evolution of ligands by exponential enrichment (SELEX)  
 CC method of the invention. This method is especially used to isolate novel  
 CC non-naturally occurring nucleic acid ligands having a specific binding  
 CC affinity for a target molecule, where the target molecule is a protein  
 CC and the nucleic acid ligand is not a nucleic acid known to bind the  
 CC target molecule. The nucleic acid ligands can be used, e.g. in assay  
 CC methods, diagnostic procedures, cell sorting, as inhibitors of target  
 CC molecule function, as probes, as sequestering agents, for therapy or as  
 CC catalysts  
 XX  
 SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV00799 (1-20)

QY 32 ValValValArgArg 36  
 DB 4 GTTGTAAACGACGG 18

RESULT 279

AAV02707  
 ID AAV02707 standard; DNA; 20 BP.

XX  
 AC AAV02707;

XX  
 DT 19-MAY-1998 (first entry)

XX  
 DE Human Class I HLA-G gene exon 2 PCR primer 1.

XX  
 KW Human leukocyte antigen class I gene; HLA-G; allele testing; donor;  
 XX tissue matching; recipient; graft rejection; class typing; ds.

XX  
 OS Synthetic.

XX  
 OS Homo sapiens.

XX  
 PN WO9723645-A1.

XX  
 XX 03-JUL-1997.

XX  
 PF 04-JAN-1996; 96WO-US000362.

XX  
 PR 04-JAN-1996; 96WO-US000362.

XX  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.

XX  
 PI Yang SY, Cereb N;

XX  
 DR WPI; 1997-351080/32.

XX  
 PT DNA-based human leukocyte antigen class I gene typing method - useful for  
 PT tissue matching and prevention of graft versus host disease.

XX  
 PS Claim 16; Page 18; 89pp; English.

XX  
 CC AAV02707 and AAV02708 are PCR primers used to amplify the human leukocyte  
 CC antigen (HLA) Class I HLA-G gene exon 2, which is used in a novel method  
 CC for testing a tissue sample to determine the allelic type of a HLA class  
 CC I gene in the sample. The HLA class I gene is selected from among HLA-A,  
 CC -B and -C genes. The method comprises of treating the tissue sample to  
 CC obtain nucleic acid polymers suitable for amplification then combining  
 CC these polymers with a first primer which hybridises with a portion of  
 CC intron 1 or intron 3 of the HLA Class I gene and a second primer which  
 CC hybridises with a different portion of the HLA Class I gene under  
 CC conditions suitable for amplification to obtain an amplified product. The  
 CC product is then evaluated to determine the allelic type of the HLA-Class  
 CC I gene. The method is useful for tissue matching HLA class I antigens

CC between donors and recipients and hence for preventing graft versus host  
 CC disease  
 XX  
 SQ Sequence 20 BP; 2 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV02707 (1-20)

QY 35 ArgArgAspSerAla 39  
 DB 5 CGACGCGACTCGCG 19

RESULT 280

AAV20877

ID AAV20877 standard; cDNA; 20 BP.

XX  
 AC AAV20877;

XX  
 DT 28-JUL-1998 (first entry)

XX  
 DE Mouse specific 5' PCR primer.

XX  
 KW Rat interferon-gamma inducing factor; IGIF; interleukin-18; IL-18;  
 XX IL-18-alpha; transfection; antibody; probe; hybridisation; PCR;  
 XX amplification; primer; ss.

XX  
 OS Synthetic.

XX  
 OS Mus sp.

XX  
 PN WO9810072-A1.

XX  
 PD 12-MAR-1998.

XX  
 PF 08-SBP-1997; 97WO-US015891.

XX  
 PR 09-SBP-1996; 96US-0025141P.

XX  
 PR 08-APR-1997; 97US-0043087P.

XX  
 PA (CORR ) CORNELL RES FOUND INC.

XX  
 PI Joh TH, Conti B;

XX  
 DR WPI; 1998-193622/17.

XX  
 PT Rat interferon-gamma inducing factors and related DNA - useful for  
 PT quantitating stress in a mammal.

XX  
 PS Example 1; Page 34; 47pp; English.

XX  
 CC This is the nucleotide sequence of the mouse specific 5' PCR primer used  
 CC in the amplification of the isolated rat interferon-gamma inducing factor  
 CC (IGIF), also known as interleukin-18 (IL-18). It can be used to transform  
 CC a cell, which upon its expression can cause the cell to produce rat IGIF,  
 CC i.e. IL-18 or IL-18 alpha. The antibody to IGIF, IGIF and probes derived  
 CC from it, are useful for detection of IL-18 or IL-18 alpha present in a  
 CC sample. The amount of IL-18 or IL-18 alpha in a sample can be used to  
 CC quantitate stress in a mammal

XX  
 SQ Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0



```

DB:      2      Gaps:      0
US-09-966-880A-8 (1-198) x AAV20877 (1-20)
QY      53 AenglyCysHisVal 57
      |||||
Db      4 AATGGCTGCCATGTC 18
      |||||
RESULT 281
AAV44624
ID      AAV44624 standard; DNA; 20 BP.
XX
AC      AAV44624;
XX
XX      24-NOV-1998 (first entry)
DT
DE
DE      Human uncoupling protein-2 UCP2 gene primer hUCP2.CDSR3.
XX
KW      Uncoupling protein-2; UCP2 gene; human; respiration; thermogenesis;
KW      obesity; hyperinsulinaemia; glucose intolerance; diabetes; syndrome X;
KW      hypothermia; wasting; cachexia; anorexia; inflammation; fever;
KW      hyperthermia; gene therapy; diagnosis; PCR; primer; ss.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
XX      MO9831396-AL.
PN
XX
XX      23-JUL-1998.
PD
XX
XX      22-APR-1997; 97WO-US006864.
PF
XX
XX      15-JAN-1997; 97US-0034960P.
PR
XX
XX      (UYDU-) UNIV DUKE.
PA
PA      (REGC) UNIV CALIFORNIA.
PA
PA      (CNRS) CENT NAT RECH SCI.
XX
XX      Surwit RS, Collins SA, Warden CH, Seldin MF, Ricquier D;
PI      Bouillaud F;
PI
XX
XX      WPI; 1998-413823/35.
DR
XX
XX      Method for treating disease associated with altered UCP-2 expression - by
PT      administering agent which enhances or inhibits UCP-2 activity,
PT      effectively to treat obesity, diabetes, fever, hyperthermia, cachexia
PT      etc.
XX
XX      Disclosure; Fig 1F; 98pp; English.
PS
XX
XX      Primer hUCP2.CDSR3 is used with forward primer hUCP2.CDSF3 (see AAV44623)
CC      in the PCR amplification of a 1096 bp region of the human uncoupling
CC      protein-2 (UCP2) gene coding sequence (see also AAV44595). The primers
CC      were also used in a RACE amplification of human UCP2 cDNA. The invention
CC      relates to a method for treating diseases associated with altered UCP2
CC      expression, such as obesity, diabetes, syndrome X, hypothermia,
CC      hyperinsulinaemia, glucose intolerance, wasting, anorexia, inflammation,
CC      cachexia, fever or hyperthermia
XX
SQ      Sequence 20 BP; 9 A; 0 C; 11 G; 0 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9.44e+03      Length:      20
Score:      5.00      Matches:      5
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      2.53%      Indels:      0
DB:      2      Gaps:      0

US-09-966-880A-8 (1-198) x AAV44624 (1-20)
QY      22 LysGlyArgArgGlu 26
      |||||

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Db      5 AAGGAGAGGAGGAA 19
RESULT 282
AAV27092/C
ID      AAV27092 standard; DNA; 20 BP.
XX
XX      AAV27092;
AC
XX
XX      25-MAR-2003 (revised)
DT      16-SEP-1998 (first entry)
DT
DE      Primer YA6.
DE
XX      ss; Human; double-stranded adenosine deaminase; neurological disorder;
XX      CNS disorder; PCR; primer; amplification.
XX      Synthetic.
XX
XX      US5763174-A.
PN
XX
XX      09-JUN-1998.
PD
XX
XX      13-NOV-1995; 95US-00555678.
PF
XX
XX      17-FEB-1994; 94US-00197794.
PR      25-JUL-1994; 94US-00280443.
PR      01-JUN-1995; 95US-00457459.
XX
XX      (WIST-) WISTAR INST ANATOMY & BIOLOGY.
PA
XX
XX      Nishikura K;
PI
XX
XX      WPI; 1998-347307/30.
DR
XX
XX      Diagnosis of disorders characterised by inappropriate expression of
PT      enzyme - comprises contacting tissue sample with labelled antibodies,
PT      oligonucleotides or protein reagent and measuring association of enzyme.
XX
XX      Example 10; Col 21; 66pp; English.
PS
XX
XX      The primers AAV27072-V27099 were used in the isolation, amplification and
CC      characterisation of double-stranded adenosine deaminase (DRADA). DRADA is
CC      specific for double-stranded RNA and is useful for the diagnosis of
CC      disorders characterised by inappropriate double-stranded ribonucleic acid
CC      adenosine deaminase expression. Particularly for diagnosis of certain
CC      neurological or CNS disorders, e.g. Alzheimer's disease, Huntington's
CC      disease, subacute sclerosing panencephalitis, measles inclusion body
CC      encephalitis or stroke, or other neurological conditions associated with
CC      aging. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence 20 BP; 7 A; 1 C; 9 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      9.44e+03      Length:      20
Score:      5.00      Matches:      5
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      2.53%      Indels:      0
DB:      2      Gaps:      0

US-09-966-880A-8 (1-198) x AAV27092 (1-20)
QY      38 SerAlaThrSerPhe 42
      |||||
Db      17 TCAGCCACATCCTTC 3
      |||||
RESULT 283
AAV27081
ID      AAV27081 standard; DNA; 20 BP.
XX
XX      AAV27081;
AC
XX
XX      25-MAR-2003 (revised)
DT

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DT 16-SEP-1998 (first entry)
XX
DE Primer YS5.
XX
KW ss; Human; double-stranded adenosine deaminase; neurological disorder;
KW CNS disorder; PCR; primer; amplification.
XX
XX Synthetic.
XX
XX US5763174-A.
XX
XX 09-JUN-1998.
XX
XX 13-NOV-1995; 95US-005555678.
XX
XX 17-FEB-1994; 94US-00197794.
XX
XX 25-JUL-1994; 94US-00280443.
XX
XX 01-JUN-1995; 95US-00457459.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Nishikura K;
XX
XX WPI; 1998-347307/30.
XX
XX Diagnosis of disorders characterised by inappropriate expression of
XX enzyme - comprises contacting tissue sample with labelled antibodies,
XX oligonucleotides or protein reagent and measuring association of enzyme.
XX
XX Example 10; Col 21; 66pp; English.
XX
XX The primers AAV27072-V27099 were used in the isolation, amplification and
XX characterisation of double-stranded adenosine deaminase (DRADA). DRADA is
XX specific for double-stranded RNA and is useful for the diagnosis of
XX disorders characterised by inappropriate double-stranded ribonucleic acid
XX adenosine deaminase expression. Particularly for diagnosis of certain
XX neurological or CNS disorders, e.g. Alzheimer's disease, Huntington's
XX disease, subacute sclerosing panencephalitis, measles inclusion body
XX encephalitis or stroke, or other neurological conditions associated with
XX aging. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 20 BP; 3 A; 9 C; 1 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV27081 (1-20)

Qy 38 SerAlaThrSerPhe 42
Db 4 TCAGCCACATCCTTC 18

RESULT 284
AAV48030
ID AAV48030 standard; DNA; 20 BP.
XX
XX AAV48030;
XX
XX 19-OCT-1998 (first entry)
XX
XX Murine B7-1 targetted oligonucleotide 14915.
XX
XX ss; mouse; B7; T cell; inflammation; autoimmune disease; cell activation;
XX cell proliferation.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX

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FH Key Location/Qualifiers
PT modified_base 1..20
PT /tag= a
PT /note= "Phosphorothioate linkages"
XX
XX W09829124-A1.
XX
XX 09-JUL-1998.
XX
XX 16-DEC-1997; 97WO-US023270.
XX
XX 31-DEC-1996; 96US-00777266.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Vickers TA;
XX
XX WPI; 1998-387783/33.
XX
XX New oligo:nucleotide(s) that modulate expression of B7 proteins - used
XX for, e.g. controlling activation and proliferation of T cells,
XX particularly for treatment, diagnosis and prevention of inflammation.
XX
XX Example 1; Page 36; 120pp; English.
XX
XX The oligonucleotides which specifically hybridise to B7 modulate its
XX expression (and thus T cell activation and proliferation). This is
XX particularly useful for treatment and prevention of inflammation and
XX autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
XX Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
XX (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
XX rhinitis, allergy, cancer and metastases. The oligonucleotides may also
XX be used to manipulate T cell activation ex vivo; to determine or detect
XX B7 protein expression; for diagnosis; as assay and purification reagents,
XX and to study physiological roles of B7 proteins
XX
XX Sequence 20 BP; 3 A; 10 C; 4 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV48030 (1-20)

Qy 176 LeuArgArgIleLeu 180
Db 1 CTGCGCGAATCCTG 15

RESULT 285
AAV14584
ID AAV14584 standard; DNA; 20 BP.
XX
XX AAV14584;
XX
XX 27-AUG-2003 (revised)
XX
XX 21-MAY-1998 (first entry)
XX
XX Sequence used in construction of SELEX template for T4 polymerase.
XX
XX High affinity RNA ligand motif; polymer binding; cell sorting; inhibitor;
XX systematic evolution of ligands by exponential enrichment; SELEX;
XX sequestering agent; bacteriophage T4 DNA polymerase; ss.
XX
XX Synthetic.
XX
XX Enterobacteria phage T4.
XX
XX US5696249-A.
XX
XX 09-DEC-1997.
XX

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XX 24-MAR-1995; 95US-00409442.
XX
XX 11-JUN-1990; 90US-00536428.
XX PR 10-JUN-1991; 91US-00714131.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Tuerk C, Gold L;
XX
XX WPI; 1998-041356/04.
XX
XX Synthetic nucleic acid ligands - that bind to target molecules other than
XX nucleic acids.
XX
XX Example 1; Col 54; 137pp; English.
XX
XX This sequence represents a sequence used to prepare the template for a
XX systematic evolution of ligands by exponential enrichment (SELEX)
XX reaction to isolate ligands specific for the bacteriophage T4 DNA
XX polymerase. The identified sequences are examples of the ligands of the
XX invention. The ligands are non-naturally occurring nucleic acid ligand
XX with specific binding affinity for a target molecule, where: the target
XX molecule is not a polynucleotide that binds to the ligand by Watson-Crick
XX base pairing or triple helix binding; the ligand is not a nucleic acid
XX having the known physiological function of being bound by the target
XX molecule; and the ligand is obtained by: (a) contacting the target
XX molecule with a candidate mixture of nucleic acids, each having a region
XX of randomised sequence; (b) separating the nucleic acids having the
XX highest affinity for the target; and (c) amplifying the separated nucleic
XX acids. Ligands as above that bind to natural or synthetic polymers, e.g.
XX proteins, polysaccharides, glycoproteins, hormones, receptors, cell
XX surfaces, drugs, metabolites, cofactors, transition-state analogues or
XX toxins, may be useful in assays, diagnostic procedures or cell sorting,
XX as inhibitors of target molecule function, as probes, as sequestering
XX agents, etc.; or may have catalytic activity. (Updated on 27-AUG-2003 to
XX correct OS field.)
XX
XX Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 9.44e+03 Length: 20
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAV14584 (1-20)
XX
XX QY 32 ValVallysArgArg 36
XX
XX DB 4 GTTGTAAACGACGG 18
XX
XX
XX RESULT 286
XX AAV28063
XX ID AAV28063 standard; DNA; 20 BP.
XX
XX AC AAV28063;
XX
XX 25-SEP-1998 (first entry)
XX
XX DE Ataxia telangiectasia exon 53 primer 2.
XX
XX ss; PCR; primer; amplification; ataxia telangiectasia; diagnosis; human;
XX radiation; breast cancer.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9822621-A1.
XX
XX 28-MAY-1998.
XX

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XX 17-NOV-1997; 97WO-US020953.
XX
XX 20-NOV-1996; 96US-00753147.
XX
XX (VIRG-) VIRGINIA MASON RES CENT.
XX
XX Concannon P;
XX
XX WPI; 1998-312503/27.
XX
XX Method of detecting ataxia telangiectasia - comprises use of primers
XX based on intron-exon boundaries, useful for diagnosing disease in
XX heterozygotes.
XX
XX Claim 6; Page 8; 47pp; English.
XX
XX The primers AAV27964-V28086 are used to amplify ataxia telangiectasia
XX (ATM) exons and their adjacent splice junction sites. These can be used
XX as a method of detecting a mutation in the ATM gene by comparing the PCR
XX products of amplification from a sample from a patient suspected of
XX having an ATM mutation with a sample from a non-mutated ATM patient. This
XX method is especially useful for diagnosing ataxia telangiectasia in
XX heterozygotes and can be used to locate the positions of the mutation.
XX The diagnosis of ataxia telangiectasia in patients needing therapeutic
XX radiation will prevent fatal radiation burns and the development of
XX breast cancer which can occur
XX
XX Sequence 20 BP; 5 A; 3 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 9.44e+03 Length: 20
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAV28063 (1-20)
XX
XX QY 97 PheLeuArgGlyAsn 101
XX
XX DB 4 TTCTTAGAGGGAAT 18
XX
XX
XX RESULT 287
XX AAZ09818
XX ID AAZ09818 standard; DNA; 20 BP.
XX
XX AC AAZ09818;
XX
XX 26-NOV-1999 (first entry)
XX
XX DE Phytophthora citricola PCR primer CITR1.
XX
XX PCR primer; detection; pathogenic; oak; beech; tree; probe; screening;
XX natural forest; infection; nursery; disease-resistant genotype;
XX asymptomatic tissue; ss.
XX
XX Phytophthora citricola.
XX
XX EP949337-A2.
XX
XX 13-OCT-1999.
XX
XX 01-APR-1999; 99EP-00105198.
XX
XX 03-APR-1998; 98DE-01015138.
XX
XX (GSFS-) GSF GES STRAHLEN & UMWELTFORSCH GMBH.
XX
XX Bahnweg G, Schubert R, Sandermann H, Mueller-Starck G;
XX
XX WPI; 1999-553461/47.
XX

```

XX Primers for species-specific detection of Phytophthora species,  
PT especially in oak and beech trees.  
XX  
PS Claim 1; Page 11; 19pp; German.  
XX  
CC This invention describes novel PCR primers for species-specific detection  
CC of Phytophthora spp. The primers can be used to detect, quantify or  
CC distinguish between Phytophthora spp. that are pathogenic to oak and  
CC beech trees, either (a) in pairs as primers per se in a conventional  
CC polymerase chain reaction or (b) individually as probes in conventional  
CC hybridization assays. The assays can be used for mass screening of  
CC natural forest trees to prevent spread of infection to nursery material,  
CC and in the development of disease-resistant genotypes. The primers do not  
CC cross-react with DNA from other species and can be used in assays capable  
CC of detecting pathogenic Phytophthora spp. in asymptomatic tissues of oak  
CC and beech trees. AA209816-209825 represent the PCR primers and probes  
CC used in the method of the invention  
XX  
SQ Sequence 20 BP; 1 A; 5 C; 4 G; 10 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AA209818 (1-20)  
  
QY 59 LeuLeuPheLeuArg 63  
DB 3 TTGCTTTTTCGA 17  
  
RESULT 288  
AA277443/C  
ID AAX77443 standard; DNA; 20 BP.  
XX  
AC AAX77443;  
XX  
XX 05-AUG-1999 (first entry)  
XX  
XX JP11127897 primer 5.  
XX  
XX  
XX Detection; primer; hybridisation; target; probe; interaction;  
KW electron current; double helix; ss.  
XX  
XX Synthetic.  
XX  
XX JP11127897-A.  
XX  
XX 18-MAY-1999.  
XX  
XX 31-OCT-1997; 97JP-00300944.  
XX  
XX 31-OCT-1997; 97JP-00300944.  
XX  
XX (CANO ) CANON KK.  
XX  
XX WPI; 1999-350344/30.  
XX  
XX  
XX Detection of a target nucleic acid - using substances capable of  
PT interaction with a phenomenon which allow electron current in the double  
PT helix structure bound via a linker.  
XX  
XX  
XX Example 3; Page 6; 7pp; Japanese.  
XX  
XX This invention describes a novel method for the detection of a target  
CC nucleic acid and a probe nucleic acid hybrid in a sample, comprising (1)  
CC substances capable of interaction with a phenomenon which allow electron  
CC current in the double helix structure bound via a linker (2)  
CC immobilisation of the base sequence of target nucleic acid and the probe  
CC

CC nucleic acid having complementary base sequence of the target nucleic  
CC acid on a predetermined site of a carrier (3) contact of the probe  
CC nucleic acid and the sample under a condition capable of forming a hybrid  
CC of the target nucleic acid and the probe nucleic acid (4) supply of the  
CC labelled unit on the predetermined site of the carrier presumed to form  
CC the hybrid (5) detection of change of 1st and/or 2nd labelled  
CC substance(s) in the labelled unit supplied to the predetermined site and  
CC (6) detection of the presence of the hybrid in the sample. This sequence  
CC represents a primer used in the method of the invention  
XX  
SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAX77443 (1-20)  
  
QY 32 ValVallyeArgArg 36  
DB 20 GTTGTAAACGACGG 6  
  
RESULT 289  
AAX77439  
ID AAX77439 standard; DNA; 20 BP.  
XX  
AC AAX77439;  
XX  
XX 05-AUG-1999 (first entry)  
XX  
XX JP11127897 primer 1.  
XX  
XX Detection; primer; hybridisation; target; probe; interaction;  
KW electron current; double helix; ss.  
XX  
XX Synthetic.  
XX  
XX JP11127897-A.  
XX  
XX 18-MAY-1999.  
XX  
XX 31-OCT-1997; 97JP-00300944.  
XX  
XX 31-OCT-1997; 97JP-00300944.  
XX  
XX (CANO ) CANON KK.  
XX  
XX WPI; 1999-350344/30.  
XX  
XX Detection of a target nucleic acid - using substances capable of  
PT interaction with a phenomenon which allow electron current in the double  
PT helix structure bound via a linker.  
XX  
XX  
XX Example 1; Page 6; 7pp; Japanese.  
XX  
XX This invention describes a novel method for the detection of a target  
CC nucleic acid and a probe nucleic acid hybrid in a sample, comprising (1)  
CC substances capable of interaction with a phenomenon which allow electron  
CC current in the double helix structure bound via a linker (2)  
CC immobilisation of the base sequence of target nucleic acid and the probe  
CC nucleic acid having complementary base sequence of the target nucleic  
CC acid on a predetermined site of a carrier (3) contact of the probe  
CC nucleic acid and the sample under a condition capable of forming a hybrid  
CC of the target nucleic acid and the probe nucleic acid (4) supply of the  
CC labelled unit on the predetermined site of the carrier presumed to form  
CC the hybrid (5) detection of change of 1st and/or 2nd labelled  
CC substance(s) in the labelled unit supplied to the predetermined site and  
CC (6) detection of the presence of the hybrid in the sample. This sequence  
CC represents a primer used in the method of the invention



AAK15307  
ID AAK15307 standard; DNA; 20 BP.  
XX  
AC AAK15307;  
XX  
DT 29-APR-1999 (first entry)  
XX  
DE PCR primer F5S1 for DNA encoding a DNA polymerase binding factor F5.  
XX  
KW Thermostable polypeptide factor; DNA synthesis activity; DNA polymerase;  
KW in vitro DNA synthesis; PCR primer; ss.  
XX  
OS Synthetic.  
OS Pyrococcus furiosus.  
XX  
FN WO9900506-A1.  
XX  
PD 07-JAN-1999.  
XX  
PF 24-JUN-1998; 98WO-JP002845.  
XX  
PR 26-JUN-1997; 97JP-00187496.  
PR 21-NOV-1997; 97JP-00320692.  
XX  
PA (TAKI ) TAKARA SHUZO CO LTD.  
XX  
PI Uemori T, Sato Y, Fujita T, Miyake K, Mukai H, Asada K, Kato I;  
XX  
DR WPI; 1999-095751/08.  
XX  
PT Thermostable polypeptide factors promoting the activity of DNA polymerase  
PT - for improvement of DNA synthesis and amplification in vitro.  
XX  
PS Example 12; Page 138; 177pp; Japanese.  
XX  
CC PCR primers AAK15307-08 were used to amplify Pyrococcus furiosus DNA  
CC encoding a thermostable polypeptide factor. This factor binds to, and  
CC promotes the DNA synthesis activity of DNA polymerase. The polymerase  
CC related factors can be used to provide more efficient in vitro DNA  
CC synthesis and amplification systems (e.g. for polymerase chain reaction)  
CC by using the factors in conjunction with a DNA polymerase  
XX  
SQ Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAK15307 (1-20)  
  
QY 156 GluArgThrPhelys 160  
Db 3 GAGAGAACTTCAAG 17  
  
RESULT 293  
AAK15307/C  
ID AAK15307 standard; DNA; 20 BP.  
XX  
AC AAK15307;  
XX  
DT 20-AUG-1999 (first entry)  
XX  
DE 3' ribonucleoside oligonucleotide probe AT-A5.  
XX  
KW Microelectronic device; multi-step reaction; microscopic format;  
KW ion-permeable permeation layer; electrode; electrical control; transport;  
KW attachment; binding; DNA/RNA hybrid; probe; ss.  
XX  
OS Synthetic.

XX Key Location/Qualifiers  
FH misc\_RNA 20  
FT /\*tag= a  
XX  
PN WO9929711-A1.  
XX  
PD 17-JUN-1999.  
XX  
PF 01-DEC-1998; 98WO-US025475.  
XX  
PR 05-DEC-1997; 97US-00986065.  
XX  
PA (NANO-) NANOGEN INC.  
XX  
PI Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;  
XX  
DR WPI; 1999-385567/32.  
XX  
PT New microelectronic device designed to carry out and control multi-step  
PT and multiplex molecular biological reactions in microscopic format.  
XX  
PS Example 1; Page 89; 179pp; English.  
XX  
CC The specification describes a self-addressable, self-assembling  
CC microelectronic device which is designed to actively carry out and  
CC control multi-step and multiplex molecular biological reactions in  
CC microscopic formats. A key aspect of this invention is played by the ion  
CC -permeable permeation layer which overlies the electrode. This permeation  
CC layer allows attachment of nucleic acids to permit immobilization but  
CC also separates the attached oligonucleotides and hybridized target DNA  
CC sequences from the highly reactive electrochemical environment generated  
CC immediately at the electrode surface. The microelectronic device is  
CC designed and fabricated to actively carry out and control reactions such  
CC as nucleic acid hybridizations, antibody/antigen reactions, sample  
CC preparation, diagnostics and biopolymer synthesis. The device can  
CC electronically control the transport and attachment of specific binding  
CC entities, such as nucleic acids and polypeptides, to specific micro-  
CC locations. The device can subsequently control the transport and reaction  
CC of analytes or reactants at the addressed specific micro-locations. The  
CC device is able to concentrate analytes and reactants, remove non-  
CC specifically bound molecules, provide stringency control for DNA  
CC hybridization reactions and improve the detection of analytes. The  
CC present sequence represents a probe used to exemplify the invention  
XX  
SQ Sequence 20 BP; 4 A; 3 C; 7 G; 5 T; 1 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 9.44e+03 Length: 20  
Score: 5.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.53% Indels: 0  
DB: 2 Gaps: 0  
  
US-09-966-880A-8 (1-198) x AAX81307 (1-20)  
  
QY 56 HisValGluLeuLeu 60  
Db 18 CAGTAGAACTGCTC 4  
  
RESULT 294  
AAX76912  
ID AAX76912 standard; DNA; 20 BP.  
XX  
AC AAX76912;  
XX  
DT 05-AUG-1999 (first entry)  
XX  
DE Probe used to test nucleic acid detection method.  
KW Nucleic acid detection; probe; ss.  
XX

OS Synthetic.  
 XX JP11127862-A.  
 PN  
 XX 18-MAY-1999.  
 PD  
 XX 31-OCT-1997; 97JP-00300943.  
 XX  
 XX 31-OCT-1997; 97JP-00300943.  
 PR  
 XX (CANO ) CANON KK.  
 PA  
 XX WPI; 1999-350323/30.  
 DR  
 XX  
 XX Detection of a target nucleic acid - using a labelled unit with labels  
 PT capable of interactive action in a phenomenon of electron flow in double  
 PT helix structure.  
 XX  
 XX Example 1; Page 4; 9pp; Japanese.  
 PS  
 XX This sequence is a probe used to test the method of the invention. The  
 CC method is for the detection of a hybrid of a target nucleic acid and a  
 CC probe nucleic acid in a sample comprises: (1) preparation of a labelled  
 CC unit composed of 1st and 2nd labelled substances capable of interactive  
 CC action in a phenomenon of electron flow in double helix structure in the  
 CC presence of a hybrid via a linker; (2) addition of a probe nucleic acid  
 CC having a complementary base sequence to the base sequence of target  
 CC nucleic acid; (3) placing the sample under conditions capable of forming  
 CC the target nucleic acid and the probe nucleic acid to give a hybrid; (4)  
 CC mixing the sample capable of forming the hybrid and the labelled unit;  
 CC (5) detection of the change in the 1st and/or 2nd labelled substances  
 CC caused by their interaction; and (6) detection of the presence of a  
 CC hybrid in the sample. The method can be used for the detection of a  
 CC target nucleic acid having a specified base sequence. The method allows  
 CC for the simple and easily operable detection of labelled nucleic acids  
 CC without complicated synthesis of labelled probe nucleic acids for  
 CC respective base sequence  
 XX  
 SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAX76912 (1-20)  
 QY 32 ValVallysArgArg 36  
 Db 1 GTTGTAACGACGG 15  
 RESULT 295  
 AAV64129  
 ID AAV64129 standard; DNA; 20 BP.  
 XX  
 XX AAV64129;  
 AC  
 XX 25-JAN-1999 (first entry)  
 DT  
 XX Bovine beta-mannosidase PCR sense primer MJ-124.  
 DE  
 XX Bovine; beta-mannosidase; beta-mannosidosis; diagnosis; goat; cattle;  
 XX primary storage product; tremor; deafness; dysmyelination; PCR primer;  
 KW ss.  
 XX Synthetic.  
 OS Bos taurus.  
 XX  
 XX US5837836-A.  
 PN  
 XX

PD 17-NOV-1998.  
 XX  
 XX 19-SEP-1995; 95US-00530524.  
 XX  
 PR 15-SEP-1994; 94US-00306546.  
 XX  
 XX (UNMS ) UNIV MICHIGAN STATE.  
 PA  
 XX Chen H, Cavanagh KT, Friderici K, Jones MZ;  
 XX WPI; 1999-023539/02.  
 DR  
 XX Bovine beta-mannosidase nucleic acid sequence and mutation(s) - useful  
 XX for diagnosis of the disease beta-mannosidosis and its carriers.  
 PT  
 XX Example 2; Col 18; 39pp; English.  
 PS  
 XX The present sequence represents a PCR primer for bovine beta-mannosidase.  
 CC The present invention also describes a nucleic acid molecule encoding  
 CC bovine beta-mannosidase, but where the adenine at position 2648 is  
 CC replaced by guanine. The nucleic acid is useful for the detection of the  
 CC disease beta-mannosidosis. This is an autosomal recessive inherited  
 CC disorder affecting mainly goats and cattle, caused a defect in the enzyme  
 CC beta-mannosidase. This mutation renders the inflicted animals incapable  
 CC of correctly processing primary storage products, resulting in tremors,  
 CC deafness and dysmyelination amongst other symptoms. The nucleic acid is  
 CC used in hybridisation assays, or other nucleic acid based assays (e.g.  
 CC PCR or restriction mapping) to detect beta-mannosidase, especially where  
 CC nucleic acid encoding bovine beta-mannosidase contains the adenine to  
 CC guanine mutation at position 2648, for specific detection of the disease.  
 CC The nucleic acid allows specific detection of presence or absence of the  
 CC disease. Previous detection methods relied on enzyme activity assays  
 CC which can be inaccurate as the range of activities greatly varies from  
 CC one individual to another, especially when tested for in cross-breeds  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x AAV64129 (1-20)  
 QY 179 IleleuleuProleu 183  
 Db 6 ATTCTTTTACCCTG 20  
 RESULT 296  
 AAZ32733  
 ID AAZ32733 standard; DNA; 20 BP.  
 XX  
 XX AAZ32733;  
 AC  
 XX 31-JAN-2000 (first entry)  
 DT  
 XX Neospora caninum GRA1 PCR primer bd219.  
 DE  
 XX GRA1; GRA2; SAG1; MIC1, MAG1; protozoan; parasite; neosporosis; abortion;  
 KW neonatal death; congenital infection; encephalitic disease; paralysis;  
 KW pathogenic; antigen; excretory; secretory; modified cell; vaccine;  
 KW differential; diagnosis; detection; antibody; screening;  
 KW antisense therapy; lambda clone; PCR; primer; ss.  
 XX  
 XX Synthetic.  
 OS Neospora caninum.  
 XX  
 XX EP953641-A2.  
 PN  
 XX 03-NOV-1999.  
 PD

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XX 09-MAR-1999; 99BP-00301746.
XX
XX 26-MAR-1998; 98US-0079389P.
XX
XX 15-DEC-1998; 98US-0112282P.
XX
XX (PFIZ ) PFIZER PROD INC.
XX
XX Brake DA, Madura RA, Durtschi BA, Krishnan BR, Yoder SC;
XX
XX WPI; 1999-621834/54.
XX
XX Polypeptides encoding Neospora caninum proteins, useful for vaccines
XX against neosporosis and as diagnostic reagents.
XX
XX Example; Page 23; 59pp; English.
XX
XX This sequence represents Neospora caninum GRA1 PCR primer bd219, used
XX with primer bd220 (AA232734) in the amplification of a fragment of cDNA
XX encoding the Neospora caninum cytoplasmic excretory/secretory antigen
XX GRA1 (AY50130), subsequently used as a probe for secondary screening of
XX GRA1 lambda clones. Neospora is a pathogenic protozoan parasite of
XX mammals that is a major cause of abortion, neonatal death, congenital
XX infection, and encephalitic disease. Neospora caninum infects dogs, and
XX congenitally infects pups, often leading to paralysis. Neospora-related
XX disease has also been reported in goats, sheep and horses. The invention
XX relates to novel isolated Neospora caninum proteins GRA1, GRA2
XX (AA50131), SAG1 (AA50132), MIC1 (AA50133) and MAG1 (AY50134) and the
XX nucleotides which encode them. Genetic constructs comprising mutated or
XX otherwise modified GRA1, GRA2, SAG1, MIC1 and/or MAG1 nucleotides can be
XX used to disable or mutate the genes encoding these proteins. This method
XX can be used to create a modified Neospora cell expressing GRA1, GRA2,
XX SAG1, MIC1 and/or MAG1 proteins with altered function. The recombinant
XX proteins, nucleotides encoding them or the modified Neospora cell may be
XX used to prepare vaccines against neosporosis. Such vaccines can be used
XX to prevent abortion, neonatal death, congenital infection and
XX encephalitic disease in mammals. The proteins or derived peptides can be
XX used as diagnostic reagents to screen for Neospora specific antibodies in
XX blood or serum samples, or as antigens to raise polyclonal or monoclonal
XX antibodies used to screen for Neospora proteins in cell or tissue samples
XX from mammals. GRA1, GRA2, SAG1, MIC1 and MAG1 nucleotides may be used in
XX differential disease diagnosis or as antisense molecules
XX
XX Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 9.44e+03 Length: 20
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AA232733 (1-20)
XX
XX QY 39 AlaThrSerPheSer 43
XX
XX Db 4 QCGACATCTTTTCT 18
XX
XX RESULT 297
XX AAV63539
XX ID AAV63539 standard; DNA; 20 BP.
XX
XX AC AAV63539;
XX
XX DT 29-JAN-1999 (first entry)
XX
XX DE Antisense oligonucleotide AS2 directed against human Napi-2 cDNA.
XX
XX KW Phosphorothioate; antisense; human; kidney disease;
XX renal sodium/phosphate cotransporter protein; Napi-2; hyperphosphataemia;
XX renal disease; cystic fibrosis; polycystic kidney disease; hypertension;
XX ss.

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XX Synthetic.
XX Homo sapiens.
XX
XX US5840875-A.
XX
XX 24-NOV-1998.
XX
XX 06-JUN-1995; 95US-00467007.
XX
XX 06-JUN-1995; 95US-00467007.
XX
XX (THER-) THERAPEUTICS CV.
XX
XX Oberbauer R, Schreiner GF, Meyer TW;
XX
XX WPI; 1999-034128/03.
XX
XX Antisense oligonucleotide to renal sodium/phosphate cotransporter mRNA -
XX useful for treating kidney diseases.
XX
XX Example 2; Col 10; 19pp; English.
XX
XX The present sequence represents a phosphorothioate antisense
XX oligonucleotide which is directed against human Napi-2. The antisense
XX molecule blocks the expression of a renal sodium/phosphate cotransporter
XX protein (Napi-2), which is useful for treating kidney diseases associated
XX with hyperphosphataemia. The antisense oligonucleotide can be used
XX against a variety of systemic or renal diseases e.g. cystic fibrosis,
XX polycystic kidney disease and various forms of hypertension
XX
XX Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 9.44e+03 Length: 20
XX Score: 5.00 Matches: 5
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 2.53% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-966-880A-8 (1-198) x AAV63539 (1-20)
XX
XX QY 102 ProAsnLeuSerLeu 106
XX
XX Db 5 CCCAATCTCTCGCTG 19
XX
XX RESULT 298
XX AAV79659
XX ID AAV79659 standard; DNA; 20 BP.
XX
XX AC AAV79659;
XX
XX DT 24-FEB-1999 (first entry)
XX
XX DE HIV RT DNA template constructing oligo.
XX
XX KW Target molecule; detection; measuring; high-affinity; ligand; SELEX;
XX systemic evolution of ligands by exponential enrichment; assay;
XX diagnostic; cell sorting; metabolite; reverse transcriptase; HIV;
XX RNA ligand; ss.
XX
XX Synthetic.
XX Human immunodeficiency virus 1.
XX
XX US5843653-A.
XX
XX PD 01-DEC-1998.
XX
XX PF 06-JUN-1995; 95US-00469609.
XX
XX 11-JUN-1990; 90US-00536428.
XX
XX 10-JUN-1991; 91US-00714131.
XX

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XX PA (NEXS-) NEXSTAR PHARM INC.
XX PI
XX PI Tuerk C, Gold L;
XX XX
XX DR WPI; 1999-044566/04.
XX XX
XX FT Detection of target molecule - by detecting binding of nucleic acid
XX FT ligand.
XX XX
XX PS Example 2; Col 54; 135pp; English.
XX CC
XX CC The invention provides methods for detecting the presence or absence of a
XX CC target molecule in a sample and measuring the amount of a target molecule
XX CC using high-affinity nucleic acid ligands. The nucleic acid ligands are
XX CC identified by the method of the invention referred to as the systemic
XX CC evolution of ligands by exponential enrichment (SELEX). The nucleic acid
XX CC products are useful in assay methods, diagnostic procedures, cell
XX CC sorting, as inhibitors of target molecule function etc. The methods are
XX CC used to detect or determine the amount of a protein, small molecule,
XX CC controlled substance or metabolite in a biological sample. Sequences
XX CC AAV79649 to AAV79659 represent oligonucleotides used for creating a HIV
XX CC reverse transcriptase (RT) template population used in the isolation of a
XX CC specific RNA ligand for HIV RT
XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAV79659 (1-20)

QY 32 ValVallysArgArg 36
Db 4 GTTGTAACACGCGG 18

RESULT 299
AA06704/C
ID AAX06704 standard; DNA; 20 BP.
XX AC
XX AC AAX06704;
XX DT
XX DT 26-APR-1999 (first entry)
XX DE
XX DE Human JAGGED1 gene exon 4-intron 4 boundary.
XX KW
XX KW JAGGED1; JAGGED1; human; notch ligand; stem cell;
XX KW progenitor cell; haematopoiesis; cell differentiation; Alagille syndrome;
XX KW leukaemia; lymphoma; diagnosis; therapy; ss.
XX OS
XX OS Homo sapiens.
XX FH
XX FH Key Location/Qualifiers
XX FT exon 1..10
XX FT /tag= a
XX FT /note= "3", end of exon 4 (exon length is 255 bp)"
XX FT intron 11..20
XX FT /tag= b
XX FT /note= "5", end of intron 4"
XX FT
XX FT
XX PN WO9858958-A2.
XX PD
XX PD 30-DEC-1998.
XX PF
XX PF 25-JUN-1998; 98WO-US013207.
XX PI
XX PI Griffais R;
XX PR
XX PR 25-JUN-1997; 97US-00882046.
XX XX

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PA (UNIW ) UNIV WASHINGTON.
PA (CHIL-) CHILDRENS HOSPITAL PHILADELPHIA.
XX FI
XX FI Li L, Hood L, Krantz ID, Spinner NB;
XX DR
XX DR WPI; 1999-081220/07.
XX PT
XX PT New Jagged peptides for inhibiting differentiation of progenitor cells -
XX PT also used for maintaining these cells in undifferentiated state, e.g. for
XX PT haematopoietic reconstitution.
XX PS
XX PS Example 4; Fig 6B; 101pp; English.
XX CC
XX CC This nucleotide sequence comprises the exon 4-intron 4 boundary of the
XX CC human JAGGED1 gene. 47 Intron/exon boundaries have been defined (see
XX CC AAX06701-47) by comparison of genomic sequences from bacterial artificial
XX CC chromosome 4D9 and an isolated cDNA clone (see AAV63753). Exon 4
XX CC corresponds to nucleotides 853-1107 of the hJAGGED1 cDNA. hJAGGED1 (see
XX CC also AAV7894) is a Notch ligand capable of inhibiting the
XX CC differentiation of haematopoietic progenitor cells. Mutation of the
XX CC hJAGGED1 gene is associated with Alagille syndrome. The Jagged1 gene has
XX CC been mapped to human chromosome 20p12
XX SQ Sequence 20 BP; 5 A; 1 C; 7 G; 7 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.44e+03 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservatative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.53% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAX06704 (1-20)

QY 27 ThrTyLeuCyStyr 31
Db 16 ACATACCTCTGTAC 2

RESULT 300
AAZ03591/C
ID AAZ03591 standard; DNA; 20 BP.
XX AC
XX AC AAZ03591;
XX DT
XX DT 07-OCT-1999 (first entry)
XX DE
XX DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX KW
XX KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
XX KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
XX KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; ss.
XX KW Bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX OS
XX OS Synthetic.
XX OS Chlamydia trachomatis.
XX PN
XX PN WO928475-A2.
XX DD
XX DD 10-JUN-1999.
XX PF
XX PF 27-NOV-1998; 98WO-IB001939.
XX XX
XX XX 28-NOV-1997; 97FR-00015041.
XX PR
XX PR 17-DEC-1997; 97FR-00016034.
XX PR
XX PR 04-NOV-1998; 98US-010707P.
XX XX
XX XX (GEST ) GENSET.
XX PA
XX PF Griffais R;
XX PI
XX PI WPI; 1999-371125/31.
XX XX

```

PT Genome sequence of Chlamydia trachomatis.  
 XX  
 PS Disclosure; Page 1619; 1755pp; English.  
 XX  
 CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames  
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs  
 CC encode polypeptides (see AAZ01425) which can be used as vaccines  
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also  
 CC be used to control growth of the microorganism. Chlamydia trachomatis is  
 CC responsible for a large number of diseases, e.g. eye diseases such as  
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion  
 CC conjunctivitis; genital diseases such as nongonococcal urethritis,  
 CC epididymitis, cervicitis, salpingitis, perihepatitis, Bartholin's;  
 CC pneumonia in breast feeding infants; and venereal lymphogranulomatosis.  
 CC The polypeptides of the invention may be of use in treating these  
 CC diseases  
 XX  
 SQ Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9.44e+03 Length: 20  
 Score: 5.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.53% Indels: 0  
 DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x AAZ03591 (1-20)

QY 179 IleLeuLeuProLeu 183  
 |||||  
 Db 15 ATACTATTGCCACTC 1

Search completed: March 5, 2004, 00:35:09  
 Job time : 412 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:50:45 ; Search time 2268.59 Seconds  
(without alignments)  
9552.848 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_1\_500

Perfect score: 500

Sequence: 1 aggttcagagagactgtggg.....gagactgcaggaggaag 500

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*\*

1: gb\_ba:\*\*

2: gb\_htg:\*\*

3: gb\_in:\*\*

4: gb\_on:\*\*

5: gb\_ov:\*\*

6: gb\_pat:\*\*

7: gb\_ph:\*\*

8: gb\_pl:\*\*

9: gb\_pr:\*\*

10: gb\_ro:\*\*

11: gb\_sts:\*\*

12: gb\_sy:\*\*

13: gb\_un:\*\*

14: gb\_vi:\*\*

15: em\_ba:\*\*

16: em\_fun:\*\*

17: em\_hum:\*\*

18: em\_in:\*\*

19: em\_mu:\*\*

20: em\_om:\*\*

21: em\_or:\*\*

22: em\_ov:\*\*

23: em\_pat:\*\*

24: em\_ph:\*\*

25: em\_pl:\*\*

26: em\_ro:\*\*

27: em\_sts:\*\*

28: em\_un:\*\*

29: em\_vi:\*\*

30: em\_htg\_hum:\*\*

31: em\_htg\_inv:\*\*

32: em\_htg\_other:\*\*

33: em\_htg\_mus:\*\*

34: em\_htg\_pln:\*\*

35: em\_htg\_rod:\*\*

36: em\_htg\_mam:\*\*

37: em\_htg\_vrt:\*\*

38: em\_sy:\*\*

39: em\_htgo\_hum:\*\*

40: em\_htgo\_mus:\*\*

41: em\_htgo\_other:\*\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	500	100.0	5514	6	BD016834	BD016834 Novel cyt
2	500	100.0	11204	6	BD016860	BD016860 Novel cyt
3	500	100.0	11204	9	AB040430	AB040430 Homo sapi
4	498.4	99.7	71132	9	AC092184	AC092184 Homo sapi
5	145.6	29.1	178130	2	AC119975	AC119975 Mus muscu
6	144	28.8	1767	10	AB091291	AB091291 Mus muscu
7	128.4	25.7	241757	2	AC094826	AC094826 Rattus no
8	128.4	25.7	25506	2	AC109119	AC109119 Rattus no
9	128.4	25.7	345098	2	AC120617	AC120617 Rattus no
10	59	11.8	87	6	BD016836	BD016836 Novel cyt
11	59	11.8	2818	9	BC006296	BC006296 Homo sapi
12	56	11.2	1828	9	BC006296	BC006296 Homo sapi
13	56	11.2	2791	9	AB040431	AB040431 Homo sapi
14	49	9.8	181060	5	EX119907	EX119907 Zebrafish
15	46.6	9.3	275142	2	AC103174	AC103174 Rattus no
16	45.8	9.2	92464	5	AL606705	AL606705 Zebrafish
17	45	9.0	160280	2	AL953909	AL953909 Danio rer
18	44.4	8.9	234545	5	EX470214	EX470214 Zebrafish
19	44.2	8.8	153687	5	EX119987	EX119987 Zebrafish
20	44.2	8.8	230614	10	AC138320	AC138320 Mus muscu
21	44.2	8.8	232304	2	AC111030	AC111030 Mus muscu
22	43.8	8.8	158639	2	EX072539	EX072539 Danio rer
23	43.8	8.8	214628	2	AC101947	AC101947 Mus muscu
24	43.8	8.8	333321	3	AC116986	AC116986 Dictyoste
25	43.6	8.7	154160	2	EX571709	EX571709 Danio rer
26	43.6	8.7	207737	2	EX640470	EX640470 Danio rer
27	43.4	8.7	173096	2	EX511094	EX511094 Danio rer
28	43.4	8.7	198645	2	EX469885	EX469885 Danio rer
29	43	8.6	158904	10	AC135807	AC135807 Mus muscu
30	43	8.6	204737	2	AC147107	AC147107 Mus muscu
31	43	8.6	211345	2	EX004890	EX004890 Danio rer
32	43	8.6	221552	2	AC112328	AC112328 Rattus no
33	43	8.6	243739	2	AC109679	AC109679 Rattus no
34	42.8	8.6	131355	2	AC139655	AC139655 Rattus no
35	42.8	8.6	243735	2	AC106614	AC106614 Rattus no
36	42.6	8.5	212722	2	AC087158	AC087158 Mus muscu
37	42.6	8.5	331039	3	AC116988	AC116988 Dictyoste
38	42.4	8.5	28670	9	AC104621	AC104621 Homo sapi
39	42.4	8.5	154930	2	EX571944	EX571944 Danio rer
40	42.4	8.5	167409	2	AC073374	AC073374 Homo sapi
41	42.4	8.5	179510	2	AC013820	AC013820 Homo sapi
42	42.2	8.4	278	8	AY023421	AY023421 Oryza sat
43	42.2	8.4	2767	3	AB039883	AB039883 Dictyoste
44	42.2	8.4	123454	8	AP005851	AP005851 Oryza sat
45	42.2	8.4	175081	2	EX085194	EX085194 Danio rer

ALIGNMENTS

RESULT 1  
BD016834

LOCUS

DEFINITION

BD016834

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

BD016834  
Novel cytidine deaminase.

BD016834

BD016834.1 GI:22558010

JP 2001245669-A/7..

Homo sapiens (human)

Homo sapiens

1 (bases 1 to 5514)

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Honjo, T. and Muramatsu, M.

Novel cytidine deaminase

Patent: JP 2001245669-A 7 11-SEP-2001;

5514 bp  
DNA  
linear  
PAT 27-AUG-2002

```
COMMENT
JAPAN TOBACCO INC,TASUKU HONJO
OS Homo sapiens (human)
PN JP 2001245669-A/7
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO,MASAMICHI MURAMATSU
PC C12N15/09,A61K39/395,A61P11/06,A61P13/12,
PC A61P17/00,
PC A61P27/02,A61P27/16,A61P37/02,A61P37/08,C07K16/18,C12N1/19,PC
C12N1/21,
PC C12N5/10,C12N9/78,C12P21/02,C12P21/08,C12N1/21,C12R1/19,PC
PC C12N5/10,C12R1/91,C12N15/00,C12N5/00,C12N5/00,C12R1/91) CC
FH Key Location/Qualifiers
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FT intron (1119)..(5514)
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/mol_type="genomic DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.2e-114;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGTTTCAGAGAGACTGTGGGAATATGGGGAAATTAGAGGCTATCTGAGGCTCTTCAACAC 60
Db 591 AGTTTCAGAGAGACTGTGGGAATATGGGGAAATTAGAGGCTATCTGAGGCTCTTCAACAC 650
QY 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAATATTACTATTCTC 120
Db 651 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAATATTACTATTCTC 710
QY 121 ATTGTGCTTTTATTTTGTGTTATCATGATTATTAATGAGTGTCTACTGTACTGCCTCC 180
Db 711 ATTGTGCTTTTATTTTGTGTTATCATGATTATTAATGAGTGTCTACTGTACTGCCTCC 770
QY 181 TGATCTTTGCTAGCTATGGAGCATGGAGCTGGGCTTTTAGAGCAGCAGCCCAAGGAACC 240
Db 771 TGATCTTTGCTAGCTATGGAGCATGGAGCTGGGCTTTTAGAGCAGCAGCCCAAGGAACC 830
QY 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGC 300
Db 831 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGC 890
QY 301 CCCACCCACCATCTTCACTGGATCCAAATCAGGAGCAAGCCGTTGGGGTACCTGGTGG 360
Db 891 CCCACCCACCATCTTCACTGGATCCAAATCAGGAGCAAGCCGTTGGGGTACCTGGTGG 950
QY 361 GGGTGATGCTGTGAGGAGAGAGCCCAAGGCGAGCTCAAAATTTGAATGTGAAGGGCC 420
Db 951 GGGTGATGCTGTGAGGAGAGAGCCCAAGGCGAGCTCAAAATTTGAATGTGAAGGGCC 1010
QY 421 AATGCACTGTGAGCTGAGAGAGAGCAATCAATTAATGAAGTGAAGTTTTCTGGCCT 480
Db 1011 AATGCACTGTGAGCTGAGAGAGAGCAATCAATTAATGAAGTGAAGTTTTCTGGCCT 1070
QY 481 GAGACTTGCAGGGAGGCAAG 500
Db 1071 GAGACTTGCAGGGAGGCAAG 1090
RESULT 2
BD016860
LOCUS BD016860 11204 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel cytidine deaminase.
ACCESSION BD016860
VERSION BD016860.1 GI:22558036
KEYWORDS JP 2001245669-A/33.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11204)
HONJO,T. and Muramatsu,M.
Novel cytidine deaminase
Patent: JP 2001245669-A 33 11-SEP-2001;
JAPAN TOBACCO INC,TASUKU HONJO
OS Homo sapiens (human)
PN JP 2001245669-A/33
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO,MASAMICHI MURAMATSU
PC C12N15/09,A61K39/395,A61P11/06,A61P13/12,
PC A61P17/00,
PC A61P27/02,A61P27/16,A61P37/02,A61P37/08,C07K16/18,C12N1/19,PC
C12N1/21,
PC C12N5/10,C12N9/78,C12P21/02,C12P21/08,C12N1/21,C12R1/19,PC
PC C12N5/10,C12R1/91,C12N15/00,C12N5/00,C12N5/00,C12R1/91) CC
FH Key Location/Qualifiers
FT intron (1032)..(1118)
FT intron (1119)..(5514)
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Best Local Similarity 100.0%; Pred. No. 4.1e-114;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AGTTTCAGAGAGACTGTGGGAATATGGGGAAATTAGAGGCTATCTGAGGCTCTTCAACAC 60
QY 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAATATTACTATTCTC 120
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Db 121 ATTGTGCTTTTATTTTGTGTTATCATGATTATTAATGAGTGTCTACTGTACTGCCTCC 180
QY 181 TGATCTTTGCTAGCTATGGAGCATGGAGCTGGGCTTTTAGAGCAGCAGCCCAAGGAACC 240
Db 181 TGATCTTTGCTAGCTATGGAGCATGGAGCTGGGCTTTTAGAGCAGCAGCCCAAGGAACC 240
QY 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGC 300
Db 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGC 300
QY 301 CCCACCCACCATCTTCACTGGATCCAAATCAGGAGCAAGCCGTTGGGGTACCTGGTGG 360
Db 301 CCCACCCACCATCTTCACTGGATCCAAATCAGGAGCAAGCCGTTGGGGTACCTGGTGG 360
QY 361 GGGTGATGCTGTGAGGAGAGAGCCCAAGGCGAGCTCAAAATTTGAATGTGAAGGGCC 420
Db 361 GGGTGATGCTGTGAGGAGAGAGCCCAAGGCGAGCTCAAAATTTGAATGTGAAGGGCC 420
QY 421 AATGCACTGTGAGCTGAGAGAGAGCAATCAATTAATGAAGTGAAGTTTTCTGGCCT 480
Db 421 AATGCACTGTGAGCTGAGAGAGAGCAATCAATTAATGAAGTGAAGTTTTCTGGCCT 480
QY 481 GAGACTTGCAGGGAGGCAAG 500
Db 481 GAGACTTGCAGGGAGGCAAG 500
RESULT 3
AB040430
LOCUS AB040430 11204 bp DNA linear PRI 03-OCT-2000
DEFINITION Homo sapiens AID gene for activation-induced cytidine deaminase,
complete cds.
ACCESSION AB040430
```



TITLE  
JOURNAL

REFERENCE  
2 (bases 1 to 71132)  
Worley,K.C.

TITLE  
JOURNAL

Submitted (25-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS

TITLE  
JOURNAL

Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS

TITLE  
JOURNAL

Submitted (25-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS

TITLE  
JOURNAL

Submitted (12-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On May 25, 2002 this sequence version replaced gi:20901754.  
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email  
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.  
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:  
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

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misc\_feature

/note="overlaps bases 1..1448 of clone AC092490"  
/function="clone overlap"  
187..408  
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439..560  
/standard\_name="92005"  
774..881  
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903..1190  
/rpt\_family="AluSq"  
1191..1213  
/rpt\_family="AT-rich"  
1591..1807  
/standard\_name="6612"  
1744..1819  
/standard\_name="8198"  
1966..2264  
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5734..6012  
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STS

STS

repeat\_region

repeat\_region

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STS

STS

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STS

repeat\_region

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repeat\_region

/rpt\_family="MIR"

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Best Local Similarity 99.8%; Pred. No. 9.2e-114;
Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGGTTACAGAGACTGTGGGAATATGGGGAAATAGAGGCTATCTGAGGCTCTTCAACAC 60
DB 34549 AGGTTACAGAGACTGTGGGAATATGGGGAAATAGAGGCTATCTGAGGCTCTTCAACAC 34508

QY 61 AATAACCAAGAAGCTATTTAAATGCTCTTTAAAGTATTTACATAATATATCTATCTC 120
DB 34609 AATAACCAAGAAGCTATTTAAATGCTCTTTAAAGTATTTACATAATATATCTATCTC 34668

QY 121 ATTGTGCTTTTATTTGTGTTATCATGATTATAATGAAGTGTCTACTGTACTGCCTCC 180
DB 34669 ATTGTGCTTTTATTTGTGTTATCATGATTATAATGAAGTGTCTACTGTACTGCCTCC 34728

QY 191 TGAATCTTGTAGCTATGGACATGGACTGGGCTTTTAGAGCAGACGCCCAAGGAACC 240
DB 34729 TGAATCTTGTAGCTATGGACATGGACTGGGCTTTTAGAGCAGACGCCCAAGGAACC 34788

QY 241 TAAACATTAAAGCAGAGTGCCTCAATGCTTTAACTGTGTGACTCTGCTATGACAGC 300
DB 34789 TAAACATTAAAGCAGAGTGCCTCAATGCTTTAACTGTGTGACTCTGCTATGACAGC 34848

QY 301 CCCACCCACCATCTTCTACTGGATCCCAATCAGAGCAGGCCCTTTGGGTACTGTGGT 360
DB 34849 CCCACCCACCATCTTCTACTGGATCCCAATCAGAGCAGGCCCTTTGGGTACTGTGGT 34908

QY 361 GGGTATGCTCTGTCAGGGGAGAGAGCCCAAGGCAAGCTCAAAATTTGAATGTGAAGGGCC 420
DB 34909 GGGTATGCTCTGTCAGGGGAGAGAGCCCAAGGCAAGCTCAAAATTTGAATGTGAAGGGCC 34968

QY 421 AATGCACTGTGAGACTGAGACAGAGACCATCATTAATGAAGTGAATTTTCTGCGCT 480
DB 34969 AATGCACTGTGAGACTGAGACAGAGACCATCATTAATGAAGTGAATTTTCTGCGCT 35028

QY 481 GAGACTTGCAGGGGCAAG 500
DB 35029 GAGACTTGCAGGGGCAAG 35048
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RESULT 5
AC119975/c
LOCUS          178130 bp      DNA      linear      HTG 14-MAR-2003
DEFINITION    Mus musculus clone RP24-483K3, WORKING DRAFT SEQUENCE, 8 unordered
               pieces.
AC119975
VERSION       AC119975.3 GI:28951252
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 178130)
               Birren, B., Nusbaum, C., Lander, E., Allen, A., Allon, N.,
               Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
               Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
               Chazaro, B., Choepel, J., Colangelo, M., Collins, S., Collumore, A.,
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               Faro, S., Ferreira, P., Fitzgerald, W., Gage, D., Galagan, J., Gardyna, S.,
               Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
               Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
               Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,
               Landers, T., Lehoczyk, J., Levine, R., Lindblad-Toh, K., Liu, G.,
               Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
               McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
               Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
               Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
               O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
               Raghupathi, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
               Spencer, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
               Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
               Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
               Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
               Direct Submission
               Submitted (14-MAR-2003) Whitehead Institute/MIT Center for Genome
               Research, 320 Charles Street, Cambridge, MA 02141, USA
               On Mar 14, 2003 this sequence version replaced gi:28195895.
               All repeats were identified using RepeatMasker:
               Smith, A.F.A. & Green, P. (1996-1997)
               http://ftp.genome.washington.edu/RM/RepeatMasker.html
               ----- Genome Center
               Center: Whitehead Institute/ MIT Center for Genome Research
               Center code: WIBR
               Web site: http://www-seq.wi.mit.edu
               Contact: sequence.submissions@genome.wi.mit.edu
               ----- Project Information
               Center project name: L25744
               Center clone name: 483_K_3
               ----- Summary Statistics
               Sequencing vector: Plasmid; n/a; 100% of reads
               Chemistry: Dye-terminator Big Dye; 100% of reads
               Assembly program: Phrap; version 0.960731
               Consensus quality: 176301 bases at least Q40
               Consensus quality: 176937 bases at least Q30
               Consensus quality: 177194 bases at least Q20
               Insert size: 176000; agarose-fp
               Insert size: 177430; sum-of-ctnigs
               Quality coverage: 9.0 in Q20 bases; agarose-fp
               Quality coverage: 8.9 in Q20 bases; sum-of-ctnigs
               -----
               * NOTE: This is a 'working draft' sequence. It currently
               * consists of 8 contigs. The true order of the pieces
               * is not known and their order in this sequence record is
               * arbitrary. Gaps between the contigs are represented as
               * runs of N, but the exact sizes of the gaps are unknown.
               * This record will be updated with the finished sequence
               * as soon as it is available and the accession number will
               * be preserved.
               *
               * 1 11982: contig of 11982 bp in length
               * 11983 12082: gap of 100 bp
               * 12083 13278: contig of 1136 bp in length
               * 13279 13378: gap of 100 bp
               * 13379 15640: contig of 2262 bp in length
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\* 15641 15740: gap of 100 bp  
 \* 15741 22800: contig of 7060 bp in length  
 \* 22900: gap of 100 bp  
 \* 22901 101338: contig of 78438 bp in length  
 \* 101339 101439: gap of 100 bp  
 \* 101439 133612: contig of 32174 bp in length  
 \* 133613 133713: gap of 100 bp  
 \* 133713 173588: contig of 39876 bp in length  
 \* 173589 173689: gap of 100 bp  
 \* 173689 178130: contig of 4442 bp in length.

## FEATURES

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misc\_feature

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misc\_feature

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misc\_feature

173689..178130  
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 vector\_side:right"

## ORIGIN

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 Best Local Similarity 69.6%; Pred. No. 8.7e-26;  
 Matches 263; Conservative 0; Mismatches 94; Indels 21; Gaps 4;  
 QY 138 TGTATCATGATTAAATGAAGTGTCTACTGTCTACTGCTCTGATCTTTGCTAGCTAT 197  
 Db 138982 TATCATGATACCAATGTGAAAGTGTCCAGTCTATTGCTCTCTGATCTTTGTTACCTGT 138923  
 QY 198 GGAGCATGACTGGGCTTTTAGAGCAGCAGCGCCCAAGAACTTAAACATTAAGACGAG 257  
 Db 138922 GGTACTGGCTGGCTTTTATAGGAAACAGCCTCGAAGAAAGTTGGACATTAAGCATGAG 138863  
 QY 258 CTG-----CCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGCCCA 304  
 Db 138862 CAGAACTGCCCGCCCGCCCAATCATTTATCCGTGTGGCTCTGCCACACACAGC----- 138807  
 QY 305 CCCACCCATCTTCACTGGATCCAAATCAGGACAGCGCGGTGGGGTACCTGGTGGGGGT 364  
 Db 138806 CCGGCCATCTTTACTGGACCAACCCAGAGGCGAG--ATGTTGGATACCTGGTGGTAGT 138749  
 QY 365 GATGCTGTC--AGGGGAGAGCCCAAGAGGCGAAGCTCAATTTGAATGTGAAGGCCAA 422  
 Db 138748 GATGCTGTCTGGGGGAGAGGCCCAAGAGCAAGCTCAGATTGAATGCCAGGGGCCAG 138689  
 QY 423 TGCATCTGCAGACTGCAGACAGAGAACCATTCATTAATTGAAGTGAGATTTTCTGSCCTGA 482  
 Db 138688 TGCTCTGTACACAAACAGCACTGAAGAGCCCTTGTGTAAGCAAGCTTCCCTTTGSCCTAA 138629  
 QY 483 GACTTGCAGGGGCGAAG 500  
 Db 138628 GACTTTGAGGGAGTCAAG 138611

RESULT 6

AB091291

LOCUS

DEFINITION

Mus musculus AID gene for activation-induced cytidine deaminase, 5'  
 flanking region and partial cds.

ACCESSION

AB091291

VERSION

AB091291.1 GI:34447115

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

misc\_feature

gene

CDS

ORIGIN

Query Match

Best Local Similarity

Matches 262; Conservative

0; Mismatches 95; Indels 21; Gaps 4;

QY 138 TGTATCATGATTAAATGAAGTGTCTACTGTCTACTGCTCTGATCTTTGCTAGCTAT 197

Db 1367 TATCATGATACCAATGTGAAAGTGTCCAGTCTATTGCTCTGATCTTTGTTACCTGT 1426

QY 198 GGAGCATGACTGGGCTTTTAGAGCAGCAGCGCCCAAGAACTTAAACATTAAGCAGAG 257

Db 1427 GATACCTGGCTGGCTTTTAGAGGACAGCCTCGAAGAAAGTTGACATTAAGCATGAG 1486

QY 258 CTG-----CCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGCCCA 304

Db 1487 CAGAACTGGCGCCCGCCCAATCATTTAATCCGTGTGGCTTTGCCACACAGC----- 1542

QY 305 CCCACCCATCTTCACTGGATCCAAATCAGGACAGCGCGGTGGGGTACCTGGTGGGGGT 364

Db 1543 CCGGCCATCTTTACTGGACCAACCCAGAGGCGAG--ATGTTGGATACCTGGTGGTAGT 1600

QY 365 GATGCTGTC--AGGGGAGAGCCCAAGAGGCGAAGCTCAATTTGAATGTGAAGGCCAA 422

Db 1601 GATGCTGTCTGGGGGAGAGGCCCAAGAGCAAGCTCAGATTGAATGCCAGGGGCCAG 1660

QY 423 TGCATCTGCAGACTGCAGACAGAGAACCATTCATTTAATTGAAGTGAGATTTTCTGSCCTGA 482

Db 1661 TGCTCTGTACACAAACAGCACTGAAGAGCCCTTGTGTAAGCAAGCTTCCCTTTGSCCTAA 1720

QY 483 GACTTGCAGGGGCGAAG 500





Db 119027 CCTGGCTGGCTAGCTTTTATGAGGAGCAGCAGCCCTCAAGAGAGCTGGCCATTTCAGCATAA 118968

Qy 257 GCTG -CCCTCAATGGTTTAACTGTGTGACTCTGCTATGACAGAGCCACCCACCCATC 314

Db 118967 GCAGAACTGTCAATCATTTATCTATGTGCTCTGGCCACCATGGC-----CCGCGCCCTC 118912

Qy 315 TTCACTGGATCCAAATCAGAGCAAGGCCCTT-TGGGGTACCTGGTGGGGGTGATGCTGTC 373

Db 118911 CTTACTGGAGCCCAACCCAGGAGGAGGAGGAGATGTTGGATACCTGGTGGCAGTGTGATCTATC 118852

Qy 374 A---GGGGAGGAGCCCAAGAGGCAAGCTCAAAATTTGAATGTCAAGGGCAATGCACTCT 430

Db 118851 ATTGGGGAGGAGACCTCAAGAGCAAGCTCAAAATTTGAATGCCAGGGCCAGTGTCTCTGT 118792

Qy 431 CAGACTGAGACAGAGCAACCATCATTAATGAAGTGAAGATTTTCTGGCTGAGACTTGCA 490

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Qy 491 GGGAGGCAAG 500

Db 118731 GGGAAACAAG 118722

RESULT 8

AC109119/c

LOCUS AC109119 259506 bp DNA linear HTG 08-OCT-2002

DEFINITION Rattus norvegicus clone CH230-98A4, \*\*\* SEQUENCING IN PROGRESS \*\*\*

ACCESSION AC109119

VERSION AC109119.5 GI:22856767

KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT; HTGS\_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 259506)

AUTHORS Muzny,D.,Marie., Metzker,M., Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswallo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregregis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mathney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwackemeleh,O., Okwono,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Perez,A., Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poidexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,R., Ruiz,S.J.,

Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,P., Williams,G., Willson,R., Wlezyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,X., Zhao,S., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 259506)

Worley,K.C.

Direct Submission

Submitted (03-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 259506)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (08-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 14, 2002 this sequence version replaced gi:22538869.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center of Medicine

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GRFZ

Center clone name: CH230-98A4

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 225337 bases at least Q40

Consensus quality: 229008 bases at least Q30

Consensus quality: 230948 bases at least Q20

Estimated insert size: 248565; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

\* This sequence will be replaced

\* By the finished sequence as soon as it is available and

\* the accession number will be preserved.

\* 1 259506: Contig of 259506 bp in length.

Location/Qualifiers

1..259506

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-98A4"

FEATURES

source



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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 330403: contig of 330403 bp in length
* 330404 330503: gap of unknown length
* 330504 331603: contig of 1100 bp in length
* 331604 331703: gap of unknown length
* 331704 337738: contig of 6035 bp in length
* 337739 337838: gap of unknown length
* 337839 345098: contig of 7260 bp in length.
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                        /clone_end:Sp6
                        site:
                        end sequence: BH328475"
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                        /note="wgs end extension"
                        clone_end:Sp6"
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Best Local Similarity 68.6%; Pred. No. 1.6e-21;
Matches 254; Conservative 0; Mismatches 101; Indels 15; Gaps 5;

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QY 202 CATGGACTGGGC-----TTTTAGACGACGAGCCCAAGAACCTTAACATTAAAGCAGA 256
DB 150110 CTGGGCTGGGCTAGCTTTTATAGAGGAGCAGCTCAAGGAGCTGGCCATTGAGCATAA 150051

QY 257 GCTG--CCCTGAATGGTTAACTGTGACTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 314
DB 150050 GCAGAACTGTCAATCAATTAATTAATGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 149995

QY 315 TTCACTGGATCAAAATCAGGAGCAAGGCCGT--TGGGGTACCTGTGGTGGGGTGATGCTGTC 373
DB 149994 CTTACTGGACCAACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 149935

QY 374 A---GGGAGGAGGCCCAAGGCGAAGCTCAAAATTTGAATGTGAAGGCCCAATGCACTGT 430
DB 149934 ATTGGGGGAGGAACTTACAAGAGCAAGCTCAAAATTTGAATGTGAAGGCCCAATGCTGT 149875

QY 431 CAGACTGACAGAGAACCATCAATTAATTTGAAGTGAAGTATTTCTGGCTGAGACTTGCA 490
DB 149874 GACACAACGGCACTGAAGCAGCCTTCTGTTGAAGCAAGCTCCCTTTGACCTAAGCTTGA 149815

QY 491 GGGAGGCAAG 500
DB 149814 GGGAAACAG 149805

RESULT 10
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LOCUS              87 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION         Novel cytidine deaminase.
ACCESSION          BD016836
VERSION            BD016836.1 GI:22558012

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KEYWORDS            JP 2001245669-A/9.
SOURCE              Homo sapiens (human)
ORGANISM            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE            1 (bases 1 to 87)
AUTHORS             Honjo, T. and Muramatsu, M.
TITLE               Novel cytidine deaminase
JOURNAL             Patent: JP 2001245669-A 9 11-SEP-2001;
                    JAPAN TOBACCO INC, TASUKU HONJO
COMMENT             OS Homo sapiens (human)
                    PN JP 2001245669-A/9
                    PD 11-SEP-2001
                    PF 28-MAR-2000 JP 2000092981
                    PI TASUKU HONJO, MASAMICHI MURAMATSU
                    PC A61P15/09, A61K39/395, A61P1/00, A61P11/06, A61P13/12,
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                    C12N1/21,
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                    PN JP 2001245669-A/9
                    PD 11-SEP-2001
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                    PN JP 2001245669-A/9
                    PD 11-SEP-2001
                    PF 28-MAR-2000 JP 2000092981
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                    PC A61P17/00,
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                    PC C12N5/10, C12N9/78, C12P21/02, C12P21/08, C12N1/21, C12R1/19, PC
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                    PD 11-SEP-2001
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                    C12N1/21,
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                    PD 11-SEP-2001
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                    PC A61P17/00,
                    PC A61P27/02, A61P27/16, A61P37/02, A61P37/08, C07K16/18, C12N1/19, PC
                    C12N1/21,
                    PC C12N5/10, C12N9/78, C12P21/02, C12P21/08, C12N1/21, C12R1/19, PC
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                    PN JP 2001245669-A/9
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RESULT 12  
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ACCESSION BC006296  
 VERSION BC006296.2 GI:33871601  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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2388257  
 1247932  
 2 (bases 1 to 1828)  
 Strausberg, R.  
 Direct Submission  
 Submitted (09-APR-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 On Aug 19, 2003 this sequence version replaced gi:13623400.  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Louis Staudt  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lalic, P., Legaspi, R.,  
 Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 17 Row: a Column: 1  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 10190699.

FEATURES  
 Location/Qualifiers

1..1828  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="MGC:12911 IMAGE:4054915"  
 /tissue\_type="Primary B-Cells from Tonsils"  
 /clone\_lib="NIH MGC 48"  
 /lab\_host="DH10B-R"  
 /note="Vector: pOTB7"  
 1..1828  
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 /note="synonyms: AID, HIGM2, CDA2, ARP2"  
 /db\_xref="LocusID:57379"  
 /db\_xref="MIM:605257"  
 77..673  
 /codon\_start=1  
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 /protein\_id="AAH06296.1"  
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 /db\_xref="LocusID:57379"  
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 DFGYRNKNGCHVELLELYRISWDLDGRCYRVFTWSVPCVDCARHVADFLRGNP  
 NLSRIPTFARLYFCDEKAPGEGRLRHRAGVQIAIMTFKDYFCWTFVENHRTFK  
 AWEGLHNSVLSQLRILLPLVEVDLDRAPFTGL"

ORIGIN  
 Query Match 11.2%; Score 56; DB 9; Length 1828;  
 Best Local Similarity 100.0%; Pred. No. 0.0024;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 GAACCATCATTAATTAATGAAGTGAGATTTTCTGGCCTGAGACTTCGAGGAGGCAAG 500  
 Db 1 GAACCATCATTAATTAATGAAGTGAGATTTTCTGGCCTGAGACTTCGAGGAGGCAAG 56

RESULT 13  
 AB040431 2791 bp mRNA linear PRI 03-OCT-2000  
 LOCUS Homo sapiens AID mRNA for activation-induced cytidine deaminase,  
 complete cds.

ACCESSION AB040431  
 VERSION AB040431.1 GI:9988409  
 KEYWORDS AID; activation-induced cytidine deaminase; Human AID.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (sites)  
 Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.  
 Isolation, tissue distribution, and chromosomal localization of the  
 human activation-induced cytidine deaminase (AID) gene  
 Genomics 68 (1), 85-88 (2000)  
 20408890  
 MEDLINE  
 PUBMED  
 REFERENCE

2 (sites)  
 Revy, P., Muto, T., Levy, Y., Geissmann, F., Plebani, A., Sanal, O.,  
 Catalan, N., Forveille, M., Dufourcq-Lagelouse, R., Gennery, A.,  
 Tazcan, I., Ersoy, F., Kayserili, H., Ugazio, A.G., Brouse, N.,  
 Muramatsu, M., Notarangelo, L.D., Kinoshita, K., Honjo, T., Fischer, A.  
 and Durandy, A.  
 Activation-induced cytidine deaminase (AID) deficiency causes the  
 autosomal recessive form of the Hyper-IgM syndrome (HIGM2)  
 Cell 102 (5), 565-575 (2000)  
 20460541

TITLE  
 JOURNAL  
 MEDLINE

11007475  
 PUBMED  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 Submitted (18-MAR-2000) Tsukuru Honjo, Kyoto University, Department  
 of Medical Chemistry, Faculty of Medicine, Yoshida, Sakyo-Ku,  
 Kyoto, Kyoto 606-8501, Japan (E-mail: honjo@med.kyoto-u.ac.jp,  
 Tel: 81-75-753-4371 (ex. 4371), Fax: 81-75-753-4388)  
 Location/Qualifiers

## FEATURES

source  
 1..2791  
 /organism="Homo sapiens"  
 /mol\_type="rRNA"  
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 /gene="AID"  
 77..673  
 /gene="AID"  
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 /product="activation-induced cytidine deaminase"  
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 /db\_xref="GI:9988410"  
 /translation="MDSLMMRRKFLVQFNVRWAKGRRETYLCVYVVRDSDATPSL  
 DFGYRNKGCHVLLFLRYISDMDLPGRCYRVTFMTSPCYDCARHVDLFGNP  
 NLSIRIFARLYFCEDKAEPEGLRRLHRAVGQIAIMTFKDYFCWNTFVENHRTFK  
 AWEGHLSNVSRLRQLRIILPLVEVDLDAFRTGL"

## ORIGIN

Query Match 11.2%; Score 56; DB 9; Length 2791;  
 Best Local Similarity 100.0%; Pred. No. 0.0024; Mismatches 0; Indels 0; Gaps 0;  
 Matches 56; Conservative 0;  
 QY 445 GAACCATCAATTAATGAAGTGGAGATTTTCTGGCTGAGACTGCAGGAGGCAAG 500  
 |||||  
 Db 1 GAACCATCAATTAATGAAGTGGAGATTTTCTGGCTGAGACTGCAGGAGGCAAG 56

## RESULT 14

BX119907  
 LOCUS  
 DEFINITION  
 BX119907  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Danio rerio (zebrafish)  
 Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 181060)  
 Smith, M.  
 Direct Submission  
 Submitted (29-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk  
 On Nov 30 2003 this sequence version replaced gi:38201264.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 -----  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e. phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest, except on the rare  
 occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information  
 on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep/Clone-derived  
 Zebrafish pUC subclones occasionally display inconsistency over the  
 length of mononucleotide A/T runs and conserved TA repeats. Where  
 this is found the longest good quality representation will be  
 submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat  
 discovery system (Zhirong Bao and Sean Eddy, submitted), and those  
 beginning 'drr' were identified by Rick Waterman (Stephen Johnson  
 lab, WashU). For further information see  
 http://www.sanger.ac.uk/Projects/D\_rerio/fishmask.shtml  
 CH211-208D14 is from a CHORI-211 BAC library  
 VECTOR: pTARBAC2.1.

## FEATURES

Location/Qualifiers  
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 /organism="Danio rerio"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:7955"  
 /clone="CH211-208D14"  
 /clone\_lib="CHORI-211"

## ORIGIN

Query Match 9.8%; Score 49; DB 5; Length 181060;  
 Best Local Similarity 56.5%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;  
 Matches 91; Conservative 0;  
 QY 39 GCTATCTGAGGCTCTCAACACATAACCCAGAGCTATTATAATGCTCTTTAAGGAT 98  
 |||||  
 Db 2100 GCGACCTCGATTATAAAGGACTAGCCAAAGAAATTAAGAATGAATTT 2159  
 QY 99 TTACATAAATATACATCTCTCATCTGCTTTTATTTTGTGTATCATGATATATGA 158  
 |||||  
 Db 2160 TATCAT 2219  
 QY 159 AGTGCTACTGTACTGCTCTGCTCTGCTATCTTTGCTAGTATGG 199  
 |||||  
 Db 2220 TATTACTACTACTACTACTACTATATTTTGTGTTGTTGTTGTTGTTGTTG 2260

## RESULT 15

AC103174  
 LOCUS  
 DEFINITION  
 AC103174  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Rattus norvegicus clone CH230-95N13, \*\*\* SEQUENCING IN PROGRESS  
 \*\*\* 4 unordered pieces.  
 AC103174.4 GI:23268241  
 HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
 Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 275142)  
 Muzny, D.Marie.; Metzker, M.Lee.; Abramson, S.; Adams, C.; Alder, J.;  
 Allen, C.; Allen, H.; Alsbrooks, S.; Amin, A.; Anguiano, D.;  
 Anyalebechi, V.; Ayodeji, A.; Ayodeji, M.; Baca, E.; Baden, H.;  
 Baldwin, D.; Bandaranaike, D.; Barber, M.; Barnstead, M.; Benahmed, F.;  
 Biswal, K.; Blair, J.; Blankenburg, K.; Blyth, P.; Brown, M.;  
 Bryant, N.; Bukay, C.; Burch, P.; Burrell, K.; Calderon, E.;  
 Cardenas, V.; Carter, K.; Cavazos, I.; Ceasar, H.; Chen, R.;  
 Chacko, J.; Chavez, D.; Chen, G.; Chen, R.; Chen, Y.; Chen, Z.; Chu, J.;  
 Cleveland, C.; Cockrell, R.; Cox, C.; Coyle, M.; Cree, A.; D'Souza, L.;  
 Davila, M.; Davis, C.; Davy-Carrroll, L.; De Anda, C.; Dederich, D.;  
 Delgado, O.; Denson, S.; Deramo, C.; Ding, Y.; Dinh, H.; Divya, K.;  
 Draper, H.; Duan-Rocha, S.; Dunn, A.; Durbin, K.; Duval, B.; Eaves, K.;  
 Egan, A.; Escotto, M.; Eugene, C.; Evans, C.A.; Falls, T.; Fan, G.;  
 Fernandez, S.; Finley, M.; Flagg, N.; Forbes, L.; Foster, M.; Foster, P.;

Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, K., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, B., Haves, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hui, Y., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseghe, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackeleneh, O., Okwunolu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Paeternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseña, D., Waldron, L., Walker, B., Wang, J., Wang, C., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zuna, D., von Niederhausern, A., Weiser, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Direct Submission  
Unpublished  
2 (bases 1 to 275142)

Worley, K.C.

Direct Submission

Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 275142)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (22-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 22, 2002 this sequence version replaced gi:21731125.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GJ02

Center clone name: CH230-95N13

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 242490 bases at least Q40

Consensus quality: 246431 bases at least Q30

Consensus quality: 248443 bases at least Q20

Estimated insert size: 282574; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/senbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/senbank_draft_data.html))  
\* NOTE: This sequence may represent more than one clone.  
\* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

## FEATURES

## source

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/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-95N13"

## misc\_feature

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## misc\_feature

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## misc\_feature

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## misc\_feature

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clone\_end:Sp6"

## ORIGIN

Query Match	9.3%	Score 46.6;	DB 2;	Length 275142;
Best Local Similarity	51.2%	Pred. No. 0.42;		
Matches	109;	Conservative	0;	Mismatches 104; Indels 0; Gaps 0;

QY 21 AATATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACACATAATTAACCTTATTAATCTATTT 80  
DB 154380 AATAGTCCATAAATACCTTCTATGCCAAAGTAAGTAATAATAACCTTATTAATCTATTT 154439

QY 81 AAATGCTCTTTAAAGTATTTACATAAATATTACTATTCTCATTTGCTTTTATTTTGTGT 140  
DB 154440 ACATTTTATATTTTATTTATTTATTAATTAATGTTTATTAATCTGTTTCAGATGGAATTTACAGT 154499

QY 141 TATCATGATTAATAATGAAGTGTCTACTGTGTACGCTCTCGATCTTTTGTAGTATGGA 200  
DB 154500 CCACATTTAGTTGATTTTATAGTACAAAGATGCTTTTATTTATTTATCTAATAGCCCTAAATA 154559

QY 201 GCATGGACTGGCTTTTAGAGCAGCAGCCCAA 233  
DB 154560 AAATACAGATCTTTTAAAGAGAGGCATAA 154592

Search completed: March 4, 2004, 15:00:18  
Job time : 2274.59 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 11:56:09 ; Search time 285.857 Seconds  
(without alignments)  
7430.646 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_1\_500  
Perfect score: 500  
Sequence: 1 aggttcagagacactgtggg.....gagacttcagaggagcaag 500

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	5514	3 AAC55313	Aac55313 Human act
2	500	100.0	11204	3 AAC55339	Aac55339 Human act
3	500	100.0	11204	6 ABS73286	Abs73286 DNA encod
4	118	23.6	772	5 AAS81193	Aas81193 DNA encod
5	59	11.8	87	3 AAC55315	Aac55315 Human act
6	59	11.8	2818	3 AAC55312	Aac55312 Human act
7	56	11.2	1543	7 ABX05468	Abx05468 Human nov
8	56	11.2	2791	6 ABS73287	Abs73287 DNA encod
9	56	11.2	2791	6 ABS73288	Abs73288 DNA encod
10	43.8	8.8	983	7 ABZ24315	Abz24315 Sclerotin
11	39.6	7.9	346	5 ABV57342	Abv57342 Human pro
12	38.4	7.7	11143	4 ABL12834	Ab112834 Drosophil
13	38.4	7.7	12024	6 AAD38807	Aad38807 CODR3 ORF
14	38.2	7.6	328	6 ABQ97746	Abq97746 Mouse ES
15	38.2	7.6	4363	4 ABL08198	Ab108198 Drosophil
16	38.2	7.6	4386	4 ABL08180	Ab108180 Drosophil
17	38	7.6	7131	6 ABK31450	Abk31450 Signal tr
18	38	7.6	7131	6 ABL70427	Ab170427 Chemical
19	38	7.6	7131	6 AAS61360	Aas61360 Human gen
20	37.8	7.6	529	7 ABZ24320	Abz24320 Sclerotin
21	37.8	7.6	5454	3 AA70236	Aa70236 Plasmodi
22	37.4	7.5	8578	4 ABL06880	Ab106880 Drosophil
23	37.2	7.4	520	5 AAS21880	Aas21880 Human col

c 24	37.2	7.4	2787	2 AAX15661	Aax15661 Protein p
c 25	37.2	7.4	2886	7 ACC59886	Acc59886 Saccharom
c 26	37.2	7.4	3300	3 AAZ55699	Aaz55699 DNA encod
27	37.2	7.4	24183	5 AAS21771	Aas21771 Human gen
28	37.2	7.4	53585	2 AAX20251	Aax20251 Botrelia
29	37.2	7.4	91552	6 AAD38803	Aad38803 BAC clone
c 30	37	7.4	758	6 AAS95261	Aas95261 Long term
31	37	7.4	26997	4 AAS46747	Aas46747 Tumour su
32	36.8	7.4	6325	6 ABN80070	Abn80070 Human che
33	36.8	7.4	9832	6 ABL32656	Ab132656 Human imm
34	36.8	7.4	14552	4 ABL03818	Ab103818 Drosophil
35	36.8	7.4	28066	9 ADC87584	Adc87584 Human GPC
c 36	36.6	7.3	110000	2 AAT42063_07	Continuation (8 of
37	36.4	7.3	1859	6 RAD42874	Rad42874 Human DNA
38	36.4	7.3	2111	4 AAH17042	Aah17042 Human CDN
c 39	36.4	7.3	4023	6 ABN79892	Abn79892 Fungal ZB
c 40	36.4	7.3	4985	4 ABL01906	Ab101906 Drosophil
41	36.4	7.3	8413	6 ABL34497	Ab134497 Human met
42	36.4	7.3	8413	6 ABL70520	Ab170520 Chemical
43	36.4	7.3	19380	6 AAS61426	Aas61426 Human gen
c 44	36.4	7.3	82952	6 ABN85766	Abn85766 Arabidops
c 45	36.2	7.2	412	5 ABV56553	Abv56553 Human pro

## ALIGNMENTS

RESULT 1  
ID AAC55313 standard; DNA; 5514 BP.  
XX  
AC AAC55313;  
DT 05-FEB-2001 (first entry)  
XX  
DE Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:9.  
XX  
KW Activation-induced cytidine deaminase; AID; cytidine deaminase;  
KW immune related disease; allergy; allergic disease; antiallergic;  
KW antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;  
KW gene therapy; B cell associated immune system disorder; food allergy;  
KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;  
KW Iga nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;  
KW drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;  
KW ataxia telangiectasia; common variable immunodeficiency disorder;  
KW major histocompatibility class II deficiency disease;  
KW auto immunodeficiency syndrome; Igg subclass selection disorder; ds.

OS Homo sapiens.

XX WO200058480-A1.

XX 05-OCT-2000.

XX 28-MAR-2000; 2000WO-JP001918.

XX 29-MAR-1999; 99JP-00087192.

XX 24-JUN-1999; 99JP-00178999.

XX 27-DEC-1999; 99JP-00371382.

XX (NISR) JAPAN TOBACCO INC.

XX (HONJ/) HONJO T.

XX Honjo T, Muramatsu M;

XX WPI; 2000-611715/58.

XX Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies.

XX Claim 17; Page 142-145; 174pp; Japanese.



CC The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class II) deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and Igg subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents a genomic DNA sequence of human AID

XX Sequence 5514 BP; 1709 A; 1045 C; 1134 G; 1623 T; 0 U; 3 Other;

Query Match 100.0%; Score 500; DB 3; Length 5514;  
Best Local Similarity 100.0%; Pred. No. 1.7e-136;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGTTTCAGAGAGACTGTGGGAATATGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC 60  
DB 591 AGGTTTCAGAGAGACTGTGGGAATATGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC 650

QY 61 AATAACCCAGAGAGCTTTAAATGCTTTAGGTTATTACATAAATTTACTATTCTC 120  
DB 651 AATAACCCAGAGAGCTTTAAATGCTTTAGGTTATTACATAAATTTACTATTCTC 710

QY 121 ATTGTGCTTTATTTTGTGTATCATGATTATTAATGAAAGTGCTACTGTCTGCTCC 180  
DB 711 ATTGTGCTTTATTTTGTGTATCATGATTATTAATGAAAGTGCTACTGTCTGCTCC 770

QY 181 TGATCTTTGTAGTATGAGAGTGGAGTGGGCTTTTGGAGCAGAGCCCAAGAAC 240  
DB 771 TGATCTTTGTAGTATGAGAGTGGAGTGGGCTTTTGGAGCAGAGCCCAAGAAC 830

QY 241 TAAACATTAAGCAGAGCTCCCTCAATGCTTTAACTGTGTGACCTCTGCTATGACAG 300  
DB 831 TAAACATTAAGCAGAGCTCCCTCAATGCTTTAACTGTGTGACCTCTGCTATGACAG 890

QY 301 CCACCCACCATCTTCACTGGATCCCAATCAGAGCAGAGCCGCTGGGTCCTGGTGG 360  
DB 891 CCACCCACCATCTTCACTGGATCCCAATCAGAGCAGAGCCGCTGGGTCCTGGTGG 950

QY 361 GGGTGTGCTGTGAGGGGAGGAGCCCAAGAGGCAAGCTCAAAATTTGAATGTGAAGGGCC 420  
DB 951 GGGTGTGCTGTGAGGGGAGGAGCCCAAGAGGCAAGCTCAAAATTTGAATGTGAAGGGCC 1010

QY 421 AATGCATGTCAGACTGAGAGCAGAGACCATCATTAATGCAAGTGAGATTTTCTGGCT 480  
DB 1011 AATGCATGTCAGACTGAGAGCAGAGACCATCATTAATGCAAGTGAGATTTTCTGGCT 1070

QY 481 GAGACTTGCAGGGAGGCAAG 500  
DB 1071 GAGACTTGCAGGGAGGCAAG 1090

RESULT 2  
AAC55339  
ID AAC55339 standard; DNA; 11204 BP.  
XX  
XX AAC55339;  
AC  
XX 05-FEB-2001 (first entry)  
DT  
DE Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:35.  
DE  
XX Activation-induced cytidine deaminase; AID; cytidine deaminase;  
KW immune related disease; allergy; allergic disease; antiallergic;  
KW

KW antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological; gene therapy; B cell associated immune system disorder; food allergy; immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; Igg subclass selection disorder; ds.  
XX Homo sapiens.  
OS  
XX WO200058480-A1.  
PN  
XX 05-OCT-2000.  
PD  
XX 28-MAR-2000; 2000WO-JP001918.  
PF  
XX 29-MAR-1999; 99JP-00087192.  
PR  
XX 24-JUN-1999; 99JP-00178999.  
PR  
XX 27-DEC-1999; 99JP-00371382.  
PA (NLSB) JAPAN TOBACCO INC.  
XX (HONJ) HONJO T.  
PI Honjo T, Muramatsu M;  
XX WPI; 2000-611715/58.  
DR  
XX Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies.

PS Claim 17; Page 163-170; 174pp; Japanese.

CC The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has antiallergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IgA) deficiency disease, IgA nephritis, gamma-globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class II) deficiency disease, AIDS (auto immunodeficiency syndrome), elevated IgE disorder, and Igg subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders. The present sequence represents a genomic DNA sequence of human AID

XX Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 U; 0 Other;

Query Match 100.0%; Score 500; DB 3; Length 11204;  
Best Local Similarity 100.0%; Pred. No. 2.4e-136;  
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGTTTCAGAGAGACTGTGGGAATATGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC 60  
DB -1 AGGTTTCAGAGAGACTGTGGGAATATGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC 60

QY 61 AATAACCCAGAGAGCTTTAAATGCTTTAAAGTATTACATAAATTTACTATTCTC 120  
DB 61 AATAACCCAGAGAGCTTTAAATGCTTTAAAGTATTACATAAATTTACTATTCTC 120

QY 121 ATTGTGCTTTATTTTGTGTATCATGATTATTAATGCAAGTGCTACTGTGCTGCTCC 180  
DB 121 ATTGTGCTTTATTTTGTGTATCATGATTATTAATGCAAGTGCTACTGTGCTGCTCC 180

QY 181 TGATCTTTGTAGTATGAGAGTGGAGTGGGCTTTTGGAGCAGAGCCCAAGAAC 240  
DB 181 TGATCTTTGTAGTATGAGAGTGGAGTGGGCTTTTGGAGCAGAGCCCAAGAAC 240

QY 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTTGCCTATGACAGC 300  
 DB 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTTGCCTATGACAGC 300  
 QY 301 CCCACCCACCCATCTTCACTGATCCAAATCAGAGCAGAGCCGTTGGGTACCTGGTGG 360  
 DB 301 CCCACCCACCCATCTTCACTGATCCAAATCAGAGCAGAGCCGTTGGGTACCTGGTGG 360  
 QY 361 GGGTGATGTGTGTCAGGGGAGGAGCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC 420  
 DB 361 GGGTGATGTGTGTCAGGGGAGGAGCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC 420  
 QY 421 AATGCACTGTGACACTGTGACAGACAGACACCATCAATTAATTTGAATGTGAGATTTTCTGGCCT 480  
 DB 421 AATGCACTGTGACACTGTGACAGACAGACACCATCAATTAATTTGAATGTGAGATTTTCTGGCCT 480  
 QY 481 GAGACTTGCAGGGAGGCAAG 500  
 DB 481 GAGACTTGCAGGGAGGCAAG 500

RESULT 3  
 ABS73286  
 ID ABS73286 standard; DNA; 11204 BP.

XX ABS73286;  
 XX 04-DEC-2002 (first entry)  
 XX DNA encoding human translocation del(12p) protein #1.

XX Chromosome aberration; oncogenic fusion protein; cancer;  
 KW proliferative disease; cellular protein isoform; heat shock protein 90;  
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
 XX Homo sapiens.  
 OS WO200269900-A2.  
 XX 12-SEP-2002.  
 XX 01-MAR-2002; 2002WO-US006518.  
 XX 01-MAR-2001; 2001US-0272751P.  
 XX (CONF-) CONFORMA THERAPEUTICS CORP.  
 XX Fritz LC, Burrows FU;  
 XX WPI; 2002-698710/75.  
 XX P-FSD; ABG95082.  
 XX Treating genetically-defined disease associated with chromosomal  
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
 PT diseases, involves administering an inhibitor of heat shock protein 90.  
 XX Disclosure; Page 242-245; 389pp; English.  
 XX The invention describes a method of treating genetically-defined disease  
 CC associated with chromosomal aberrations yielding oncogenic fusion  
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
 CC cell population, treating proliferative diseases associated with mutant  
 CC protein or cellular protein isoforms (II) dependent on heat shock protein  
 CC (HSP)-90, or selectively treating cells expressing (II) involving  
 CC administering HSP90-inhibitor. The method is useful for treating  
 CC genetically-defined disease with chromosomal aberration yielding  
 CC oncogenic fusion protein, treating cancerous cells containing fusion

CC protein in heterogeneous cell population, treating proliferative disease  
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
 CC p53), or selectively treating cells expressing mutant protein or cellular  
 CC protein isoform in a patient heterozygous for (II). The method is useful  
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
 CC or a disease characterised by a solid tumour such as papillary thyroid  
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
 CC synovial sarcoma. The method is also useful for treating viral  
 CC infections. This represents the DNA sequence of a chromosome aberration  
 XX  
 SQ Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 U; 0 Other;

Query Match 100.0%; Score 500; DB 6; Length 11204;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-136; Indels 0; Gaps 0;  
 Matches 500; Conservative 0; Mismatches 0;

QY 1 AGGTTCCAGAGAGACTGTGGGAATATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC 60  
 DB 1 AGGTTCCAGAGAGACTGTGGGAATATGGGGGAATTAGAGGCTATCTGAGGCTCTTCAACAC 60  
 QY 61 AATAACCCAGAGACTATTAAATGCTCTTTAAGGTATTACATAAATATTACTATCTC 120  
 DB 61 AATAACCCAGAGACTATTAAATGCTCTTTAAGGTATTACATAAATATTACTATCTC 120  
 QY 121 ATTGTGCTTTTATTGTTGTTATCATGATTATAATTGAAGTGTCTACTGTACTGCTCC 180  
 DB 121 ATTGTGCTTTTATTGTTGTTATCATGATTATAATTGAAGTGTCTACTGTACTGCTCC 180  
 QY 181 TGATCTTTGCTAGCTATGGAGCATGAGCTGGGCTTTTAGAGCAGCAGCCCCAAGGAACC 240  
 DB 181 TGATCTTTGCTAGCTATGGAGCATGAGCTGGGCTTTTAGAGCAGCAGCCCCAAGGAACC 240  
 QY 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTTGCCTATGACAGC 300  
 DB 241 TAAACATTAAAGCAGAGCTGCCCTCAATGGTTTAACTGTGTGACTTGCCTATGACAGC 300  
 QY 301 CCCACCCACCCATCTTCACTGATCCAAATCAGAGCAGAGCCGTTGGGTACCTGGTGG 360  
 DB 301 CCCACCCACCCATCTTCACTGATCCAAATCAGAGCAGAGCCGTTGGGTACCTGGTGG 360  
 QY 361 GGGTGATGTGTGTCAGGGGAGGAGCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC 420  
 DB 361 GGGTGATGTGTGTCAGGGGAGGAGCCAAAAGGGCAAGCTCAAATTTGAATGTGAAGGGCC 420  
 QY 421 AATGCACTGTGACACTGTGACAGACAGACACCATCAATTAATTTGAATGTGAGATTTTCTGGCCT 480  
 DB 421 AATGCACTGTGACACTGTGACAGACAGACACCATCAATTAATTTGAATGTGAGATTTTCTGGCCT 480  
 QY 481 GAGACTTGCAGGGAGGCAAG 500  
 DB 481 GAGACTTGCAGGGAGGCAAG 500

RESULT 4  
 AAS81193/C  
 ID AAS81193 standard; cDNA; 772 BP.

XX AAS81193;  
 XX 13-FEB-2002 (first entry)  
 DT DNA encoding novel human diagnostic protein #16997.  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX Homo sapiens.  
 XX WO200175067-A2.  
 XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.  
 XX PF  
 XX 31-MAR-2000; 2000US-00540217.  
 XX PR  
 XX 23-AUG-2000; 2000US-00649167.  
 XX PR  
 XX (HYSE-) HYSEQ INC.  
 XX PA  
 XX Drmanac RT, Liu C, Tang YT;  
 XX PI  
 XX WPI; 2001-539362/73.  
 XX DR  
 XX P-PSDE; ABGL7006.  
 XX  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 XX PT diagnostics, forensics, gene mapping, identification of mutations  
 XX PT responsible for genetic disorders or other traits and to assess  
 XX PT biodiversity.  
 XX PT  
 XX Claim 1; SEQ ID NO 16997; 103pp; English.  
 XX PS  
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 XX CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 XX CC and in recombinant production of (II). The polynucleotides are also used  
 XX CC in diagnostics as expressed sequence tags for identifying expressed  
 XX CC genes. (I) is useful in gene therapy techniques to restore normal  
 XX CC activity of (II) or to treat disease states involving (II). (II) is  
 XX CC useful for generating antibodies against it, detecting or quantitating a  
 XX CC polypeptide in tissue, as molecular weight markers and as a food  
 XX CC supplement. (II) and its binding partners are useful in medical imaging  
 XX CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 XX CC involving aberrant protein expression or biological activity. The  
 XX CC polypeptide and polynucleotide sequences have applications in  
 XX CC diagnostics, forensics, gene mapping, identification of mutations  
 XX CC responsible for genetic disorders or other traits to assess biodiversity  
 XX CC and to produce other types of data and products dependent on DNA and  
 XX CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 XX CC coding sequences of the invention. Note: The sequence data for this  
 XX CC parent did not appear in the printed specification, but was obtained in  
 XX CC electronic format directly from WIPO at  
 XX CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX CC  
 XX SQ Sequence 772 BP; 166 A; 204 C; 222 G; 180 T; 0 U; 0 Other;  
 Query Match 23.6%; Score 118; DB 5; Length 772;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-24;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 310 CCATCTTCACTGATCCAAATCAGGACGAGGCGGTTGGGGTACCTGGTGGGGGTGATGC 369  
 DB 638 CCATCTTCACTGATCCAAATCAGGACGAGGCGGTTGGGGTACCTGGTGGGGGTGATGC 579  
 QY 370 TGTTCAGGGGAGGAGCCCAAGGCGCAAGCTCAAAATTTGAATGTGAAGGGCCCAATGCAC 427  
 DB 578 TGTTCAGGGGAGGAGCCCAAGGCGCAAGCTCAAAATTTGAATGTGAAGGGCCCAATGCAC 521  
 RESULT 5  
 AAC55315  
 ID AAC55315 standard; DNA; 87 BP.  
 XX AC  
 XX AAC55315;  
 XX AC  
 XX 05-FEB-2001 (first entry)  
 DT  
 XX Human activation-induced cytidine deaminase exon 1 SEQ ID NO:11.  
 DE  
 XX Activation-induced cytidine deaminase; AID; cytidine deaminase;  
 KW immune related disease; allergy; allergic disease; anti-allergic;  
 KW antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;  
 KW gene therapy; B cell associated immune system disorder; food allergy;  
 KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;  
 KW IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;

XX drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;  
 KW ataxia telangiectasia; common variable immunodeficiency disorder;  
 KW major histocompatibility class II deficiency disease;  
 KW auto immunodeficiency syndrome; IgG subclass selection disorder; ds.  
 XX OS  
 XX Homo sapiens.  
 XX PN WO200058480-A1.  
 XX XX  
 XX PD 05-OCT-2000.  
 XX XX  
 XX PF 28-MAR-2000; 2000WO-JP001918.  
 XX XX  
 XX PR 29-MAR-1999; 99JP-00087192.  
 XX PR 24-JUN-1999; 99JP-00178999.  
 XX PR 27-DEC-1999; 99JP-00371382.  
 XX XX  
 XX (NLSB ) JAPAN TOBACCO INC.  
 XX PA (HONJ/) HONJO T.  
 XX PI  
 XX Honjo T, Muramatsu M;  
 XX WPI; 2000-611715/58.  
 XX DR  
 XX Nucleic acid encoding activation induced cytidine deaminase, useful as a  
 XX PT target for drug development for immune-related diseases including  
 XX PT allergies.  
 XX PT  
 XX Claim 18; Page 150; 174pp; Japanese.  
 XX  
 XX The present invention describes an activation-induced cytidine deaminase  
 XX (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has  
 XX cytidine activity similar to APOBEC-1. AID has anti-allergic, antianemic,  
 XX antiasthmatic, ophthalmological, anti-HIV and dermatological activities,  
 XX and can be used in gene therapy. AID polynucleotides are useful in  
 XX methods for identifying drugs for the treatment of B cell associated  
 XX immune system disorders, immunodeficiency diseases and allergies, such as  
 XX immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-  
 XX globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy,  
 XX drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia  
 XX telangiectasia, common variable immunodeficiency disorder, MHC (major  
 XX histocompatibility class II deficiency disease, AIDS (auto  
 XX immunodeficiency syndrome), elevated IgG disorder, and IgG subclass  
 XX selection disorder. The DNA sequences encoding AID may be used for gene  
 XX therapy and the antibodies to the AID protein may be used for diagnosis  
 XX and treatment of these disorders. The present sequence represents the  
 XX exon 1 genomic DNA sequence of human AID  
 XX  
 XX SQ Sequence 87 BP; 28 A; 17 C; 23 G; 19 T; 0 U; 0 Other;  
 Query Match 11.8%; Score 59; DB 3; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 442 AGAGAACCATCATTAATTGAAGTGAGATTTTCTGGCCTGAGACTTGCAGGAGGCAAG 500  
 DB 1 AGAGAACCATCATTAATTGAAGTGAGATTTTCTGGCCTGAGACTTGCAGGAGGCAAG 59  
 RESULT 6  
 AAC55312  
 ID AAC55312 standard; cDNA; 2818 BP.  
 XX AC  
 XX AAC55312;  
 XX AC  
 XX 05-FEB-2001 (first entry)  
 DT  
 XX Human activation-induced cytidine deaminase encoding cDNA SEQ ID NO:7.  
 DE  
 XX Activation-induced cytidine deaminase; AID; cytidine deaminase;  
 KW immune related disease; allergy; allergic disease; anti-allergic;  
 KW antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;  
 KW gene therapy; B cell associated immune system disorder; food allergy;  
 KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;  
 KW IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;

immunodeficiency disease; immunoglobulin A deficiency disease; asthma; IgA nephritis; gamma-globulinemia; atopic dermatitis; allergic colitis; drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS; ataxia telangiectasia; common variable immunodeficiency disorder; major histocompatibility class II deficiency disease; auto immunodeficiency syndrome; IGA subclass selection disorder; ss.

XX Homo sapiens.

OS Key Location/Qualifiers

XX FH 80..676

XX FT /\*tag= a

XX FT /product= "activation-induced cytidine deaminase"

XX PN WO200058480-A1.

XX PD 05-OCT-2000.

XX PF 28-MAR-2000; 2000WO-JP001918.

XX PR 29-MAR-1999; 99JP-00087192.

XX PR 24-JUN-1999; 99JP-00178999.

XX PR 27-DEC-1999; 99JP-00371382.

XX PA (NISE ) JAPAN TOBACCO INC.

XX PA (HONJ/) HONJO T.

XX PI Honjo T, Muramatsu M;

XX DR WPI; 2000-611715/58.

XX DR P-PSDB; AAS24198.

XX Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies.

XX Claim 3; Page 135-139; 174pp; Japanese.

XX The present sequence encodes human activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has anti-allergic, antianaemic, antitasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated immune system disorders, immunodeficiency diseases and allergies, such as immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-globulinemia, atopic dermatitis, allergic colitis, asthma, food allergy, drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia telangiectasia, common variable immunodeficiency disorder, MHC (major histocompatibility class II) deficiency disease, AIDS (auto immunodeficiency syndrome), elevated Ige disorder, and IGA subclass selection disorder. The DNA sequences encoding AID may be used for gene therapy and the antibodies to the AID protein may be used for diagnosis and treatment of these disorders

XX Query Match 11.8%; Score 59; DB 3; Length 2818;

XX Best Local Similarity 100.0%; Pred. No. 1.3e-06;

XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 AGAAGACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCAGGGAGGCAAG 500

DB 1 AGAAGACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCAGGGAGGCAAG 59

RESULT 7

ABX05468

ID ABX05468 standard; cDNA; 1543 BP.

XX AC ABX05468;

XX 17-JAN-2003 (first entry)

Human novel polynucleotide #483.

XX Human; gene; ss; genetic disorder; gene mapping; medical imaging; cancer; neurodegenerative disorder; lymphoid cell disorder; osteoporosis; Parkinson's disease; Alzheimer's disease; bone degenerative disorder; osteoarthritis; periodontal disease; liver fibrosis; viral infection; fungal infection; bacterial infection; autoimmune disease; diabetes; atopic dermatitis.

XX Homo sapiens.

XX WO200274961-A1.

XX 26-SEP-2002.

XX 14-MAR-2002; 2002WO-US005109.

XX 15-MAR-2001; 2001US-00810173.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;

XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;

XX Wehrman T, Wang J, Wang D, Drmanac RT;

XX WPI; 2003-040556/03.

XX P-PSDB; ABU00390.

XX New isolated polypeptides and polynucleotides, useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, lymphoid cell disorders, bone degenerative disorders, and infections.

XX Claim 1; SEQ ID NO 483; 235pp; English.

XX The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, medical imaging, identification of mutations, responsible for genetic disorders or other traits, assessing biodiversity and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell disorders, osteoporosis, osteoarthritis, bone degenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis). Sequences ABX04986-ABX05511 represent human polynucleotides of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office

XX Query Match 11.2%; Score 56; DB 7; Length 1543;

XX Best Local Similarity 100.0%; Pred. No. 7.3e-06;

XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 GAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCAGGGAGGCAAG 500

DB 2 GAACCATCATTAATTGAAGTGAGATTTTCTGCGCTGAGACTTGCAGGGAGGCAAG 57

RESULT 8

ABX73287

ID ABS73287 standard; DNA; 2791 BP.

XX AC ABS73287;

XX 04-DEC-2002 (first entry)

XX DNA encoding human translocation del(12p) protein #2.

KW Chromosome aberration; oncogenic fusion protein; cancer;  
 KW proliferative disease; cellular protein isoform; heat shock protein 90;  
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200269900-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 01-MAR-2002; 2002WO-US006518.  
 XX  
 PR 01-MAR-2001; 2001US-0272751P.  
 XX  
 PA (CONF-) CONFORMA THERAPEUTICS CORP.  
 XX  
 PI Fritz LC, Burrows FU;  
 XX  
 PI WPI: 2002-698710/75.  
 XX  
 DR P-PSDB; ABG95083.  
 DR  
 XX  
 PT Treating genetically-defined disease associated with chromosomal  
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
 PT diseases, involves administering an inhibitor of heat shock protein 90.  
 PT  
 XX  
 PS Disclosure; Page 246-247; 389pp; English.  
 XX  
 CC The invention describes a method of treating genetically-defined disease  
 CC associated with chromosomal aberrations yielding oncogenic fusion  
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
 CC cell population, treating proliferative diseases associated with mutant  
 CC protein or cellular protein isoforms (II) dependent on heat shock protein  
 CC (HSP)-90, or selectively treating cells expressing (II) involving  
 CC administering HSP90-inhibitor. The method is useful for treating  
 CC genetically-defined disease with chromosomal aberration yielding  
 CC oncogenic fusion protein, treating cancerous cells containing fusion  
 CC protein in heterogeneous cell population, treating proliferative disease  
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
 CC p53), or selectively treating cells expressing mutant protein or cellular  
 CC protein isoform in a patient heterozygous for (II). The method is useful  
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
 CC or a disease characterised by a solid tumour such as papillary thyroid  
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
 CC synovial sarcoma. The method is also useful for treating viral  
 CC infections. This represents the DNA sequence of a chromosome aberration  
 XX  
 SQ Sequence 2791 BP; 842 A; 548 C; 625 G; 776 T; 0 U; 0 Other;  
 Query Match 11.2%; Score 56; DB 6; Length 2791;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 445 GAACCATCATTAATGAAGTGAGATTTTCTGGCCCTGAGACTTGCAGGGAGGCAAG 500  
 DB 1 GAACCATCATTAATGAAGTGAGATTTTCTGGCCCTGAGACTTGCAGGGAGGCAAG 56  
 RESULT 9  
 ABS73288  
 ID ABS73288 standard; DNA; 2791 BP.  
 XX  
 AC ABS73288;  
 XX  
 XX 04-DEC-2002 (first entry)  
 DT  
 XX DNA encoding human translocation del(12p) protein #3.  
 DE

XX Chromosome aberration; oncogenic fusion protein; cancer;  
 KW proliferative disease; cellular protein isoform; heat shock protein 90;  
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200269900-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 01-MAR-2002; 2002WO-US006518.  
 XX  
 PR 01-MAR-2001; 2001US-0272751P.  
 XX  
 PA (CONF-) CONFORMA THERAPEUTICS CORP.  
 XX  
 PI Fritz LC, Burrows FU;  
 XX  
 PI WPI: 2002-698710/75.  
 XX  
 DR P-PSDB; ABG95084.  
 DR  
 XX  
 PT Treating genetically-defined disease associated with chromosomal  
 PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
 PT diseases, involves administering an inhibitor of heat shock protein 90.  
 PT  
 XX  
 PS Disclosure; Page 248-249; 389pp; English.  
 XX  
 CC The invention describes a method of treating genetically-defined disease  
 CC associated with chromosomal aberrations yielding oncogenic fusion  
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
 CC cell population, treating proliferative diseases associated with mutant  
 CC protein or cellular protein isoforms (II) dependent on heat shock protein  
 CC (HSP)-90, or selectively treating cells expressing (II) involving  
 CC administering HSP90-inhibitor. The method is useful for treating  
 CC genetically-defined disease with chromosomal aberration yielding  
 CC oncogenic fusion protein, treating cancerous cells containing fusion  
 CC protein in heterogeneous cell population, treating proliferative disease  
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
 CC p53), or selectively treating cells expressing mutant protein or cellular  
 CC protein isoform in a patient heterozygous for (II). The method is useful  
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
 CC or a disease characterised by a solid tumour such as papillary thyroid  
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
 CC synovial sarcoma. The method is also useful for treating viral  
 CC infections. This represents the DNA sequence of a chromosome aberration  
 XX  
 SQ Sequence 2791 BP; 842 A; 548 C; 625 G; 776 T; 0 U; 0 Other;  
 Query Match 11.2%; Score 56; DB 6; Length 2791;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 445 GAACCATCATTAATGAAGTGAGATTTTCTGGCCCTGAGACTTGCAGGGAGGCAAG 500  
 DB 1 GAACCATCATTAATGAAGTGAGATTTTCTGGCCCTGAGACTTGCAGGGAGGCAAG 56  
 RESULT 10  
 ABS24315  
 ID ABS24315 standard; DNA; 983 BP.  
 XX  
 AC ABS24315;  
 XX  
 XX 18-MAR-2003 (first entry)  
 DT  
 XX

DE Sclerotinia stem rot resistance quantitative trait locus Satt329.  
 XX  
 KW Sclerotinia; stem rot; disease resistance; transgenic plant; plant;  
 KW soybean; quantitative trait locus; QTL; marker; ds.  
 XX  
 OS Glycine max.  
 XX  
 PN WO200299385-A2.  
 XX  
 PD 12-DEC-2002.  
 XX  
 PF 07-JUN-2002; 2002WO-US018173.  
 XX  
 PR 07-JUN-2001; 2001US-0297044P.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX  
 PI Han F, Katt M, Schuh W, Webb DM;  
 XX  
 XX WPI; 2003-148684/14.  
 XX  
 XX Identifying a Sclerotinia stem rot or white mold resistant or susceptible  
 PT dicot plants e.g. soybean, by identifying a quantitative trait loci or  
 PT markers associated with Sclerotinia stem rot resistance.  
 XX  
 PS Disclosure; Page 63; 65pp; English.  
 XX  
 XX The present sequence is the nucleotide sequence of soybean quantitative  
 CC trait locus (QTL) Satt329, a marker for Sclerotinia stem rot resistance.  
 CC The invention relates to the identification of genetic markers correlated  
 CC with Sclerotinia stem rot resistance. The markers are used to identify  
 CC plants, especially soybean, that are resistant or exhibit improved  
 CC resistance to Sclerotinia stem rot, or white mold. A claimed method  
 CC involves the identification of a nucleic acid that is flanked by the  
 CC marker pair Satt329 and Sat 129 (see AB224314). The markers are useful  
 CC for marker-assisted selection and breeding of Sclerotinia stem rot  
 CC resistant plants, and for the identification of susceptible plants. The  
 CC markers are also used to identify and define chromosome intervals  
 CC corresponding to, or including, QTL associated with Sclerotinia stem rot  
 CC resistance. The QTL can be isolated by positional cloning e.g. of genetic  
 CC intervals defined by a pair of markers. The QTL can be used to produce  
 CC transgenic cells and plants exhibiting improved resistance to  
 CC Sclerotinia. QTL nucleic acids isolated from e.g. soybean can be used to  
 CC identify homologues of QTLs for Sclerotinia stem rot resistance from  
 CC other susceptible plants, including canola, alfalfa and sunflower  
 XX  
 SQ Sequence 983 BP; 325 A; 129 C; 118 G; 402 T; 0 U; 9 Other;  
 Query Match 8.8%; Score 43.8; DB 7; Length 983;  
 Best Local Similarity 54.5%; Pred. No. 0.023; Mismatches 0; Gaps 0;  
 Matches 78; Conservative 0; Indels 65; Indels 0; Gaps 0;  
 QY 30 GAATTAGGCTATCTGAGGCTCTTCAACACAAATACCCAAAGCTATTTAAATGCTCT 89  
 DB 361 GAATCAAACTTATCTATCTTCTTCAANCCATGATTTTNGGGTGNANTCACATATTT 420  
 QY 90 TTAAGTATTTCATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 149  
 DB 421 TATNCTCTANATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480  
 QY 150 TATAATTGAAGTCTACTGTTA 172  
 DB 481 TATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 503  
 RESULT 11  
 ABV57342/c  
 ID ABV57342 standard; cDNA; 346 BP.  
 XX  
 AC ABV57342;  
 XX  
 DT 17-SEP-2002 (first entry)  
 XX

DE Human prostate expression marker cDNA 57333.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US005171.  
 XX  
 PR 17-FEB-2000; 2000US-0183319P.  
 PR 16-MAR-2000; 2000US-0189862P.  
 PR 23-MAY-2000; 2000US-0207454P.  
 PR 09-JUN-2000; 2000US-0211314P.  
 PR 18-JUL-2000; 2000US-0219007P.  
 PR 13-DEC-2000; 2000US-0255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 XX WPI; 2001-662795/76.  
 XX  
 XX Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful  
 PT for detecting presence of prostate cancer, stage of prostate cancer.  
 XX  
 PS Claim 1; Page 11032; 11750pp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the efficacy  
 CC of progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 346 BP; 194 A; 66 C; 47 G; 39 T; 0 U; 0 Other;  
 Query Match 7.9%; Score 39.6; DB 5; Length 346;  
 Best Local Similarity 54.0%; Pred. No. 0.25; Mismatches 0; Gaps 0;  
 Matches 81; Conservative 0; Indels 69; Indels 0; Gaps 0;  
 QY 76 TATTTAAATGCTCTTTAAGGTATTTACATAAATATTACTATTCATTCGCTTTTATTT 135  
 DB 232 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 173  
 QY 136 TGTGTTATCATGATTAATTAATGAAGTCTACTGTTACTGCTCCCTGATCTTGTAGCT 195  
 DB 172 TTTTCTTTTCTTTGAGTTTGAATGTTTAATTAATTAATTAATTAATTAATTAATTA 113  
 QY 196 ATGAGCATGAGCTGGGCTTTTAGACGAC 225  
 DB 112 CTCGTGCTGCACAGCTATTAGTAGCACC 83  
 RESULT 12  
 ABL12834/c  
 ID ABL12834 standard; cDNA; 11143 BP.  
 XX  
 AC ABL12834;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 32984.



XX (FRIE//) FRIEDRICH G.  
PA (ZAMB//) ZAMBROWICZ B.  
PA (SAND//) SANDS A T.  
XX  
XX Friedrich G, Zambrowicz B, Sands AT;  
XX WPI; 2002-626541/67.  
XX  
XX Novel murine polynucleotides that individually identify novel genes into  
PT which a retroviral gene trap vector has been integrated, useful in  
PT genomic analysis and in discovery, development of therapeutic and  
PT diagnostic agents.  
XX  
XX Claim 2; SEQ ID NO 1014; 29pp + Sequence Listing; English.  
XX  
XX The invention relates to isolated murine polynucleotides (I) comprising a  
CC contiguous stretch of at least about 60 nucleotides of a sequence  
CC (ABQ96733-ABQ98191) chosen from 1461 OMIBANK gene trapped sequences  
CC (GTSs). The novel genes can be used in a process to identify novel  
CC polynucleotide sequences by comparing them to the novel gene sequences.  
CC The novel genes and cells are useful in functional genomic analysis and  
CC in the discovery and development of new therapeutic and diagnostic agents  
CC and methods. (I) is useful for identifying the coding regions of the  
CC murine genome, to isolate cDNAs, genomic clones or full-length  
CC genes/polynucleotides or homologues, heterologues, paralogues or  
CC orthologues that are capable of hybridising to one or more of the GTSs  
CC under stringent conditions. (I) can be incorporated into a phage display  
CC system that can be used to screen for proteins or other ligands, that are  
CC capable of binding an amino acid sequence encoded by an oligonucleotide  
CC or polynucleotide sequence in at least one of the GTS sequences. (I) is  
CC useful in arrays, such as gene chips, to identify and characterise  
CC temporal and tissue specific gene expression, to identify the gene of  
CC interest from many sources and for genetic manipulations such as  
CC antisense inhibition and gene targeting. Decreasing the level of  
CC expression of (I) and/or down regulating the activity of peptides or  
CC proteins encoded by (I) is useful for treating development and cell  
CC differentiation disorders. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=20020081668  
XX  
XX Sequence 328 BP; 97 A; 74 C; 99 G; 56 T; 0 U; 2 Other;  
SQ  
Query Match 7.6%; Score 38.2; DB 6; Length 328;  
Best Local Similarity 66.3%; Pred. NO. 0.62; Mismatches 0; Gaps 0;  
Matches 55; Conservative 0; Indels 28; Indels 0; Gaps 0;  
QY 418 GCCAATGCACTGTGACACTGACAGACAGAGAACCATTAATTAAGTGCAGATTTTCG 477  
Db 79 GACACAGGGGCTGGGACAGAGACAGACAGAACCCACGAGCTTGGAGGAGAGGATCCGA 138  
QY 478 CCTGACACTTGCAGGAGGAGCAAG 500  
Db 139 TGTCAGAGCTGCAGGAAGAAG 161  
  
RESULT 15  
ABL08198/C  
ID ABL08198 standard; cDNA; 4363 BP.  
XX  
XX ABL08198;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 19076.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
XX Drosophila melanogaster.  
OS  
XX WO200171042-A2.  
PN

XX 27-SEP-2001.  
XX PD  
XX PF 23-MAR-2001; 2001WO-US009231.  
XX  
XX 23-MAR-2000; 2000US-0191637P.  
XX PR 11-JUL-2000; 2000US-00614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI WPI; 2001-656960/75.  
XX DR P-PSDB; ABB54095.  
XX  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signaling and cell-cell  
PT interactions.  
XX  
XX Claim 1; SEQ ID NO 19076; 21pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at fip.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 4363 BP; 1461 A; 939 C; 974 G; 989 T; 0 U; 0 Other;  
SQ  
Query Match 7.6%; Score 38.2; DB 4; Length 4363;  
Best Local Similarity 55.7%; Pred. NO. 2.1;  
Matches 73; Conservative 0; Mismatches 58; Indels 0; Gaps 0;  
QY 87 TCCTTAAGGTATTACATAAATATTACTATTCTCATTTGCTTTTATTTTGTGTTATCAT 146  
Db 3656 TATTTGTTATTTTATTTATTTGTTTAAATGTGCTTTTTCCTTTTGTGTTTATTTAT 3597  
QY 147 GATTATAATTTGAAGTGTCTACTGTCTTACTGCTCCTGATCTTTGCTAGCTATGAGCATGG 206  
Db 3596 ATTTTAGTGTGTTATGTATAGAGTTGTTGTGTAAGTCTGCTGATTTGTTATGTTCTG 3537  
QY 207 ACTGGGCTTTT 217  
Db 3536 CCTATGCTTTT 3526  
  
Search completed: March 4, 2004, 13:06:14  
Job time : 288.857 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 13:06:29 ; Search time 55.4449 Seconds  
(without alignments)  
5004.527 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_1\_500

Perfect score: 500

Sequence: 1 aggttcagagactgtggg.....gagacttcaggagggaag 500

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgm2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgm2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgm2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgm2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgm2\_6/ptodata/2/ina/PTCUS\_COMB.seq.\*  
6: /cgm2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	41.8	8.4	2237	4	US-08-914-999-7
2	37.2	7.4	520	3	US-08-943-731-112
3	37.2	7.4	24183	3	US-08-943-731-3
C 4	36.6	7.3	1830121	4	US-09-557-884-1
C 5	36.6	7.3	1830121	4	US-09-643-990A-1
6	36.2	7.2	3155	2	US-08-591-629-7
C 7	36	7.2	7605	3	US-09-417-455-8
C 8	36	7.2	7605	4	US-09-348-942-8
C 9	36	7.2	7605	4	US-09-457-626-8
C 10	36	7.2	7605	4	US-09-576-008-8
11	35.6	7.1	3836	4	US-09-976-594-59
12	35.2	7.0	832	4	US-09-621-976-2813
13	35	7.0	2540	4	US-09-684-708A-4
14	35	7.0	1664976	4	US-08-916-421B-1
C 15	34.4	6.9	13124	2	US-08-487-826B-13
16	34.2	6.8	246240	2	US-08-724-394A-20
17	34.2	6.8	246240	2	US-08-724-394A-21
18	34.2	6.8	246240	2	US-08-724-394A-22
19	33.8	6.8	3707	3	US-09-276-531-42
20	33.8	6.8	5714	4	US-09-620-312D-393
21	33.8	6.8	6709	3	US-09-285-601-3
22	33.8	6.8	13233	4	US-10-204-708-46
23	33.8	6.8	640681	4	US-09-790-988-1
24	33.4	6.7	12571	4	US-09-322-478-20
C 25	33.4	6.7	640681	4	US-09-790-988-1
26	33.4	6.7	1230025	4	US-09-198-452A-1
C 27	33.2	6.6	1631	3	US-09-118-319-1

28	33.2	6.6	3156	4	US-09-134-001C-2168	Sequence 2168, Ap
C 29	33.2	6.6	4000	2	US-08-861-464-5	Sequence 5, Appli
C 30	33.2	6.6	4000	2	US-08-395-001-5	Sequence 5, Appli
C 31	33.2	6.6	4000	3	US-08-323-433A-5	Sequence 5, Appli
32	33.2	6.6	786431	4	US-09-751-389-3	Sequence 3, Appli
33	33	6.6	975	4	US-09-601-198-32	Sequence 32, Appli
34	33	6.6	2075	1	US-08-238-163-3	Sequence 3, Appli
C 35	32.8	6.6	789	4	US-09-134-001C-2581	Sequence 2581, Ap
C 36	32.8	6.6	4185	4	US-09-417-485D-7	Sequence 7, Appli
C 37	32.8	6.6	5340	4	US-09-627-122-21	Sequence 21, Appli
C 38	32.8	6.6	6070	4	US-10-204-708-9	Sequence 9, Appli
39	32.8	6.6	6669	4	US-10-204-708-6	Sequence 6, Appli
40	32.8	6.6	9347	4	US-10-204-708-35	Sequence 35, Appli
C 41	32.8	6.6	10640	4	US-09-417-485D-5	Sequence 5, Appli
42	32.6	6.5	63000	4	US-09-780-172-18	Sequence 18, Appli
C 43	32.4	6.5	972	3	US-09-286-690-1	Sequence 1, Appli
C 44	32.4	6.5	11485	4	US-09-410-464-9	Sequence 9, Appli
45	32.2	6.4	1173	3	US-09-285-601-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-08-914-999-7/c  
; Sequence 7, Application US/08914999  
; Patent No. 6346406  
; GENERAL INFORMATION:  
; APPLICANT: Ryazanov, Alexey G.  
; APPLICANT: Hait, William N.  
; APPLICANT: Pavur, Karen S.  
; TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)  
; TITLE OF INVENTION: AND METHODS OF USE THEREFOR  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/914,999  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 601-1-078  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2237 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Dictyostelium discoideum  
; US-08-914-999-7

Query Match 8.4%; Score 41.8; DB 4; Length 2237;  
Best Local Similarity 59.8%; Pred. No. 0.0065;  
Matches 70; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

[illegible]

RESULT 2  
US-08-943-731-112  
/ Sequence 112, Application US/08943731  
/ Patent No. 6265157  
/ GENERAL INFORMATION:  
/ APPLICANT: PROCKOP, DARWIN J.  
/ APPLICANT: SPOTILA, LORETTA D.  
/ APPLICANT: DELTAS, CONSTANTINOS D.  
/ APPLICANT: SEREDA, LARISA A.  
/ APPLICANT: LARSON, ANDREA W.  
/ APPLICANT: PACK, MICHAEL  
/ APPLICANT: COLIGE, ALAIN  
/ APPLICANT: EARLY, JAMES  
/ APPLICANT: KORKKO, JARMO  
/ APPLICANT: ALA-KORKKO, LEENA, et al.  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
/ TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES  
/ NUMBER OF SEQUENCES: 666  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: PANITCH SCHWARZ JACOBS & NADEL, P.C.  
/ STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND  
/

Query Match 7.4%; Score 37.2; DB 3; Length 520;  
Best Local Similarity 77.6%; Pred. No. 0.079;  
Matches 45; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QV 104 TAAATATTACATCTCATTTGGTTTTTTTGTCTTATCATGATTATATTTGAAGT 161

DB      422    TAAATTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAAAGT    47

RESULT 3  
US-08-943-731-3  
; Sequence 3, Application US/08943731  
; Patent No. 6265157  
; GENERAL INFORMATION:  
; APPLICANT: PROCKOP, DARWIN J.  
; APPLICANT: SPOTILA, LORETTA D.  
; APPLICANT: DELTAS, CONSTANTINOS D.  
; APPLICANT: SEREDA, LARISA  
; APPLICANT: LARSON, ANDREA W.  
; APPLICANT: PACK, MICHAEL  
; APPLICANT: COLIGE, ALAIN  
; APPLICANT: EARLY, JAMES  
; APPLICANT: KORKKO, JARMO  
; APPLICANT: ALA-KORKKO, LEENA, et al.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES  
; NUMBER OF SEQUENCES: 666  
; CORRESPONDENCE ADDRESS:  
ADDRESSES: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND

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Query Match      7.4%; Score 37.2; DB 3; Length 24183;
Best Local Similarity 77.6%; Pred. No. 0.6;
Matches 45; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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RESULT 4  
US-09-557-884-1/c

Sequence 1, Application US/09557884  
Patent No. 6506581  
GENERAL INFORMATION:  
APPLICANT: Fleischmann et al.  
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/557.884  
FILING DATE: 25-Apr-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/476.102  
FILING DATE: JUN-5-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Michelle S. Marks  
REGISTRATION NUMBER: 41.971  
REFERENCE/DOCKET NUMBER: PB186P3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-557-884-1  
Query Match 7.3%; Score 36.6; DB 4; Length 1830121;  
Best Local Similarity 48.3%; Pred. No. 9;  
Matches 102; Conservative 0; Mismatches 109; Indels 0; Gaps 0;  
QY 40 CTATCTGAGGCTCTTCAACACAAATACCAAGAGCTATTATAATGCTCTTTAAGGTATT 99  
Db 710070 CTATTAAATGAACCTGAACCTAATAATCAAGGAATTTTCCGCACTTTTCTCT 710011  
QY 100 TACATAAATATTACTTCTCAATGCTGCTTTTATTTGTTATCATGATTATAATTGAA 159  
Db 710010 AACAAAAAATCGCACCTTTAACAGTGCATTTTCTTATTAATTAATTAGGACATTCG 709951  
QY 160 GTGCTACTGTTACTGCTCTCTGATCTTTGCTAGCTATGAGCATGGAGCTGGCTTTTAG 219  
Db 709950 CGTTTTCATGCCAATTAACCTGATGATCAAAATGCCAATGCTAGTAGTGGCGGTGCTGACG 709891  
QY 220 AGCAGCAGCCCCAAAGGAACCTAAACATTAA 250  
Db 709890 AGAATAATCAATTTTTCAGCTTTCACATTGA 709860

RESULT 5  
US-09-643-990A-1/c  
Sequence 1, Application US/09643990A  
Patent No. 6528289  
GENERAL INFORMATION:  
APPLICANT: Robert D. Fleischmann  
Mark D. Adams  
Owen White  
Hamilton O. Smith

J. Craig Venter  
TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3 1/2 inch diskette  
COMPUTER: Dell Pentium  
OPERATING SYSTEM: MS DOS v6.22  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/643.990A  
FILING DATE: 23-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/487.429  
FILING DATE: 1995-06-07  
APPLICATION NUMBER: 08/426.787  
FILING DATE: 1995-04-21  
ATTORNEY/AGENT INFORMATION:  
NAME: Kenley K. Hoover  
REGISTRATION NUMBER: 40.302  
REFERENCE/DOCKET NUMBER: PB186P1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-610-5790  
TELEFAX: 310-309-8439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1830121 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-643-990A-1  
Query Match 7.3%; Score 36.6; DB 4; Length 1830121;  
Best Local Similarity 48.3%; Pred. No. 9;  
Matches 102; Conservative 0; Mismatches 109; Indels 0; Gaps 0;  
QY 40 CTATCTGAGGCTCTTCAACACAAATACCAAGAGCTATTATAATGCTCTTTAAGGTATT 99  
Db 710070 CTATTAAATGAACCTGAACCTAATAATCAAGGAATTTTCCGCACTTTTCTCT 710011  
QY 100 TACATAAATATTACTTCTCAATGCTGCTTTTATTTGTTATCATGATTATAATTGAA 159  
Db 710010 AACAAAAAATCGCACCTTTAACAGTGCATTTTCTTATTAATTAATTAGGACATTCG 709951  
QY 160 GTGCTACTGTTACTGCTCTCTGATCTTTGCTAGCTATGAGCATGGAGCTGGCTTTTAG 219  
Db 709950 CGTTTTCATGCCAATTAACCTGATGATCAAAATGCCAATGCTAGTAGTGGCGGTGCTGACG 709891  
QY 220 AGCAGCAGCCCCAAAGGAACCTAAACATTAA 250  
Db 709890 AGAATAATCAATTTTTCAGCTTTCACATTGA 709860

RESULT 6  
US-08-591-629-7  
Sequence 7, Application US/08591629  
Patent No. 5993808  
GENERAL INFORMATION:  
APPLICANT: MELCHERS, Leo Sjoerd  
APPLICANT: APOTHEKER-DE GROOT, Marion  
APPLICANT: BOL, John Ferdinand  
APPLICANT: CORNELISSEN, Bernardus Johannes Clemens  
APPLICANT: LINTHORST, Hubertus Josephus Maria

APPLICANT: PONSTEIN, Anne Silene  
 APPLICANT: SELA-BUURLEA, Marianne Beatrix  
 TITLE OF INVENTION: Plant chitinases, DNA coding therefor and  
 TITLE OF INVENTION: Plant chitinases, DNA coding therefor and  
 TITLE OF INVENTION: plants containing same  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ladass & Parry  
 STREET: 26 West 61st Street  
 CITY: New York  
 STATE: NY

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Query Match      7.2%; Score 36.2; DB 2; Length 3155;  
Best Local Similarity 51.6%; Pred. No. 0.42;  
Matches 83; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
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77 ATTTAAATGCTTTPAAGTGATTTCACATAAATTAATCATTTCTCATTGTGTTTTATTTT 136

2731 AATTAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 2790

Qy	137	GGTATCATGATTATTAATTGAAGTGTCTACTGTGTACTGCCTCCCTGATCTTTGCTAGCTA	196
Db	2791	TTATATTATTATTATTATTATTATTATTATTATTTCCCTCCACTGTGTGTCTTGCAGCTTC	2850
Qy	197	TGAGCATGACGTGGGCTTTTAGAGCAGCAGCCCCAAAGGA	237
Db	2851	ACAAACATGGGAGTGTCAATTCAGAGATGAAGTGATGGA	2891

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RESULT 7
US-09-417-455-8/c
; Sequence 8, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Page, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; PRIORITY FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-417-455-8

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RESULT 8  
US-09-348-942-8/c  
; Sequence 8, Application US/09348942  
; Patent No. 6337072  
; GENERAL INFORMATION:  
; APPLICANT: John Ford  
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF  
; FILE REFERENCE: 28110/35801  
; CURRENT APPLICATION NUMBER: US/09/348,942  
; CURRENT FILING DATE: 1999-07-07  
; EARLIER APPLICATION NUMBER: PCT/US99/04291

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; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-348-942-8

Query Match
Best Local Similarity 7.2%; Score 36; DB 4; Length 7605;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTCTTTAAAGTATTACATAAATATTACTATTCTCATTCGCTTTTATTG 139
Db 632 TAAATTTATTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTTA 573

QY 140 TTATCATGATTATTAATGAAGTGT 163
Db 572 TTATTATTATTACTTTAAAGTTT 549

RESULT 9
US-09-457-626-8/c
; Sequence 8, Application US/09457626
; Patent No. 642619
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US 09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-348-942-8

Query Match
Best Local Similarity 7.2%; Score 36; DB 4; Length 7605;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTCTTTAAAGTATTACATAAATATTACTATTCTCATTCGCTTTTATTG 139
Db 632 TAAATTTATTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTTA 573

QY 140 TTATCATGATTATTAATGAAGTGT 163
Db 572 TTATTATTATTACTTTAAAGTTT 549

RESULT 9
US-09-457-626-8/c
; Sequence 8, Application US/09457626
; Patent No. 642619
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36010
; CURRENT APPLICATION NUMBER: US 09/457,626
; CURRENT FILING DATE: 1999-12-08
; EARLIER APPLICATION NUMBER: US 09/417,455
; EARLIER FILING DATE: 1999-10-13
; EARLIER APPLICATION NUMBER: US 09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-348-942-8

Query Match
Best Local Similarity 7.2%; Score 36; DB 4; Length 7605;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTCTTTAAAGTATTACATAAATATTACTATTCTCATTCGCTTTTATTG 139
Db 632 TAAATTTATTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTTA 573

QY 140 TTATCATGATTATTAATGAAGTGT 163
Db 572 TTATTATTATTACTTTAAAGTTT 549

RESULT 10
US-09-576-008-8/c
; Sequence 8, Application US/09576008
; Patent No. 6541623
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice Suk-Yue
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36456
; CURRENT APPLICATION NUMBER: US 09/576,008
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/523,552
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/457,626
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 09/417,455
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7605
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-576-008-8

Query Match
Best Local Similarity 7.2%; Score 36; DB 4; Length 7605;
Matches 54; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 80 TAAATGCTCTTTAAAGTATTACATAAATATTACTATTCTCATTCGCTTTTATTG 139
Db 632 TAAATTTATTGTTAAAGCATACACTTTATTTTAAAGTTTATTTTCTTTTCTTTTA 573

QY 140 TTATCATGATTATTAATGAAGTGT 163
Db 572 TTATTATTATTACTTTAAAGTTT 549
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QY 140 TTATCATGATTATAAATGAAGTCT 163
Db 572 TTATATTATTATACATTGAAGTTT 549

RESULT 11
US-09-976-594-59
; Sequence 59 Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 59
; LENGTH: 3836
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 344524.1
; NAME/KEY: unsure
; LOCATION: 834, 946, 3201, 3614-3638
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-59

Query Match 7.1%; Score 35.6; DB 4; Length 3836;
Best Local Similarity 57.0%; Pred. No. 0.71;
Matches 65; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 61 AATACCCCAAGAGCTATTAAAGTCTTTAAAGTATTACATAAATATTACTATTCTC 120
Db 2132 AAGAACCCAGGCTCAAAATTTACTGTCTTTAAACAACTCTCATAGATATTCTTTTC 2191

QY 121 ATTGTGCTTTTATTGTGTATCATGATTATAAATGAAGTGTCTACTGTACT 174
Db 2192 ATGGGATTTCTTCCATAATATCTCATTTTAAAAAGAGTCTTTTATGAAGT 2245

RESULT 12
US-09-621-976-2813
; Sequence 2813 Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235...399
US-09-621-976-2813

Query Match 7.0%; Score 35.2; DB 4; Length 832;
Best Local Similarity 10.1%; Pred. No. 0.42;
Matches 28; Conservative 131; Mismatches 119; Indels 0; Gaps 0;

QY 91 TAAGGTATTACATAAATATTACTATTCTCATGTGCTTTTATTGTGTTATCATGATT 150
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Db 1 YKTYWKYTTWYAKWTWKWSNSYWMYKWKYWKTYWRWRKKKAWYKWTWTWYWM 60
QY 151 ATAATGAAGTGTCTACTGTCTCTCTGCTCTGCTGCTCTGCTAGCTATGGAGCATGGACTG 210
Db 61 RYAMWGTYYKKGAMCRITTKKKKKGGYMMWYMGWRRSYNAWTRTWTGTGYAYRSMYTWWR 120
QY 211 GGCTTTTAGACAGCAGCCCCCAAGAACCTAAACATTAAAGCAGAGCTGCCCTCAATGG 270
Db 121 YRCWKKAYYKTTTCYSSKGTWTKRWKKAWTTWKKTYWATRYWMMWMTKRWAS 180
QY 271 TTTAACCTGTGTGACTGTGCTGTATGACAGCCCCCACCACCACTTCTCCTGGATCCAAAT 330
Db 181 WYWCWNGKAKWSTWKRSTYSASARSAXKCCYCSWGMWSWKYMMWRRWATGAGM 240
QY 331 CAGGAGCAAGGCCCTGTGGGTACTCTGTGGGGGTGATG 368
Db 241 KAWRASCMRRRYAGKSKTSYKSMWMCWTRSKYCYTK 278

RESULT 13
US-09-684-708A-4
; Sequence 4 Application US/09684708A
; Patent No. 6602851
; GENERAL INFORMATION:
; APPLICANT: Carrioll, Steven, M.D., Ph.D
; TITLE OF INVENTION: SMDF Neuregulin Splice Variant Isoforms and Uses
; FILE REFERENCE: D6240
; CURRENT APPLICATION NUMBER: US/09/684,708A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/158,622
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 4
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 370...2458
; OTHER INFORMATION: SMDF_2a amino acid sequence
US-09-684-708A-4

Query Match 7.0%; Score 35; DB 4; Length 2540;
Best Local Similarity 51.6%; Pred. No. 0.88;
Matches 80; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 61 AATAACCCCAAGAGCTATTAAATGCTCTTTAAGGTATTACATAAATATTACTATTCTC 120
Db 109 AACAACAGCTCAAGATATTTCCGTACACTTCTATTTCATAGTTGCTAGAGCCCTTTCTT 168
QY 121 ATTGTGCTTTTATTGTGTATCATGATTATAATGAAGTGTCTACTGTACTGCTCTCC 180
Db 169 TTTTCGTTTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 228
QY 181 TGATCTTTCTAGCTATGAGCATGGACTGGGCTT 215
Db 229 TAAGCTCTGCTACTTTGGGTAAATTCCTTGGACTT 263

RESULT 14
US-08-916-421B-1
; Sequence 1 Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
; PATENT NO. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
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;; PRIOR APPLICATION NUMBER: US 60/024,428
;; PRIOR FILING DATE: 1996-08-22
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 1664976
;; TYPE: DNA
;; ORGANISM: Methanococcus jannaschii
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (28222)..(28222)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (28257)..(28258)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (84773)..(84773)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (84808)..(84808)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (84812)..(84812)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (98120)..(98120)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (98159)..(98159)
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;; LOCATION: (1349491)..(1349491)
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NAME/KEY: misc\_feature  
LOCATION: (1664854)..(1664854)  
OTHER INFORMATION: n equals a, t, c, or g  
US-08-916-421B-1

Query Match 7.0%; Score 35; DB 4; Length 1664976;  
Best Local Similarity 50.9%; Pred. No. 26;  
Matches 83; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
QY 1 AGTTTCAGAGAGACTGTGGGAATATGGGGAAATTAGAGGCTATCTGAGGCTCTTCAACAC 60  
Db 482394 AGTTAGAAGAGAAATTTGAAACCTTAAGAAGAGAAATGGCCCAAAATTAG 482453  
QY 61 AATAACCAAGAGCTATTAAATGCTCTTTAAAGGTATTACATAAATATTACTATCTC 120  
Db 482454 AAAAGGTTAAGAGAGAGTTGAAGAGAGTTTAAAGTGAATTAGAGAAATTAATTTTG 482513  
QY 121 ATTGCTTTTATTTTGTGTATCATGATTAATTAATGAAGTGT 163  
Db 482514 ATCTATTTTATTTTGTGCTTTTATTTATTTTATCAATTTT 482556

RESULT 15  
US-08-487-826B-13/c  
Sequence 13, Application US/08487826B  
Patent No. 5993827  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
APPLICANT: Chitnis, Chetan  
APPLICANT: Miller, Louis H.  
APPLICANT: Peterson, David S.  
APPLICANT: Su, Xin-zhaun  
APPLICANT: Wellens, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH121.001CPI  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-487-826B-13  
Query Match 6.9%; Score 34.4; DB 2; Length 19124;  
Best Local Similarity 65.8%; Pred. No. 3.9;  
Matches 50; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
QY 99 TTACATAAATATTAATCTCAATTTGCTTTTATTTTGTGTATCATGATTAATTAATGA 158  
Db 2325 TTACATATATATTAATTTGCTATTTAGTGCATACGTGATATTAAGATATATCTTAA 2266  
QY 159 AGTGCTCTACTGTACT 174  
Db 2265 ATTGACGACATATAAT 2250

Search completed: March 4, 2004, 16:41:57  
Job time : 88.4449 secs



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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 15:00:30 ; Search time 243.692 Seconds  
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Title: US-09-966-880A-35\_COPY\_1\_500

Perfect score: 500

Sequence: 1 aggttcagagactgtggg.....gagacttcgagggaggaag 500

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	500	100.0	5514	9	US-09-966-880A-9
2	500	100.0	11204	9	US-09-966-880A-35
3	59	11.8	87	9	US-09-966-880A-11
4	59	11.8	2818	9	US-09-966-880A-7
5	43.8	8.8	983	14	US-10-165-617B-26
6	41.8	8.4	2237	9	US-09-994-485-7
7	41.8	8.4	2237	9	US-09-832-292-11
8	39.2	7.8	3673778	14	US-10-312-841-2
9	38.6	7.7	2001	9	US-09-801-368-35
10	38.2	7.6	328	9	US-09-728-445-1014
11	38	7.6	7131	12	US-10-221-613-323
12	37.8	7.6	529	14	US-10-165-617B-31
13	37.6	7.5	3673778	14	US-10-312-841-1
14	37.2	7.4	2787	9	US-09-801-368-281
15	37.2	7.4	2787	15	US-10-369-493-25437

c	16	37.2	7.4	2886	9	US-09-801-368-131	Sequence 131, Appl
	17	37	7.4	380	9	US-09-969-373-85	Sequence 85, Appl
	18	37	7.4	380	9	US-09-969-373-85	Sequence 86, Appl
	19	36.8	7.4	9832	14	US-10-311-455-829	Sequence 629, Appl
	20	36.8	7.4	28066	14	US-10-017-161-3395	Sequence 2395, Ap
	21	36.8	7.4	28066	15	US-10-292-798-2037	Sequence 2037, Ap
c	22	36.8	7.4	3673778	14	US-10-312-841-1	Sequence 1, Appl
	23	36.6	7.3	572	15	US-10-027-632-244183	Sequence 244183,
	24	36.6	7.3	572	15	US-10-027-632-244184	Sequence 244184,
c	25	36.6	7.3	714	12	US-10-424-599-65277	Sequence 65277, A
c	26	36.6	7.3	1830121	14	US-10-329-960-1	Sequence 1, Appl
c	27	36.6	7.3	1830121	15	US-10-329-960-1	Sequence 1, Appl
c	28	36.4	7.3	1859	9	US-09-880-192-33	Sequence 33, Appl
	29	36.4	7.3	1859	14	US-10-427-348-33	Sequence 33, Appl
	30	36.4	7.3	8413	14	US-10-240-485-50	Sequence 50, Appl
	31	36.4	7.3	19380	12	US-10-221-613-389	Sequence 389, Appl
	32	36.2	7.2	748	15	US-10-027-632-15365	Sequence 15365, A
c	33	36.2	7.2	6827	14	US-10-311-455-1154	Sequence 1154, Ap
	34	36.2	7.2	8346	14	US-10-240-433-201	Sequence 201, Appl
	35	36	7.2	4985	14	US-10-094-240-10	Sequence 10, Appl
	36	36	7.2	4985	14	US-10-056-405-10	Sequence 10, Appl
	37	36	7.2	6861	14	US-10-311-455-1201	Sequence 1201, Ap
	38	36	7.2	7605	14	US-10-205-821-6	Sequence 6, Appl
c	39	35.8	7.2	774	15	US-10-027-632-150736	Sequence 150736,
c	40	35.8	7.2	774	15	US-10-027-632-150737	Sequence 150737,
	41	35.8	7.2	7560	14	US-10-311-455-1195	Sequence 1195, Ap
c	42	35.6	7.1	254	9	US-09-969-373-1027	Sequence 1027, Ap
	43	35.6	7.1	693	15	US-10-027-632-268730	Sequence 268730,
	44	35.6	7.1	5273	14	US-10-311-455-847	Sequence 847, Appl
c	45	35.6	7.1	5328	14	US-10-311-455-534	Sequence 534, Appl

## ALIGNMENTS

### RESULT 1

US-09-966-880A-9  
; Sequence 9, Application US/09966880A  
; Patent No. US20020164743A1  
; GENERAL INFORMATION:  
; APPLICANT: Honjo, Tasuku  
; APPLICANT: Muramatsu, Masamichi  
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE  
; FILE REFERENCE: 06501-088001  
; CURRENT APPLICATION NUMBER: US/09/966,880A  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR FILING DATE: 1999-06-24  
; PRIOR FILING DATE: 1999-03-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 5514  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1)...(1031)  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1032)...(1118)  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: (1119)...(5514)  
; US-09-966-880A-9

Query Match 100.0%; Score 500; DB 9; Length 5514;  
Best Local Similarity 100.0%; Pred. No. 4.2e-131;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGTTTCAGAGAGCTGGGATATGGGGATATAGAGCTATCTGAGGCTCTTCAACAC 60  
 Db 591 AGGTTTCAGAGAGCTGGGATATGGGGATATAGAGCTATCTGAGGCTCTTCAACAC 650

QY 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAAATATTACTATTCTC 120  
 Db 651 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAAATATTACTATTCTC 710

QY 121 ATTGTGCTTTTATTTTGTATCATGATTAATTAAGTGTCTACTGTGCTGCTCC 180  
 Db 711 ATTGTGCTTTTATTTTGTATCATGATTAATTAAGTGTCTACTGTGCTGCTCC 770

QY 181 TGATCTTTTGTAGCTATGAGCATGGAGTGGGCTTTTAAAGTGTCTACTGTGCTGCTCC 240  
 Db 771 TGATCTTTTGTAGCTATGAGCATGGAGTGGGCTTTTAAAGTGTCTACTGTGCTGCTCC 830

QY 241 TAAACATTTAAAGCAGAGCTGCTCAATGGTTTAACTGTGTGACTCTGCTTATGACAGC 300  
 Db 831 TAAACATTTAAAGCAGAGCTGCTCAATGGTTTAACTGTGTGACTCTGCTTATGACAGC 890

QY 301 CCCACCCACCCATCTTCACTGGATCCAAATCAGAGCAAGGCCGTTGGGGTACCTGGTGG 360  
 Db 891 CCCACCCACCCATCTTCACTGGATCCAAATCAGAGCAAGGCCGTTGGGGTACCTGGTGG 950

QY 361 GGGTGATGCTGTGAGGGAGGAGCCCAAAAGGCGAAGCTCAAAATTTGAATGTGAAGGCC 420  
 Db 951 GGGTGATGCTGTGAGGGAGGAGCCCAAAAGGCGAAGCTCAAAATTTGAATGTGAAGGCC 1010

QY 421 AATGCACTCTCAGACTGACAGACAGAACCATCATTAATTTGAAGTGTGAGATTTTCTGGCCT 480  
 Db 1011 AATGCACTCTCAGACTGACAGACAGAACCATCATTAATTTGAAGTGTGAGATTTTCTGGCCT 1070

QY 481 GAGACTTGCAGGAGGCAAG 500  
 Db 1071 GAGACTTGCAGGAGGCAAG 1090

RESULT 2

US-09-966-880A-35  
 ; Sequence 35, Application US/09966880A  
 ; Patent No. US20020164743A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Honjo, Tasuku  
 ; APPLICANT: Muramatsu, Masamichi  
 ; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE  
 ; FILE REFERENCE: 06501-088001  
 ; CURRENT APPLICATION NUMBER: US/09/966,880A  
 ; PRIOR FILING DATE: 2001-09-28  
 ; PRIOR APPLICATION NUMBER: PCT/JP00/01918  
 ; PRIOR FILING DATE: 2000-03-28  
 ; PRIOR APPLICATION NUMBER: JP 11-371382  
 ; PRIOR FILING DATE: 1999-12-27  
 ; PRIOR APPLICATION NUMBER: JP 11-178999  
 ; PRIOR FILING DATE: 1999-06-24  
 ; PRIOR FILING DATE: 1999-03-29  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 35  
 ; LENGTH: 11204  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-966-880A-35

Query Match 100.0%; Score 500; DB 9; Length 11204;

Best Local Similarity 100.0%; Pred. No. 6.2e-131;  
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGTTTCAGAGAGCTGGGATATGGGGATATAGAGCTATCTGAGGCTCTTCAACAC 60  
 Db 1 AGGTTTCAGAGAGCTGGGATATGGGGATATAGAGCTATCTGAGGCTCTTCAACAC 60

QY 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAAATATTACTATTCTC 120  
 Db 61 AATAACCCCAAGAGCTATTTAAATGCTCTTTAAAGTATTTACATAAAATATTACTATTCTC 120

QY 121 ATTGTGCTTTTATTTTGTATCATGATTAATTAAGTGTCTACTGTGCTGCTCC 180  
 Db 121 ATTGTGCTTTTATTTTGTATCATGATTAATTAAGTGTCTACTGTGCTGCTCC 180

QY 181 TGATCTTTTGTAGCTATGAGCATGGAGTGGGCTTTTAAAGTGTCTACTGTGCTGCTCC 240  
 Db 181 TGATCTTTTGTAGCTATGAGCATGGAGTGGGCTTTTAAAGTGTCTACTGTGCTGCTCC 240

QY 241 TAAACATTTAAAGCAGAGCTGCTCAATGGTTTAACTGTGTGACTCTGCTTATGACAGC 300  
 Db 241 TAAACATTTAAAGCAGAGCTGCTCAATGGTTTAACTGTGTGACTCTGCTTATGACAGC 300

QY 301 CCCACCCACCCATCTTCACTGGATCCAAATCAGAGCAAGGCCGTTGGGGTACCTGGTGG 360  
 Db 301 CCCACCCACCCATCTTCACTGGATCCAAATCAGAGCAAGGCCGTTGGGGTACCTGGTGG 360

QY 361 GGGTGATGCTGTGAGGGAGGAGCCCAAAAGGCGAAGCTCAAAATTTGAATGTGAAGGCC 420  
 Db 361 GGGTGATGCTGTGAGGGAGGAGCCCAAAAGGCGAAGCTCAAAATTTGAATGTGAAGGCC 420

QY 421 AATGCACTCTCAGACTGACAGACAGAACCATCATTAATTTGAAGTGTGAGATTTTCTGGCCT 480  
 Db 421 AATGCACTCTCAGACTGACAGACAGAACCATCATTAATTTGAAGTGTGAGATTTTCTGGCCT 480

QY 481 GAGACTTGCAGGAGGCAAG 500  
 Db 481 GAGACTTGCAGGAGGCAAG 500

RESULT 3

US-09-966-880A-11  
 ; Sequence 11, Application US/09966880A  
 ; Patent No. US20020164743A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Honjo, Tasuku  
 ; APPLICANT: Muramatsu, Masamichi  
 ; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE  
 ; FILE REFERENCE: 06501-088001  
 ; CURRENT APPLICATION NUMBER: US/09/966,880A  
 ; PRIOR FILING DATE: 2001-09-28  
 ; PRIOR APPLICATION NUMBER: PCT/JP00/01918  
 ; PRIOR FILING DATE: 2000-03-28  
 ; PRIOR APPLICATION NUMBER: JP 11-371382  
 ; PRIOR FILING DATE: 1999-12-27  
 ; PRIOR APPLICATION NUMBER: JP 11-178999  
 ; PRIOR FILING DATE: 1999-06-24  
 ; PRIOR APPLICATION NUMBER: JP 11-87192  
 ; PRIOR FILING DATE: 1999-03-29  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 11  
 ; LENGTH: 87  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-966-880A-11

Query Match 11.8%; Score 59; DB 9; Length 87;

Best Local Similarity 100.0%; Pred. No. 8.7e-07;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 AGAGAACCATCATTAATTAAGTGTGAGATTTTCTGGCCTGAGACTTGCAGGAGGCAAG 500  
 Db 1 AGAGAACCATCATTAATTAAGTGTGAGATTTTCTGGCCTGAGACTTGCAGGAGGCAAG 59

RESULT 4

US-09-966-880A-7  
 ; Sequence 7, Application US/09966880A





Qy	82	AATGCTCTTTAAAGTATATTACATAAAATATACATCTCATGTGCTTTATTTTGGTGT	141
Db	1128	ATTAGTATTGACATTTATTAATATTATTAATATTATTATTTGTTATTATTATTATT	1069
Qy	142	ATCATGATTTAAATTGAAGTGTCTACTGTACT	174
Db	1068	ATTATTATTATTATTATTGTTACTATTATTACT	1036

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RESULT 10
US-09-728-446-1014
; Sequence 1014, Application US/09728446
; Patent No. US2002081668A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US2002081668A1el
; TITLE OF INVENTION: and Mutant Cells and
; FILE REFERENCE: LEX-0101-USA
; CURRENT APPLICATION NUMBER: US/09/728,446
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,270
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 1461
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1014
; LENGTH: 328
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(328)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-446-1014

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Query Match	7.6%	Score 38.2	DB 9	Length 328
Best Local Similarity	66.13%	Fred.No.1.5		
Matches 55	Conservative 0	Mismatches 28	Indels 0	Gaps 0
QY	418	GCCAATGCACCTGTCCAGCTGAGACAGAGAACCATCATTTAATTGAAGTGGAGATTTTTTCGG	477	
DB	79	GACACAGCGCTTCGGAGACAGACAGAGAACCCACGAGACTTTGGAGGAGAGAGGATCCGA	138	

QY 478 CCTGAGACTTGCAGGGAGGCAAG 500  
DB 139 TGTGAGAGCTGCAGGAAAGAAG 161

RESULT 11  
US-10-221-613-323  
; Sequence 323, Application US/10221613  
; Publication No. US20040029123A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: PIEPENROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle  
; FILE REFERENCE: 5013.1004  
; CURRENT APPLICATION NUMBER: US/10/221.613  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: PCT/EP01/02945  
; DE 10013847.00  
; DE 10019058.8  
; DE 10019173.8  
; DE 10032529.7  
; DE 10043826.1  
; PRIOR FILING DATE: 2001-03-15  
; 2000-03-15  
; 2000-04-06  
; 2000-04-07  
; 2000-06-30  
; 2000-09-01

```

; NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 323
; LENGTH: 7131
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-613-323

Query Match          7.6%; Score 38; DB 12; Length 7131;
Best Local Similarity 54.4%; Pred. No. 8.9; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 65;

QY 1 AGGTTCCAGAGAGACTGTGGGAATATGGGGAAATAGAGGCTATCTGAGGCTCTTCAACAC 60
Db 2029 AGGTTTAGAATTTATTTTGGGTTAAATATGCCAATGTTGGGTTGATGTAATATATGTTT 2088

QY 61 AATAACCCAGAGACATTTAAATGCTCTTTAAGGTATTTACATAAAATATTACATTCTC 120
Db 2089 GATATTATAAGAAATTTGTTAAATGTTTTTTTAGAGGTTGTTATTTAATAGTAATATA 2148

QY 121 ATTGTGCTCTTTTATTGTTGTTA 142
Db 2149 AGAGAGTTTTTAAGTTGTTTTAA 2170

RESULT 12
US-10-165-617B-31/c
; Sequence 31, Application US/10165617B
; Publication No. US20030150016A1
; GENERAL INFORMATION:
; APPLICANT: Pioneer Hi-Bred International, Inc.
; APPLICANT: Han, Feng
; APPLICANT: Katt, Maria
; APPLICANT: Schuh, Wolfgang
; APPLICANT: Webb, David M
; TITLE OF INVENTION: QTL Controlling Sclerotinia Stem Rot Resistance in Soybean
; FILE REFERENCE: 04-010210US
; CURRENT APPLICATION NUMBER: US/10/165,617B
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 31
; LENGTH: 529

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1  / 5000000
2  / LENGTH: 529
3  /
4  / TYPE: DNA
5  / ORGANISM: Glycine max
6  /
7  / FEATURE:
8  /
9  / NAME/KEY: misc_feature
10 / LOCATION: (471)..(472)
11 /
12 / OTHER INFORMATION: unknown (a,c,g or t)
13 /
14 / FEATURE:
15 /
16 / NAME/KEY: misc_feature
17 / LOCATION: (493)..(493)
18 /
19 / OTHER INFORMATION: unknown (a,c,g or t)
20 /
21 / FEATURE:
22 /
23 / NAME/KEY: misc_feature
24 / LOCATION: (528)..(528)
25 /
26 / OTHER INFORMATION: unknown (a,c,g or t)
27 /
28 / US-10-165-617B-31

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	Query Match	7.6%	Score 37.8;	DB 14;	Length 529;
	Best Local Similarity	51.5%;	Pred. No. 2.5;		
	Matches	87;	Conservative 0;	Mismatches 82;	Indels 0; Gaps 0;
QY	78	TTTAAATGCTTTTAAAGTATTACATAAATATTACTATTCTCATGTGCTTTTATTATTG	137		
Db	212	TATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAT	153		
QY	138	TGTTATCATGATTATAATTGAAGTGTCTACTGTGTACTGCCCTCCCTGATCTTTTGCTAGCTAT	197		
Db	152	TATTATTATTATTATTATTATTATTATTATTATTATTAAAGTGCATTTATTCTTAATTTCTAA	93		
QY	198	GGAGCATGGACTGGGCGTTTTAGACGACGAGCCCCCAAGAACCTTAAACA	246		



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:54:45 ; Search time 1955.18 Seconds  
(without alignments)  
7836.686 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_1\_500

Perfect score: 500

Sequence: 1 aggttcagagactgtggg.....gagactgcaggagggaag 500

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_ges\_hum:\*  
18: em\_ges\_inv:\*  
19: em\_ges\_pln:\*  
20: em\_ges\_vrt:\*  
21: em\_ges\_fun:\*  
22: em\_ges\_mam:\*  
23: em\_ges\_mus:\*  
24: em\_ges\_pro:\*  
25: em\_ges\_rtd:\*  
26: em\_ges\_phg:\*  
27: em\_ges\_vrl:\*  
28: gb\_ges1:\*  
29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	106.8	21.4	765	29	CC915486 t087k19ba
2	73	14.6	1201	13	BX402063 BX402063
3	71	14.2	535	14	CD707143
4	62.4	12.5	820	12	BG757089 602715124

#### ALIGNMENTS

RESULT 1  
CC915486/c  
LOCUS t087k19ba.r1 TAMBT Bos taurus genomic clone t087k19ba, genomic survey sequence.  
DEFINITION CC915486 765 bp DNA linear GSS 08-AUG-2003  
ACCESSION CC915486  
VERSION CC915486.1 GI:33542955  
KEYWORDS GSS.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
REFERENCE 1. (bases 1 to 765)  
Lin, S., Najjar, F.Z., Adelson, D., Gill, C.A. and Roe, B.A.  
AUTHORS Bovine BAC End Sequences from Library TAMBT  
TITLE Unpublished (2003)  
JOURNAL Contact: Bruce A. Roe  
COMMENT Advanced Center for Genome Technology  
University of Oklahoma Department of Chemistry and Biochemistry  
620 Parrington Oval, Room 208, Norman, OK 73019, USA  
Tel: 405 325 4912  
Fax: 405 325 7762  
Email: broe@ou.edu  
Class: BAC ends  
High quality sequence start: 12  
High quality sequence stop: 461.

5	59	11.8	693	12	BG757392
6	56	11.2	541	10	BP238155
7	56	11.2	743	12	BG68133
8	56	11.2	942	10	BP75166
9	46.4	9.3	1201	13	BX403812
C 10	44.4	8.9	429	9	AU270161
C 11	43.8	8.7	983	28	BH126520
C 12	43.4	8.7	560	12	BJ328375
C 13	43	8.6	410	28	BH126608
C 14	43	8.6	512	28	BH841403
C 15	43	8.6	953	13	BQ065440
C 16	43	8.6	1052	13	BQ055935
C 17	42.8	8.6	464	28	BH126691
C 18	42.4	8.5	872	12	BG758510
C 19	42.2	8.4	663	12	BM164461
C 20	42	8.4	505	9	AI668763
C 21	41.8	8.4	321	28	BZ713536
C 22	41.8	8.4	609	12	BZ415548
C 23	41.8	8.4	694	28	BZ013305
C 24	41.8	8.4	728	28	BH728612
C 25	41.6	8.3	458	28	BZ386931
C 26	41.6	8.3	459	12	BM276124
C 27	41.6	8.3	705	28	AZ962863
C 28	41.4	8.3	607	13	BQ739557
C 29	41.2	8.2	276	9	AU51814
C 30	41.2	8.2	555	28	BZ678338
C 31	41.2	8.2	770	29	CC726004
C 32	41.2	8.2	776	29	CE071267
C 33	41.2	8.2	908	28	CC454033
C 34	41.2	8.2	937	29	CC726011
C 35	41	8.2	269	12	BJ439114
C 36	41	8.2	362	12	BJ351256
C 37	41	8.2	554	28	AZ159643
C 38	41	8.2	785	28	AQ739211
C 39	41	8.2	868	28	BH126559
C 40	40.8	8.2	500	29	CE727726
C 41	40.8	8.2	625	12	BJ396037
C 42	40.8	8.2	690	28	BZ389657
C 43	40.8	8.2	801	28	CC363214
C 44	40.8	8.2	821	29	CG059191
C 45	40.8	8.2	827	29	CG370251

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BP238155 601811880  
BG68133 603638412  
BP75166 602244557  
BX403812 60403812  
AU270161 AU270161  
BH126520 BAC-Satt  
BJ328375 BJ328375  
BH126608 BAC-Satt  
BH841403 TC3-55G15  
BQ065440 AGENCOURT  
BQ055935 AGENCOURT  
BH126691 BAC-Satt  
BG758510 602712721  
BM164461 EST1566984  
AI668763 TENG01062  
BZ713536 OGEAG31TM  
BZ415548 BJ415548  
BZ013305 OE100309  
BH728612 BOMJ023TR  
BZ386931 EINDW39TF  
BM276124 PFEST0a7  
AZ962863 2M0231P15  
BQ739557 PFEST0a4  
AU51814 AU051814  
BZ678338 PUBU59TD  
CC726004 OGUDL86TH  
CE071267 tigr-gss-  
CC454033 BAC-Satt  
CC726011 OGUDL86TV  
BJ439114 BJ439114  
BJ351256 BJ351256  
AZ159643 SP\_0064\_A  
AQ739211 HS-5382\_B  
BH126559 BAC-Satt  
CE727726 tigr-gss-  
BJ396037 BJ396037  
BZ389657 EINCQ56TR  
CC363214 PUHIV63TD  
CG059191 PUHIF59TB  
CG370251 OG3CF43TH

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    /organism="Bos taurus"
    /mol_type="genomic DNA"
    /strain="Angus bull T A M U Shoshone Y6 11519666"
    /db_xref="taxon:9913"
    /clone="t097k19ba"
    /sex="Male"
    /cell_type="Blood"
    /clone_lib="TAMBT"
    /note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; TAMBT Bovine BAC library (Male) produced by Texas A&M University, Department of Animal Science."

ORIGIN
  Query Match      21.4%; Score 106.8; DB 29; Length 765;
  Best Local Similarity 65.8%; Pred. No. 7.4e-16;
  Matches 217; Conservative 0; Mismatches 107; Indels 6; Gaps 4;

QY 123 TGTGCTTTTATTTGTTATCATGATTAATTAAGTGTCTACTGTACTGTCTCTG 182
DB 341 TATCTTTTATTTTATTTTACAGGATTACAATATACAACTGTCTACTCTCTGCTCTG 282

QY 183 ATCTTGTAGTATGAGTGGAGTGGCTTTTGTAGAGCAGAGCCCAAGAACTTA 242
DB 281 ATCTTTACTACTGTGGAGGGTAGACTGCATTTTAAAGACGAACTAAAGAACTTA 222

QY 243 AACATTAAAGCAGAGTGCCTCAATGGTTTAACTGTGTGA--CTCTGCCCTATGACAGC 300
DB 221 TACATT-AGGCAGATGGGCCGAGTCATTTTCTCTGTGATTTTGTGCTATGAAGAAC 163

QY 301 CCCACCCAC--CCATCTTCACTGGATCAATCAGAGCAAGCGGTGGGTACCTGGT 358
DB 162 CCCACCCACCTCCAGTGGACCCAAACAGAGGAAGCCCTGTGGGTATGGGTACCTGGT 103

QY 359 GGGGGTGATGTGTG--TCAGGGGAGGAGCCCAAGGCAAGCTCAATTTGAATGTGAAGG 417
DB 102 GGTGGTGTGCTGCTGCGGGGAGGAGCCTTAAGGCGTGAATTTGAATGTGTGAG 43

QY 418 GCAATGCACTGTCACTGACATGACACAGAGA 447
DB 42 ACCGGTGCCTGTGTCAGCCAGTGCAGCAGAA 13

RESULT 2
BX402063 1201 bp mRNA linear EST 13-MAY-2003
LOCUS
DEFINITION
  Homo sapiens cDNA clone CSODL012YD18 5-PRIME, mRNA sequence.
ACCESSION
  BX402063
VERSION
  BX402063.1 GI:30626645
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 1201)
  Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  BP 191 91006 Evry cedex - France
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  Library was constructed by Life Technologies, a division of
  Invitrogen. This sequence belongs to sequence cluster 6672.r For
  more information about this cluster, see
  http://www.genoscope.cns.fr/
  cgi-bin/cluster.cgi?seq=CSODL012YD1809Q1&cluster=6672.r. Contact :
  Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
  Faraday Avenue Genoscope sequence ID : CSODL012YD1809Q1.
  Location/Qualifiers

FEATURES
source
  Location/Qualifiers
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /tissue_type="normal nasopharynx"
    /clone_lib="human nasopharynx"
    /note="ESTs generated from a normal nasopharynx cDNA
    library from southern Chinese"

ORIGIN
  Query Match      14.2%; Score 71; DB 14; Length 535;
  Best Local Similarity 93.7%; Pred. No. 5.3e-07;
  Matches 74; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 422 ATGCACCTGTCTGAGACTGAGACAGAACCAATCATTAATGAAGTGAGATTTTCTGCCTG 481
DB 22 ATGCCGGGGAGACTGAGACAGAACCAATCATTAATGAAGTGAGATTTTCTGCCTG 81

QY 482 AGACTTCAGGGAGGCAAG 500
DB 82 AGACTTCAGGGAGGCAAG 100
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## source

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1. 541
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/db_xref="taxon:9606"
/clone="IMAGE:4054915"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

## ORIGIN

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Query Match 11.2%; Score 56; DB 10; Length 541;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 500
Db 2 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 57

```

```

RESULT 7
BG686133
LOCUS
DEFINITION
602538412F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:476234 5',
mRNA sequence.
ACCESSION
BG686133
VERSION
BG686133.1 GI:13917530
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 743)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1626 row: g column: 03
High quality sequence stop: 740.
Location/Qualifiers
1. 743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:476234"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

## FEATURES

## source

```

Query Match 11.2%; Score 56; DB 10; Length 942;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 500
Db 2 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 57

```

```

RESULT 9
EX403812
LOCUS
DEFINITION
EX403812 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOB80022C04 5-PRIME, mRNA sequence.
ACCESSION
EX403812

```

## ORIGIN

```

Query Match 11.2%; Score 56; DB 12; Length 743;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 500
Db 2 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 57

```

```

RESULT 8
BF975166
LOCUS
DEFINITION
602244657F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4335639 5',
mRNA sequence.
ACCESSION
BF975166
VERSION
BF975166.1 GI:12342381
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 942)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1207 row: a column: 16
High quality sequence stop: 707.
Location/Qualifiers
1. 942
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="PH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

```

## FEATURES

## source

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Query Match 11.2%; Score 56; DB 10; Length 942;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 445 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 500
Db 2 GAACCATCATTAATTGAAGTGAAGATTTTCTGGCTGAGACTTCGAGGAGGCAAG 57

```

```

RESULT 9
EX403812
LOCUS
DEFINITION
EX403812 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOB80022C04 5-PRIME, mRNA sequence.
ACCESSION
EX403812

```



ORIGIN

Query Match 8.8%; Score 43.8; DB 28; Length 983;  
 Best Local Similarity 54.5%; Pred. No. 3;  
 Matches 78; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 30 GAATAGAGGCTATCGAGCTCTTCAACACAAATACCAAGAGCTATTAAATGCTCT 89  
 |||||  
 DB 361 GAATCAAAATCTATCTAAATCTTCAANCAACCAATGATTTTNGGGTGNANTCACATATTT 420  
 |||||

QY 90 TTAAGGTATTTACATAATATATCTATCTCTCATCTGCTTTTATTTTGTGTATCATGAT 149  
 |||||

DB 421 TATNTGCTAT 480  
 |||||

QY 150 TATAATGAAGTCTACTGTTA 172  
 |||||

DB 481 TATTATTATTATTATTATTA 503  
 |||||

RESULT 12

BJ328375/c  
 LOCUS  
 DEFINITION  
 accession  
 version  
 keywords  
 source  
 organism  
 reference  
 authors  
 title  
 journal  
 comment

BJ328375 560 bp mRNA linear EST 05-MAR-2002  
 Dictyostelium discoideum cDNA library, AF Dictyostelium  
 discoideum cDNA clone dda23023 5', mRNA sequence.

BJ328375  
 accession  
 version  
 keywords  
 source  
 organism  
 reference  
 authors  
 title  
 journal  
 comment

BJ328375.1 GI:191589505  
 EST.  
 Dictyostelium discoideum  
 Dictyostelium discoideum  
 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
 1 (bases 1 to 560)  
 Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.  
 Full length cDNA of Dictyostelium discoideum at the aggregation  
 stage  
 Unpublished (2002)  
 Contact: Tadao Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tsunigenes.nig.ac.jp.

FEATURES

source  
 Location/Qualifiers  
 1..560  
 /organism="Dictyostelium discoideum"  
 /mol\_type="mRNA"  
 /strain="AX4"  
 /db\_xref="taxon:44689"  
 /clone="dda23023"  
 /sex="mat A"  
 /dev\_stage="Aggregation stage"  
 /clone\_lib="Dictyostelium discoideum cDNA library, AF"

ORIGIN

Query Match 8.7%; Score 43.4; DB 12; Length 560;  
 Best Local Similarity 60.7%; Pred. No. 3.7;  
 Matches 71; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 72 AAGTATTAAATGCTTTAAGGATTTTACATAAATATTAATCTATCTATGCTTTT 131  
 |||||

DB 217 ATGATATTGAATCTACTATTGTTTATTTATTTATTTATTTATTTATTTATTTAT 158  
 |||||

QY 132 ATTCTGTATCATGATTTAATTAATGAAGTGTCTACTGTCTCTCTCTCTCTTT 188  
 |||||

DB 157 TATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTAT 101  
 |||||

RESULT 13

BJ326608  
 LOCUS  
 DEFINITION  
 accession  
 version  
 keywords  
 source  
 organism  
 reference  
 authors  
 title  
 journal  
 comment

BJ326608 410 bp DNA linear GSS 19-JUL-2001  
 BARC-Satt429 Size-selected soybean genomic Glycine max genomic,  
 genomic survey sequence.

BJ326608  
 accession  
 version  
 keywords  
 source  
 organism  
 reference  
 authors  
 title  
 journal  
 comment

BJ326608.1 GI:14970111  
 GSS.  
 Glycine max (soybean)  
 Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 410)  
 Cregan, P.B., Jarvik, T., Bush, A.L., Shoemaker, R.C., Lark, K.G.,  
 Kahler, A.L., Kaya, N., VanToai, T.T., Lohnes, D.G., Chung, J. and  
 Specht, J.E.  
 An integrated Genetic Linkage Map of the Soybean Genome  
 Crop Sci. 39, 1464-1490 (1999)  
 Contact: Cregan PB  
 Soybean Genomics and Improvement Lab  
 USDA-ARS  
 BARC-West, Bldg. 006, Beltsville, MD 20705, USA  
 Tel: 301-504-5070  
 Fax: 301-504-5728  
 Email: cregan@ba.ars.usda.gov  
 Single pass sequence. See the SoyBase home page  
 (http://soybase.agron.iastate.edu) for PCR primer sequences and  
 amplification conditions.  
 Class: SSR-containing genome clone.

FEATURES

source  
 Location/Qualifiers  
 1..410  
 /organism="Glycine max"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:3847"  
 /clone\_lib="Size-selected soybean genomic"  
 /note="Simple sequence repeat containing clones from  
 genomic DNA of the cultivar 'Williams' as described by  
 Cregan, P.B., Bhagwat, A.A., Akkaya, M.S. and Rongwen, J.  
 (1994). Methods Cell. Mol. Biol. 5:49-61"

ORIGIN

Query Match 8.6%; Score 43; DB 28; Length 410;  
 Best Local Similarity 58.0%; Pred. No. 4.5;  
 Matches 76; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 44 CTGAGCTCTTCAACACATATACCAAGAGCTATTAAATGCTCTTTAAGTATTACA 103  
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DB 39 CTGTTGATTTTATATAATAATTTACTTTAAAGTTATATAAATGATTTGTGATTAATT 98  
 |||||

QY 104 TAAATATTACTATTTCTCATTTGCTTTTATTTGTTTATCATGATTATTAATGAAGTGT 163  
 |||||

DB 99 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTA 158  
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QY 164 CTTCTCTTACT 174  
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DB 159 TTATTATTATT 169  
 |||||

RESULT 14

BJ326608  
 LOCUS  
 DEFINITION  
 accession  
 version  
 keywords  
 source  
 organism  
 reference

BJ326608 512 bp DNA linear GSS 13-JUN-2002  
 TC3-55G15-TV TC3 Trypanosoma cruzi genomic clone TC3-55G15, genomic  
 survey sequence.

BJ326608  
 accession  
 version  
 keywords  
 source  
 organism  
 reference

BJ326608.1 GI:21408618  
 GSS.  
 Trypanosoma cruzi  
 Trypanosoma cruzi  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma; Schizotrypanum.  
 1 (bases 1 to 512)

## AUTHORS

Myler, P.J., Aggarwal, G., Fazelinia, G., Mack, J., Marty, A.,  
Munden, H., Nelson, S., Pentony, M., Rinta, J., Robertson, L.,  
Seyler, A., Slak, B., Stuart, K., Vogt, C., Worthey, E., El-Sayed, N.M.,  
Chedin, E., and Anderson, B.  
Trypanosoma cruzi CL-Brener TC3 BAC-end sequencing  
Other GSSs: TC3-55G15.TP  
Contact: Peter Myler  
Seattle Biomedical Research Institute  
4 Nickerson Street, Seattle, WA 98109, USA  
Tel: 206 284 8846  
Fax: 206 284 0313  
Email: mylerp@bri.org

Clones are derived from the Trypanosoma cruzi CL-Brener BAC library  
TC3. For clone availability, please contact Dr. Bjorn Andersson at  
Uppsala University (bjorn.andersson@genpat.uu.se).  
Seq primer: T7  
Class: BAC ends.

## FEATURES

source  
Location/Qualifiers

1..512  
/organism="Trypanosoma cruzi"  
/mol\_type="genomic DNA"  
/strain="CL Brener"  
/db\_xref="taxon:5693"  
/clone="TC3-55G15"  
/clone\_lib="TC3"

/note="Vector: pBelosAC11; Site 1: Hin dIII; Constructed  
for Uppsala University by Marie-Christine Le Paslier in  
the laboratory of Denis Le Paslier at the Centre d'Etude  
du Polymorphisme Humain (CEPH), Paris, France. Briefly,  
Trypanosoma cruzi CL-Brener agarose embedded DNA (obtained  
from Dr. Franco da Silveira) was partially digested with  
Hin dIII. High molecular weight fragments were ligated in  
pBelosAC11 digested with Hin dIII. The average insert  
size is 100 kb. Total clone coverage: approx. 33 X the  
haploid genome."

## ORIGIN

Query Match 8.6%; Score 43; DB 28; Length 512;  
Best Local Similarity 62.6%; Pred. No. 4.6;  
Matches 67; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 59 ACAATAACCCAGAGCTATTAAATGCTCTTTAAGGTATTACATAAATACTATTC 118  
Db 181 ACAACCAACATGCATACATTATATGCGCTTTATATTATTATTATTATTATTA 240  
QY 119 TCATGTGCTTTTATTTGCTTATCATGATTAATGAAGTCTCT 165  
Db 241 TTATTATTATTATTATTATTATTATTATTATTATTATTATTCGCGTGT 287

## RESULT 15

LOCUS

BO065440 953 bp mRNA linear EST 02-APR-2002  
AGENCOURT\_6955061 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5929977

5', mRNA sequence.

ACCESSION

BO065440

VERSION

BO065440.1

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

REFERENCE

1 (bases 1 to 953)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lou Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LLCM2108 row: p column: 10

High quality sequence stop: 634.

## FEATURES

source

1..953  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5929977"  
/tissue\_type="lymphoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 99"  
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCACGAG(G). Size-selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

## ORIGIN

Query Match 8.6%; Score 43; DB 13; Length 953;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 TTGAAGTGAGATTTTCTGGCCTGAGACTTCAGGAGGCAAG 500

Db 1 TTGAAGTGAGATTTTCTGGCCTGAGACTTCAGGAGGCAAG 43

Search completed: March 4, 2004, 16:38:33  
Job time: 1959.18 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:50:45 ; Search time 2273.13 Seconds  
(without alignments)  
9552.848 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_5000\_5500

Perfect score: 501

Sequence: 1 atacattataaacacaggtgt.....ggtcttcagcatgggaatgg 501

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg.hum.\*

31: em.htg.inv.\*

32: em.htg.other.\*

33: em.htg.mus.\*

34: em.htg.pln.\*

35: em.htg.tod.\*

36: em.htg.nam.\*

37: em.htg.vrt.\*

38: em.sy.\*

39: em.htgo.hum.\*

40: em.htgo.mus.\*

41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	501	100.0	11204	6	BD016860	BD016860 Novel cyt
2	501	100.0	11204	9	AB040430	AB040430 Homo sapi
3	501	100.0	71132	9	AC092184	AC092184 Homo sapi
4	283.4	56.6	6564	6	BD016835	BD016835 Novel cyt
5	220.2	44.0	47177	9	AL157391	AL157391 Human DNA
6	216.8	43.3	79528	6	BD176843	BD176843 A method
7	216.8	43.3	79528	9	HS468N1	297630 Human DNA s
8	215.6	43.0	139961	9	AL606477	AL606477 Human DNA
9	212.8	42.5	81278	9	AC091062	AC091062 Homo sapi
10	210.8	42.1	125304	9	AC080044	AC080044 Homo sapi
11	207.4	41.4	65489	9	AF108083	AF108083 Homo sapi
12	207.4	41.4	157075	9	AC005486	AC005486 Homo sapi
13	207.2	41.4	157075	9	CNS01DXI	AL133117 Human chr
14	207	41.3	182555	9	AC088531	AC088531 Homo sapi
15	206.2	41.2	50125	9	AL353708	AL353708 Human DNA
16	206	41.1	161090	9	AC117415	AC117415 Homo sapi
17	205	40.9	67524	2	AC134649	AC134649 Homo sapi
18	205	40.9	92472	9	HS181C9	298743 Human DNA s
19	205	40.9	107480	9	AL596094	AL596094 Human DNA
20	205	40.9	144878	2	AC145422	AC145422 Homo sapi
21	205	40.9	208024	9	AC010900	AC010900 Homo sapi
22	205	40.9	208145	2	AC033504	AC033504 Homo sapi
23	204.6	40.8	184168	9	AL135927	AL135927 Human DNA
24	204.4	40.8	3010	6	AX834001	AX834001 Sequence
25	204.4	40.8	3010	9	AK096194	AK096194 Homo sapi
26	204.4	40.8	173052	9	AP001885	AP001885 Homo sapi
27	204.2	40.8	96625	9	AC000118	AC000118 Homo sapi
28	203.5	40.6	185847	9	AC121334	AC121334 Homo sapi
29	203.2	40.6	93582	9	AC090681	AC090681 Homo sapi
30	203.2	40.6	146017	2	AC027473	AC027473 Homo sapi
31	203.2	40.6	154608	2	AC073620	AC073620 Homo sapi
32	203	40.5	85311	2	AL354912	AL354912 Homo sapi
33	203	40.5	146120	2	AL138794	AL138794 Homo sapi
34	203	40.5	164179	9	AC007227	AC007227 Homo sapi
35	203	40.5	192462	9	CNS01RHC	AL161669 Human chr
36	202.6	40.4	73041	9	AL356155	AL356155 Human DNA
37	202.4	40.4	169089	9	AC055725	AC055725 Homo sapi
38	202	40.3	110000	2	AP002753_1	Continuation (2 of
39	202	40.3	110000	2	AP002753_2	Continuation (3 of
40	201.8	40.3	112366	9	AL591804	AL591804 Human DNA
41	201.8	40.3	179947	2	AL591853	AL591853 Homo sapi
42	201.8	40.3	182897	2	AL158202	AL158202 Homo sapi
43	201.8	40.3	204679	9	AC099676	AC099676 Homo sapi
44	201.6	40.2	2762	9	AK125252	AK125252 Homo sapi
45	201.6	40.2	23301	9	AC137633	AC137633 Homo sapi

# ALIGNMENTS

RESULT 1	BD016860	BD016860	11204 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD016860	Novel cytidine deaminase.				
DEFINITION	BD016860	Novel cytidine deaminase.				
ACCESSION	BD016860	BD016860				
VERSION	BD016860.1	GI:22558036				
KEYWORDS	JP 2001245669-A/33.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
REFERENCE	1 (bases 1 to 11204)					
AUTHORS	Honjo, T. and Muramatsu, M.					
TITLE	Novel cytidine deaminase					
JOURNAL	Patent: JP 2001245669-A 33 11-SEP-2001;					

[illegible]

RESULT 2	AB040430	11204 bp	DNA	linear	PRI 03-OCT-2000
LOCUS	AB040430				
DEFINITION	Homo sapiens AID gene for activation-induced cytidine deaminase, complete cds.				
ACCESSION	AB040430				
VERSION	AB040430.1	GI:9888407			
KEYWORDS	AID; activation-induced cytidine deaminase.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				

REFERENCE	1 (sites)	Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.
AUTHORS		Isolation, tissue distribution, and chromosomal localization of the
TITLE		human activation-induced cytidine deaminase (AID) gene
JOURNAL		Genomics 68 (1), 85-88 (2000)
MEDLINE		20408890
PUBMED		10950930
REFERENCE	2 (sites)	Rev. P., Muto, T., Levy, Y., Geissmann, F., Plebani, A., Sanal, O.,
AUTHORS		Catalan, N., Forville, M., Dufourcq-Lagelouse, R., Gennery, A.,
TITLE		Tezcan, I., Ersoy, F., Kayserili, H., Ugazio, A. G., Brousse, N.,
JOURNAL		Muramatsu, M., Notarangelo, L. D., Kinoshita, K., Honjo, T., Fischer, A.
MEDLINE		and Durandy, A.
PUBMED		Activation-induced cytidine deaminase (AID) deficiency causes the
REFERENCE		autosomal recessive form of the Hyper-IGM syndrome (HIGM2)
AUTHORS		Cell 102 (5), 565-575 (2000)
TITLE		20460541
JOURNAL		3 (bases 1 to 11204)
MEDLINE		Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.
PUBMED		Direct Submission
REFERENCE		Submitted (18-MAR-2000) Tasuku Honjo, Kyoto University, Department
AUTHORS		of Medical Chemistry, Faculty of Medicine; Yoshida, Sakyo-ku,
TITLE		Kyoto, Kyoto 606-8501, Japan (E-mail: honjomcfour.med.kyoto-u.ac.jp,
JOURNAL		Tel:81-75-7573-4371 (ex.4371), Fax:81-75-7573-4388)
MEDLINE		Location/Qualifiers
PUBMED		1. 11204
REFERENCE		/organism="Homo sapiens"
AUTHORS		/mol_type="genomic DNA"
TITLE		/db_xref="caxon:9606"
JOURNAL		Join(521). 528, 6280. 6427, 7807. 8077, 8371. 8486, 8956. 9009
MEDLINE		/gene="AID"
PUBMED		Join(521). 528, 6280. 6427, 7807. 8077, 8371. 8486, 8956. 9009
REFERENCE		CDS.
AUTHORS		gene
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JOURNAL		gene
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PUBMED		gene
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AUTHORS		gene
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AUTHORS		gene
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AUTHORS		gene
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MEDLINE		CDS.
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AUTHORS		gene
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JOURNAL		gene
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PUBMED		gene
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AUTHORS		gene
TITLE		CDS.
JOURNAL		gene
MEDLINE		CDS.
PUBMED		gene
REFERENCE		CDS.

## ORIGIN

Query Match	100.0%;	Score 501;	DB 9;	Length 11204;
Best Local Similarity	100.0%;	Pred. No. 1.7e-117;		
Matches 501;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATACATTAAAAACAGCGTGTGAGCCACTCGGCCAGCCAGGATTGCTCTTATACATTAA	60	
Db	5000	ATACATTAAAAACAGCGTGTGAGCCACTCGGCCAGCCAGGATTGCTCTTATACATTAA	5059	
Qy	61	AAAATAGGCGGCTGTCAGTGGCTCACGCCCTGTATATCCAGCACCTTTGGGAAGCCAAGSCGG	120	
Db	5060	AAAATAGGCGGCTGTCAGTGGCTCACGCCCTGTATATCCAGCACCTTTGGGAAGCCAAGSCGG	5119	
Qy	121	GCAGAACACCCGAGGTCAGGAGTCCAAAGCGACGCTGGGCCAAGATGGTGAACCCCGTCT	180	
Db	5120	GCAGAACACCCGAGGTCAGGAGTCCAAAGCGACGCTGGGCCAAGATGGTGAACCCCGTCT	5179	
Qy	181	CTATTAAAAATACAAACATTACTCTGGGCATGATGGTGGGCGCTCTGTAATCCCAAGCTACTC	240	
Db	5180	CTATTAAAAATACAAACATTACTCTGGGCATGATGGTGGGCGCTCTGTAATCCCAAGCTACTC	5339	
Qy	241	AGAGGCTGAGGCGAGGATCCGCGAGCCCTGGCAGATCTGCCTCAGCGCTGGAGGTTG	300	
Db	5240	AGAGGCTGAGGCGAGGATCCGCGAGCCCTGGCAGATCTGCCTCAGCGCTGGAGGTTG	5299	
Qy	301	AGGCTACGTAGCCCAAGATCATGCCAGTATATCTCAGCGCTGGGCGACAAAGTGAGACCG	360	
Db	5300	AGGCTACGTAGCCCAAGATCATGCCAGTATATCTCAGCGCTGGGCGACAAAGTGAGACCG	5359	
Qy	361	TAACAAAAAAATAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCCACTGTAAAAAGTG	420	







Best Local Similarity 99.6%; Pred. No. 7.4e-62;  
Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 217 GGGCGCTGTATATCCAGCTACTCAGGAGCTGAGCGAGGATCCGGAGCTGGCA 276
Db 1 GGGGGCTGTATATCCAGCTACTCAGGAGCTGAGCGAGGATCCGGAGCTGGCA 60
QY 277 GATCTGCTGAGCTGGGAGTTGAGCTACAGTAAAGCAAGATGATGATATATTC 336
Db 61 GATCTGCTGAGCTGGGAGTTGAGCTACAGTAAAGCAAGATGATGATATATTC 120
QY 337 AGCTGGGACAACTGAGCGCTAACAAAAAATAAATAAATAAATAAATAAATAA 396
Db 121 AGCTGGGACAACTGAGCGCTAACAAAAAATAAATAAATAAATAAATAAATAA 180
QY 397 ATCAAGATCAACTGTAAAGTGGCTTAACACCACTTAAGAGTTTGGATTATTC 456
Db 181 ATCAAGATCAACTGTAAAGTGGCTTAACACCACTTAAGAGTTTGGATTATTC 240
QY 457 TGCAGGACAGAGACCATCAGGGGCTTTCAGCATGGGATGG 501
Db 241 TGCAGGACAGAGACCATCAGGGGCTTTCAGCATGGGATGG 285

```

## RESULT 5

AL157391/C  
LOCUS Human DNA sequence from clone RP11-271M1 on chromosome 10, complete  
DEFINITION sequence.  
ACCESSION AL157391  
VERSION AL157391.11 GI:15149560  
KEYWORDS HTO.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 47177)

## REFERENCE

AUTHORS Chapman,J.  
TITLE Direct Submission  
JOURNAL Submitted (10-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequest@sanger.ac.uk  
On Aug 13, 2001 this sequence version replaced gi:15021290.

## COMMENT

During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em:, EMBL; Swi:  
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/projects/c\_elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 10, constructed by the Sanger Centre Chromosome 10  
Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr10  
RP11-271M1 is from the library RP11-11.1 constructed by the group  
of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBACe3.6  
IMPORTANT: This sequence is not the entire insert of clone  
RP11-271M1. It may be shorter because we sequence overlapping  
sections only once, except for a 100 base overlap.  
The true left end of clone RP11-271M1 is at 1 in this sequence. The

FEATURES  
Source 1..47177  
Location/Qualifiers true left end of clone RP11-455B2 is at 45178 in this sequence.

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/mol_type="genomic DNA"
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/chromosome="10"
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1..2296
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repeat_region 2726..2883
/notes="2 copies 79 mer 82% conserved"
repeat_region 2797..3100
/notes="4 copies 76 mer 70% conserved"
repeat_region 3348..3581
/notes="3 copies 78 mer 79% conserved"
misc_feature 3371..3895
/notes="CpG island"
/evidence=not_experimental
repeat_region 3499..3806
/notes="4 copies 77 mer 75% conserved"
repeat_region 3616..3843
/notes="3 copies 76 mer 78% conserved"
repeat_region 3734..3889
/notes="2 copies 78 mer 82% conserved"
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/notes="3 copies 62 mer 75% conserved"
repeat_region 4101..4352
/notes="4 copies 63 mer 77% conserved"
repeat_region 4290..4413
/notes="2 copies 62 mer 83% conserved"
repeat_region 4525..4902
/notes="6 copies 63 mer 77% conserved"
repeat_region 4813..5122
/notes="5 copies 62 mer 68% conserved"
repeat_region 4947..5072
/notes="2 copies 63 mer 85% conserved"
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/notes="4 copies 63 mer 75% conserved"
repeat_region 5501..5815
/notes="5 copies 63 mer 75% conserved"
repeat_region 5772..6005
/notes="3 copies 78 mer 85% conserved"
repeat_region 6094..6245
/notes="2 copies 76 mer 85% conserved"
repeat_region 6294..6445
/notes="2 copies 76 mer 86% conserved"
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/notes="match: STS: Em:HSPH09B8"
repeat_region 8157..8457
/notes="AluSq repeat: matches 1..299 of consensus"
repeat_region 8524..8636
/notes="L2 repeat: matches 2596..2710 of consensus"
repeat_region 9039..9348
/notes="AluSg repeat: matches 1..308 of consensus"
repeat_region 9743..9955
/notes="MIR repeat: matches 32..252 of consensus"
repeat_region 10799..11045
/notes="L1MB3 repeat: matches 5896..6151 of consensus"
repeat_region 11046..11335
/notes="AluX repeat: matches 12..304 of consensus"
repeat_region 11336..11461
/notes="L1MB3 repeat: matches 5765..5896 of consensus"
repeat_region 11462..11771
/notes="AluX repeat: matches 6..312 of consensus"
repeat_region 11772..12766
/notes="L1MB3 repeat: matches 4818..5766 of consensus"
repeat_region 12812..13119
/notes="AluSg repeat: matches 1..308 of consensus"
repeat_region 13200..13406

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13407. .13686
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13687. .13865
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14056. .14388
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14547. .14692
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14798. .14995
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complement(15721. .16199)
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16895. .17117
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/note="2 copies 63 mer 83% conserved"
17446. .17597
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19355. .19654
/note="2 copies 150 mer 86% conserved"
19845. .19800
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23280. .23589
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23984. .24293
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24761. .25049
/note="AluSx repeat: matches 4. .296 of consensus"
25132. .25437
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25926. .26093
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26303. .26691
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26722. .27017
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27043. .27341
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28338. .28559
/note="MLT1A1 repeat: matches 1. .216 of consensus"
28560. .28862
/note="AluSx repeat: matches 1. .296 of consensus"
28863. .29010
/note="MLT1A1 repeat: matches 216. .365 of consensus"
29103. .29144
/note="tRNA-Cys-TGC repeat: matches 1. .41 of consensus"
29683. .29977
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30007. .30086
/note="L2 repeat: matches 2670. .2746 of consensus"

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/note="AluSx repeat: matches 1. .294 of consensus"
repeat_region 30693. .31004
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/note="23 copies 2 mer ac 78% conserved"
repeat_region 32274. .32578

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Best Local Similarity 80.4%; Pred. No. 1.le-45;
Matches 258; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 71 GGTGAGTGGCTCAGCGCTGTAATCCAGACATCTTGGAGCCCAAGATGGTGAACCCCGTCTCTATTAAAAA 190
Db 41836 GGTGAGTGGCTTACTCTGTATATCCAGTACTCTGGAGCCGAGGTGGGAGATCACC 41777

QY 131 CGAGTCCAGGAGTCCAAAGGCCAGCTGGCCCAAGATGGTGAACCCCGTCTCTATTAAAAA 190
Db 41776 TGAGTCCAGGAGTTCAAAGGTCCAGACTGGGCAACATGCGCAACCCCGTCTCTACTAAAAA 41717

QY 191 TACAAACATTACTTGGGCATGATGGTGGCGCTGTAAATCCAGTACTCAGGAGGCTGA 250
Db 41716 TACAAAAATTAGCCAGCATGGTGGGAGCCCTGTAAATCCAGTACTTGGAGGCTGA 41657

QY 251 GGCAGGAGGATCCCGGAGCGCTGCGACATCTGCTGAGCCTGGGAGGTTGAGGCTACAGT 310
Db 41656 GGCAGGAGATCTCTTGAACCCAGGAGATTGCTTGAACCTGGAGGCGGAGGTTGCACT 41597

QY 311 AAGCCAGATCATGCCAGTATCTTACGCTGGCGCAAGATGAGACCCCTTAACAAAAA 370
Db 41596 GAGCCAGATCTTCCCATTTGCATCCAGCCTGGGTGGTGGAGAGAGATCCCGTCTCAAAA 41537

QY 371 AAAAAAATTTAAAAAAGAAA 391
Db 41536 AAAAAAAGAAAAA 41516

RESULT 6
BD176843 79528 bp DNA linear PAT 18-MAR-2003
LOCUS A method of predicting cancer condition.
DEFINITION
ACCESSION BD176843
VERSION BD176843.1 GI:29122555
KEYWORDS WO 02072828-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
1 (bases 1 to 79528)
AUTHORS Kato, K., Iwao, K., Noguchi, S. and Matoba, R.
TITLE A method of predicting cancer condition
JOURNAL Patent: WO 02072828-A 6 19-SEP-2002;
DNA CHIP RESEARCH INC./HITACHI SOFTWARE ENGINEERING CO LTD, KIKUYA
KATO, KYOKO IWAO, SHINZABURO NOGUCHI, RYO MATOBA
COMMENT
OS Homo sapiens (human)
PN WO 02072828-A/6
PD 19-SEP-2002
PR 07-MAR-2002 WO 2002JP002153
PI 14-MAR-2001 JP 01P 073063, 06-APR-2001 JP 01P 108503 PR
02-AUG-2001 JP 01P 234807
P1 KIKUYA KATO, KYOKO IWAO, SHINZABURO NOGUCHI, RYO MATOBA PC
C12N15/12, C12Q1/68, G06F19/00
CC A method of predicting cancer condition
FH Key Location/Qualifiers
FT source 1..79528
FT /organism="Homo sapiens (human)".
FEATURES
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1..79528
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
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Query Match 43.3%; Score 216.8; DB 6; Length 79528;  
 Best Local Similarity 77.4%; Pred. No. 8e-45;  
 Matches 263; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 71 GGTGAGTGGCTCACGCTGTATCCAGCACTTTGGGAAGCAAGCGGGGAGACACC 130  
 DB 64240 GGTGCGGTGCTCATCCCTATATCTAGACATTTGGGAGGCTGAGGTGGGGAATCACC 64181

QY 131 CGAGGTGAGGATGCCAAGGCGAGCTGGGCAAGATGTTGAAACCCCGTCTCTATTAAAAA 190  
 DB 64180 TGACGTGACAGTTCGAGACCAAGCTGGCAACACAGGTGAAACCCCGTCTCTATTAAAAA 64121

QY 191 TACAACATTTACTGGGCGATGATGGTGGGCGCTGTAAATCCAGCTACTCAGAGGCTGA 250  
 DB 64120 TACAATAATTTAGTGGGCGGTGGTGGGCGGCGCTGTAAATCCAGCTACTCAGAGGCTGA 64061

QY 251 GGCAGGAGGATCGCGGAGCGCTGGCAGATCTGCTGAGCTGGGAGGTTGAGGCTACAGT 310  
 DB 64060 GGTAGGAGATTTGCTTTGAACCTAGGAGATCGCTTGAACCTGGGAGGCGAGTTGCAGT 64001

QY 311 AAGCGAAGATCATGCCAGTATATCTTCAAGCTGGGCGACAAAGTGAGACCGTTAAACAAAAA 370  
 DB 64000 GAGCCAGATTTGCCCACTGTACTTCAGCTGGGAGACAGACGAGCTCCATCTCAAAA 63941

QY 371 AAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAACT 410  
 DB 63940 AAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAACT 63901

RESULT 7  
 HS466N1/c  
 LOCUS  
 DEFINITION

HS466N1 79528 bp DNA linear PRI 05-JUN-2003  
 Human DNA sequence from clone Rp3-466N1 on chromosome 22q12-13  
 Contains the H1F0 gene for H1 histone family member 0, the GCAT  
 gene for glycine C-acetyltransferase (2-amino-3-ketobutyrate  
 coenzyme A ligase), the GALR3 gene for galanin receptor, the gene  
 for a novel protein similar to ANK3 (ankyrin 3, node of Ranvier  
 (ankyrin G)), the 5' end of the gene for proteins HSPC025 and  
 HSPC021 (similar to C. elegans FAT-3 alcohol dehydrogenase), ESTs,  
 STSS, GSSs and eight putative CpG islands, complete sequence.

257630  
 257630.11 GI:4582128  
 H1F0; alcohol dehydrogenase; ANK3; ankyrin; CpG island; FAT-3;  
 galanin receptor; GALR3; GCAT; H1F0; histone; HSPC021; HSPC025.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 79528)  
 Pearce, A.  
 Direct Submission  
 Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 On Apr 13, 1999 this sequence version replaced gi:4581359.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information  
 on the WORMPEP database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep -----  
 Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk  
 -----  
 This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the rare  
 occasion of the clone being a YAC.  
 This sequence was generated from part of bacterial clone contigs of  
 human chromosome 22, constructed by the Sanger Centre Chromosome 22  
 Mapping Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr22  
 Rp3-466N1 is from the library RPI-3 constructed by the group of  
 Pieter de Jong. For further details see  
 http://www.chori.org/bacpac/home.htm  
 VECTOR: pCYFAC2  
 IMPORTANT: This sequence is not the entire insert of clone  
 Rp3-466N1. It may be shorter because we sequence overlapping  
 sections only once, except for a short overlap.  
 The true left end of clone Rp3-1014D13 is at 79429 in this  
 sequence. The true right end of clone RPI-37E16 is at 100 in this  
 sequence.

FEATURES  
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 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
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 8..17  
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 39..174  
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 175..492  
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 494..505  
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 850..1133  
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 1134..1446  
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 1514..1597  
 /note="MIR repeat: matches 180..262 of consensus"  
 1837..2110  
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 2113..2253  
 /note="FLAM\_C repeat: matches 1..133 of consensus"  
 2261..2280  
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 2537..2555  
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 complement(2760..3070)  
 /note="AluY2 repeat: matches 1..310 of consensus"  
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 3205..3215  
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 complement(3220..3532)  
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 3555..3766  
 /note="L2 repeat: matches 2443..2691 of consensus"  
 3842..3908  
 /note="L1ME repeat: matches 5672..5727 of consensus"  
 3909..4040  
 /note="FLAM\_C repeat: matches 3..133 of consensus"  
 4041..4072  
 /note="L1ME repeat: matches 5727..5761 of consensus"  
 complement(4073..4399)



assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: En: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chrl> RP11-130H11 is from the library RP01-11.1 constructed by the group of Fiecer de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pRCe3.6  
This sequence is the entire insert of clone RP11-190H11. The true left end of clone RP11-138J20 is at 32632 in this sequence. The true right end of clone RP5-930J4 is at 48503 in this sequence.

## FEATURES

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dye terminator reads only."
60787..61315
/note="Single clone region. Reads generated from a
transposon library derived from a single pUC clone.
Restriction digest data confirm the assembly."
61098..61144
/note="Sequence from uni-directional dGTP big dye
terminator reads only."
61283..61315
/note="Sequence from uni-directional dGTP big dye
terminator reads only."
61324
complement(61316..61324)
/note="1372 bases of IS186 transposon (X03123) removed
here. This sequence represents the duplicated flanking
sequence of the IS186."

ORIGIN
Query Match 43.0%; Score 215.6; DB 9; Length 139961;
Best Local Similarity 78.3%; Pred. No. 1.6e-44;
Matches 271; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

QY 44 TTGCTCTTATACATTAAAAATAGCCGGTGCAGTGGCTCACGCTGTATATCCAGCACT 103
Db |||||TTCTTTTGTGAACAAAGCAGAGCTGGCGCAGTGGCTCACAGCTGTATATCCAGCACT 117945

QY 104 TTGGGAAGCCCAAGSCGGCGCAGAACCCGAGGTCAGGAGTCCAAGGCCAGCCTGGGCCAAG 163
Db |||||TTGGGAGCCAGGCGCAGCGGATTACTTGAGTTCAGGTCAGGAGTTCAGGCCAGCCTGGCCAC 117944

QY 164 ATGFTGAAAACCCCGTCTCTTATAAATAACAACATTACCTGGGCATGATGTGGCGGCC 223
Db |||||ATGFTGAAAACCCCATCTCTACTAAAAATAACAAAAATAGCTGGGCATGTTGGCGCATGCC 117884

QY 224 TGTATCCCACTACTCAGGAGGCTGAGGCAGGAGGATCCGCGAGCCTGGCGATCTGC 283
Db |||||TGTATCCCACTACTTGGGAGGCTGAGGCAGGAGAAATTCCTTGAAGCAGG-AGAAATTCG 117824

QY 284 CTGAGCCTGGGAGGTTGAGGCTACAGTAAGCAAGATCATGCCAGCTATATCTTCAAGCTGG 343
Db |||||CTGAGCAGGAGGTTGAGGTTGAGTGAGTGCAGTGAGTGCATATGCCATCTGCATCCAGCTGG 117765

QY 344 GGCACAAAGTGAGACCGGTAAACAAAAAATAAATTTAAAAAAGA 389
Db |||||CGCAGAGTGAGGCTCTGTCTCAAAAAAATAAATAAATAAATAAATAA 117705

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QY 232 CAGCTACTCAGGAGCTGAGGAGGAGGATCCGGGAGCTGGCAGATCTGCTGAGCCT 291
Db 43020 CAGCTACTCAGGAGCTGAGCAGGAGGAGATCGCTTGAACCTGGGAGAT-GGAGGTTGCAT 42962

QY 292 GGGAGGTTGAGGCTACAGTAAGCAAGATCATCCAGTATACCTTCAGCCTGGCGGACAAA 351
Db 42961 GGGAGGTTGAGGCTACAGTAAGCAAGATCGCTTGAACCTGGGAGAT-GGAGGTTGCAT 42962

QY 352 GTGAGCCGTAAACAAAAAATTTTAAAAAGAAA 391
Db 42901 GCGAGCTCCATCTCAAAAAAATTTTAAAAAGAAA 42862

RESULT 10
AC008044/c 125304 bp DNA linear PRI 07-OCT-1999
LOCUS Homo sapiens chromosome 14 BAC containing genes for ABH and nuclear
DEFINITION receptor coactivator NCoA-62, complete sequence.
ACCESSION AC008044
VERSION AC008044.4 GI:6015188
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 125304)
AUTHORS Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,
Bloom, S., Dors, M., Dickhoff, R., Harrison, G., James, R., Lasky, S.,
Madan, A., Ratcliffe, A., Shaffer, T. and Hood, L.
Sequencing of human chromosome 14
Unpublished
2 (bases 1 to 125304)
AUTHORS Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R.,
Harrison, G., James, R., Lasky, S., Madan, A., Prescott, S.,
Ratcliffe, A., Shaffer, T. and Hood, L.
Direct Submission
Submitted (14-JUL-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
3 (bases 1 to 125304)
AUTHORS Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B.,
Bloom, S., Dors, M., Dickhoff, R., Harrison, G., James, R., Lasky, S.,
Madan, A., Ratcliffe, A., Shaffer, T. and Hood, L.
Direct Submission
Submitted (07-OCT-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
On Oct 7, 1999 this sequence version replaced gi:5708444.
FEATURES
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/notes="This clone overlaps BAC 50114, Accession AF111168
and BAC 111016, Accession AC008372"
misc_feature
1. 21034
/notes="Overlap with BAC 50114, Accession AF111168, at
positions 210429-231464."
exon
complement(8617..8748)
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gene
complement(65213..100168)
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/notes="ALK B protein homologue"
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86902..87064,96533..96641,99985..100168)
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86902..87064,96533..96641,99985..100168))
/notes="ALK B protein homologue; Intron-exon boundaries
defined in relation to cDNA in X9192. There are
differences in the conceptual translation between this CDS
and the cDNA due to frameshift variations. The genomic
sequence is all high quality data"

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PRSLLEKLVWTVGVHYWDSKYSADHYTPSPDLGLFLSEVAAAGCFDEFERAGI
LNYRLDSTLGIHVDRELDSKPLLSFSFQQAIFLGLGLQRLDEATPMFMHSGDIM
IMSGFRLNHAVERVLPFEEGELPHCLREAPLPAVLPRDSMVEFCFSEMDWQVCASYL
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complement(join(110239..110437,110518..110681,
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DEFINITION Homo sapiens chromosome 7 BAC clone F5, complete sequence.
ACCESSION AF108083
VERSION AF108083.1 GI:3941729
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 65489)
AUTHORS Rump, A., Rosenthal, A., Drescher, B., Weber, J., Schattevooy, R. and
Korenberg, J.
Direct Submission
TITLE

```



JOURNAL	Submitted (20-NOV-1998)	Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
FEATURES	Location/Qualifiers	
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**MAPPING INFORMATION:**  
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the

Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information contact Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://baopac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

#### SOURCE INFORMATION:

This clone was derived from human PAC library RPI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://baopac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc.

(http://www.genomesystems.com) or Research Genetics, Inc.

(http://www.geneng.com); or from Pieter de Jong.

VECTOR: pCYPAC2

#### NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP4-555L14, 200 bp overlap. Actual start of this clone is at base position 88584 of RP4-555L14; actual end is at base position 157075 of RP5-1070G24.

#### FEATURES

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1886. 1975

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2732. 2775

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3218. 3276

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4956. 5132

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5547. 5841

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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens chromosome 17, clone RP11-463M16, complete sequence.  
AC068531  
AC068531.9 GI:24080707  
HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 182555)

Birren,B., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 17, clone RP11-463M16

Unpublished

2 (bases 1 to 182555)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,

Campbell,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,  
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,  
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

Klein,J., Laroque,K., Lamazares,R., Landers,T., Lehotzky,J.,  
Levine,R., Liu,G., Liu,G., Locke,K., Macdonald,P., Marquis,N.,  
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,  
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,

Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (03-MAY-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 182555)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,  
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,

Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,  
Gardyna,S., Gird,S., Graham,L., Grand-Pierre,N., Hagos,B.,

Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A.,  
Karatas,A., Kellis,C., Landers,T., Levine,R., Lindblad-Toh,K.,  
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,

McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,  
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,  
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,

Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,  
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,

Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,  
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (11-SEP-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 182555)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,  
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,

Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,  
Gardyna,S., Gird,S., Graham,L., Grand-Pierre,N., Hafez,N.,

Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kanat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,

Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,  
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,  
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,

Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,  
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R.,  
Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,

Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,  
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (11-SEP-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

5 (bases 1 to 182555)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,  
Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgalter,B.,  
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,

Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,  
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,  
Gardyna,S., Gird,S., Graham,L., Grand-Pierre,N., Hafez,N.,

Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
Kanat,A., Karatas,A., Kellis,C., Landers,T., Levine,R.,  
Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J.,

Matthews,C., McCarthy,M., Meldrim,J., Meneus,L., Mihova,T.,  
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,  
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,

Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,  
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Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K.,  
Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X.,  
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

On Oct 17, 2002 this sequence version replaced gi:22779575.

All repeats were identified using RepeatMasker:

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WITBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

Project Information

Center project name: L9798

Center clone name: 463\_M16

Location/Qualifiers

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complement(28973..29210)
/rpt_family="HAL1"

Query Match      41.3%; Score 207; DB 9; Length 182555;
Best Local Similarity 72.7%; Pred. No. 2.6e-42;
Matches 290; Conservative 0; Mismatches 90; Indels 19; Gaps 1;

QY 19 GTGAGCCACTGGCCAGCCAGGTATGCTCTTATACATTAAATAATAGCCGGTGCAGT 78
DB 149980 GGGAGCCCTAGGCTTTGAAATAATTCATGAATAATAGAAATTTGGCCGGTGCAGT 149921
QY 79 GGCTCACGCTGTATATCCAGCACTTTGGGAAGCCAGGCGGGGAGAACACCCAGGTCA 138
DB 149920 GGCTCACACCTGTATATCCAGCACTTTGGGAGCGGAGGTGGTGGTATCACCAGGTCA 149861
QY 139 GGAGTCCAGGCGCCAGCTGGCCAGATGTTGAACCCCGTCTCTTATTAATAATCAACA 198
DB 149860 GGAGTTTGAGACCGCTAGCCATGCAATGGCAAAACCCCGTCTCTTACTAAATAACAAAA 149801
QY 199 TTACTTGGCGCATGATGGTGGGCGCTGTAAATCCAGCTTACTCAGGAGGCTGAGGAGGAG 258
DB 149800 TTAGCCGGGCATCGTGGCGGGTGCCTGTAAATCCAGCTTACTCAGGAGGCTGAGGAGGAG 149741
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QY 259 GATCGCGGAGCCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGCTACAGTACGCAAG 318  
DB 149740 AAT-----AGCTTGAGCCCGGAGGTGGAGTGCAGTGTGAGCTGAG 149700  
QY 319 ATCATGCGCAGTATATTTCAGCCTGGGCGACAAAAGTGAGACCGTAAACAAAAAATAAT 378  
DB 149699 ATCAGTTCAGCGCACTCCACACTGGTGGTACAGACGACGACTGTCTCAAAAAAATAA 149640  
QY 379 TTAATAAAGAAATTTAGATCAAGATCCACTGTAAAAA 417  
DB 149639 AAAAAAATAAATAATATATATATATAAATAAAGAA 149601

AL353708 90125 bp DNA linear PRI 30-MAY-2001  
Human DNA sequence from clone RP11-533E19 on chromosome 1, complete  
sequence.  
AL353708  
AL353708.10 GI:14272261  
HTG.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 90125)  
Direct Submission  
Submitted (30-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On May 31, 2001 this sequence version replaced gi:13992256.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chrl  
RP11-533E19 is from the library RPCI-11.2 constructed by the group  
of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBACE3.6  
IMPORTANT: This sequence is not the entire insert of clone  
RP11-533E19. It may be shorter because we sequence overlapping  
sections only once, except for a 100 base overlap.  
The true right end of clone RP11-533E19 is at 90125 in this  
sequence. The true left end of clone RP11-52118 is at 15352 in this  
sequence. The true right end of clone RP11-12M5 is at 100 in this  
sequence.

RESULT 15  
LOCUS AL353708  
DEFINITION Human DNA sequence from clone RP11-533E19 on chromosome 1, complete  
sequence.  
ACCESSION AL353708  
VERSION AL353708.10 GI:14272261  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 90125)  
AUTHORS Martin, S.  
TITLE Direct Submission  
JOURNAL Submitted (30-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,  
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
requests: clonerequests@sanger.ac.uk  
On May 31, 2001 this sequence version replaced gi:13992256.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chrl  
RP11-533E19 is from the library RPCI-11.2 constructed by the group  
of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBACE3.6  
IMPORTANT: This sequence is not the entire insert of clone  
RP11-533E19. It may be shorter because we sequence overlapping  
sections only once, except for a 100 base overlap.  
The true right end of clone RP11-533E19 is at 90125 in this  
sequence. The true left end of clone RP11-52118 is at 15352 in this  
sequence. The true right end of clone RP11-12M5 is at 100 in this  
sequence.

FEATURES  
source  
1..90125  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="1"  
/clone="RP11-533E19"

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repeat_region 418..449
repeat_region /note="16 copies 2 mer tg 100% conserved"
misc_feature 1208..1517
misc_feature /note="AluY repeat: matches 1..311 of consensus"
misc_feature 2723..3611
misc_feature /note="CpG island"
misc_feature /evidence=not_experimental
repeat_region 5279..5413
repeat_region /note="MIR repeat: matches 28..175 of consensus"
repeat_region 6111..6415
repeat_region /note="AluX repeat: matches 1..305 of consensus"
repeat_region 7493..7784
repeat_region /note="AluSg repeat: matches 1..291 of consensus"
repeat_region 8219..8308
repeat_region /note="L2 repeat: matches 2659..2747 of consensus"
repeat_region 8655..8840
repeat_region /note="AluJo repeat: matches 85..298 of consensus"
repeat_region 10020..10324
repeat_region /note="AluY repeat: matches 1..308 of consensus"
repeat_region 10969..11294
repeat_region /note="AluY repeat: matches 1..306 of consensus"
repeat_region 11591..11697
repeat_region /note="AluSg repeat: matches 1..304 of consensus"
repeat_region 11929..12240
repeat_region /note="L2 repeat: matches 1..312 of consensus"
repeat_region 12585..12863
repeat_region /note="AluSg repeat: matches 1..298 of consensus"
repeat_region 12867..13146
repeat_region /note="AluY repeat: matches 37..309 of consensus"
repeat_region 13334..13647
repeat_region /note="AluX repeat: matches 1..312 of consensus"
repeat_region 13819..14115
repeat_region /note="AluX repeat: matches 2..297 of consensus"
repeat_region 14230..14324
repeat_region /note="MER58C repeat: matches 119..89 of consensus"
repeat_region 14357..14648
repeat_region /note="AluYa5 repeat: matches 1..304 of consensus"
repeat_region 14780..15076
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repeat_region 15706..15990
repeat_region /note="AluY repeat: matches 1..290 of consensus"
repeat_region 15993..16322
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repeat_region /note="AluSg/x repeat: matches 207..301 of consensus"
repeat_region 16945..17071
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repeat_region 18171..18190
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repeat_region 18191..18489
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repeat_region 18490..18511
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repeat_region /note="FLAM A repeat: matches 43..116 of consensus"
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repeat_region 20637..20960
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repeat_region 22762..22926
repeat_region /note="AluY repeat: matches 137..301 of consensus"
repeat_region 23039..23207
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repeat_region 23328..23394
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repeat_region 23877..24183
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repeat_region 24994..25299

/note="AluJo repeat: matches 1..308 of consensus"
25470..25778
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26048..26340
/note="AluX repeat: matches 3..295 of consensus"
27036..27118
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27119..27411
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27412..27462
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27477..27586
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27588..27835
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27967..28014
/note="24 copies 2 mer ta 93% conserved"
28282..28582
/note="AluY repeat: matches 1..309 of consensus"
29259..29559
/note="AluY repeat: matches 1..305 of consensus"
29774..30110
/note="AluSg repeat: matches 1..310 of consensus"
30131..30438
/note="AluX repeat: matches 1..304 of consensus"
32010..32180
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34889..35188
/note="AluSg repeat: matches 1..300 of consensus"
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35860..36148
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37071..37361
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/note="AluSg repeat: matches 44..295 of consensus"
40695..40828
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44492..44705
/note="MIR repeat: matches 3..246 of consensus"
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45075..45198
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45199..45548
/note="TIGER2 repeat: matches 2..374 of consensus"
45551..45664
/note="L1P3 repeat: matches 6035..6149 of consensus"
45686..46081
/note="TIGER2 repeat: matches 347..744 of consensus"
46161..46385
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46387..46564
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Query Match 41.2%; Score 206.2; DB 9; Length 90125;
Best Local Similarity 73.0%; Pred. No. 4.1e-42;
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Db	15982	CAGAAAAAGAGCCGCGCACGGTGTCTCACACCTGTATATCCAGCACTTCGGAGGCGG	16041						
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Db	16042	AGCAGGTGGATCACCTGAGATCAGGAGTTCAAGACCGCCTGGCCCAACATGGCGAAACC	16101						
Qy	175	CCGTCTCTATTAAAAATACAAACATTACCTGGGCATGATGGTGGCGCCTGTAAATCCCAG	234						
Db	16102	CCGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTGGCACAAAGCCTGTAGTCCCAG	16161						
Qy	235	CTACTCAGGAGGTGAGGAGGAGGATCCGCGAGCCTGGCAGATCTGCCTGAGCTGGG	294						
Db	16162	CTACTCGGGAACCTGAGGAGGAGGATCACTTGAAACCCGGGAGATCACTTGAACCCCGG	16221						
Qy	295	AGGTTGAGGCTACAGTAAGCCAGATCATGCCAGTATATCTTCAAGCCTGGCGCACAAAGTG	354						
Db	16222	AGGCAGAGGTTGCAGTGAGCCGACATTCACCACTGCACCTCCAGCCTGGTGCACAGATG	16281						
Qy	355	AGACCGTAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCCACTGTAA	414						
Db	16282	AGACTCTGTCTCAAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCCACTGTAA	16341						
Qy	415	AAA	417						
Db	16342	ACA	16344						

Search completed: March 4, 2004, 15:00:23  
 Job time : 2278.13 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 11:56:09 ; Search time 286.428 Seconds  
(without alignments)  
7430.646 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_5000\_5500

Perfect score: 501  
Sequence: 1 ataccataaaacaggtgt.....ggcttcacgatgggaatgg 501

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: Geneseqn29Jan04:\*  
2: Geneseqn1980s:\*  
3: Geneseqn1990s:\*  
4: Geneseqn2000s:\*  
5: Geneseqn2001as:\*  
6: Geneseqn2002bs:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	501	100.0	11204	3 AAC55339	Aac55339 Human act
2	501	100.0	11204	6 ABS73286	Abst73286 DNA encod
3	283.4	56.6	6564	3 AAC55314	Aac55314 Human act
4	216.8	43.3	79528	6 AAL50814	Aal50814 Human can
5	197.4	39.4	164702	7 ACF62730	Acf62730 Cancer ba
6	197.4	39.4	164702	7 ADB20845	Adb20845 MRP1 base
7	197.4	39.4	164702	9 ADB87934	Adb87934 Human UGT
8	197.4	39.4	164702	9 ADB96917	Adb96917 Human MDR
9	197.4	39.4	164702	9 ADB92108	Adb92108 Human MDR
10	197.4	39.4	207433	5 ABZ72040	Abz72040 Gene 216
11	197.4	39.4	207433	7 ABX74891	Abx74891 BAC1098L2
12	196.8	39.3	1877	3 AAC93353	Aac93353 Human sec
13	196.6	39.2	8321	7 ADA98848	Ada98848 Human sec
14	196.6	39.2	8321	7 ADA44471	Ada44471 Human sec
15	196.6	39.2	8321	9 ADC20851	Adc20851 Human sec
16	196.6	39.2	1743	4 AAI62586	Aai62586 Human bre
17	196.2	39.2	1743	4 AAL03368	Aal03368 Human rep
18	196.2	39.2	1746	4 AAI62587	Aai62587 Human bre
19	196.2	39.2	1746	4 AAL03369	Aal03369 Human rep
20	196.2	39.2	249999	7 ABZ80229	Abz80229 Human tra
21	195.6	39.0	10642	5 ABA20382	Aba20382 Human ner
22	195	38.9	66566	3 AAA53450	Aaa53450 Human thi
23	195	38.9	100301	6 ABQ88176	Abq88176 Human ost

## ALIGNMENTS

### RESULT 1

AAC55339

ID AAC55339 standard; DNA; 11204 BP.

XX AC AAC55339;

XX AC AAC55339;

DT 05-FEB-2001 (first entry)

XX DE Human activation-induced cytidine deaminase genomic DNA SEQ ID NO.35.

XX KW Activation-induced cytidine deaminase; AID; cytidine deaminase;

XX KW immune related disease; allergy; allergic disease; anti-allergic;

XX KW antianemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;

XX KW gene therapy; B cell associated immune system disorder; food allergy;

XX KW immunodeficiency disease; immunoglobulin A deficiency disease; ashma;

XX KW IgA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;

XX KW drug allergy; allergic rhinitis; Rosen disease; Digeorge disease; AIDS;

XX KW ataxia telangiectasia; common variable immunodeficiency disorder;

XX KW major histocompatibility class II deficiency disease;

XX KW auto immunodeficiency syndrome; IgG subclass selection disorder; ds.

XX OS Homo sapiens.

XX PN WO200058480-A1.

XX PD 05-OCT-2000.

XX PF 28-MAR-2000; 2000WO-JP001918.

XX PR 29-MAR-1999; 99JP-00087192.

XX PR 24-JUN-1999; 99JP-00178999.

XX PR 27-DEC-1999; 99JP-00371382.

XX PA (NISH) JAPAN TOBACCO INC.

XX PA (HONJ/) HONJO T.

XX PI Honjo T, Muramatsu M;

XX DR WPI; 2000-611715/58.

XX PT Nucleic acid encoding activation induced cytidine deaminase, useful as a

XX PT target for drug development for immune-related diseases including

XX PT allergies.

XX XX Claim 17; Page 163-170; 174pp; Japanese.

XX PS

XX XX

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XX XX

XX XX

CC The present invention describes an activation-induced cytidine deaminase  
CC (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has  
CC cytidine activity similar to APOBEC-1. AID has anti-allelic, antileukemic,  
CC antiasthmatic, ophthalmological, anti-HIV and dermatological activities,  
CC and can be used in gene therapy. AID polynucleotides are useful in  
CC methods for identifying drugs for the treatment of B cell associated  
CC immune system disorders, immunodeficiency diseases and allergies, such as  
CC immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-  
CC globulinemia, atopic dermatitis, allergic colitis, asthma, food allergy,  
CC drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia  
CC telangiectasia, common variable immunodeficiency disorder, MHC (major  
CC histocompatibility class II deficiency disease, AIDS (auto  
CC immunodeficiency syndrome), elevated IGE disorder, and IGG subclases  
CC selection disorder. The DNA sequences encoding AID may be used for gene  
CC therapy and the antibodies to the AID protein may be used for diagnosis  
CC and treatment of these disorders. The present sequence represents a  
CC genomic DNA sequence of human AID  
XX

SQ Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 U; 0 Other;

Query Match 100.0%; Score 501; DB 3; Length 11204;  
Best Local Similarity 100.0%; Pred. No. 1.4e-113;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACATTAATAAACAGGTGTGAGCCATCGCCAGCAGGTATGCTTTATACATTAA 60  
DB 5000 ATACATTAATAAACAGGTGTGAGCCATCGCCAGCAGGTATGCTTTATACATTAA 5059  
QY 61 AAAATAGCCGTCAGTGGCTCAGCGCTGAATCCAGACACTTTGGAGCCCAAGCGG 120  
DB 5060 AAAATAGCCGTCAGTGGCTCAGCGCTGAATCCAGACACTTTGGAGCCCAAGCGG 5119  
QY 121 GCAGAACACCCGAGGTCTAGGAGTCCAGGCCAGCGTGGCCAAAGATGGTGAACCCCGTCT 180  
DB 5120 GCAGAACACCCGAGGTCTAGGAGTCCAGGCCAGCGTGGCCAAAGATGGTGAACCCCGTCT 5179  
QY 181 CTATTAAATAACAAACAGTCTAGGAGTCCAGGCCAGCGTGGCCAAAGATGGTGAACCCCGTCT 240  
DB 5180 CTATTAAATAACAAACAGTCTAGGAGTCCAGGCCAGCGTGGCCAAAGATGGTGAACCCCGTCT 5239  
QY 241 AGGAGGCTGAGGACGAGGATCCGGGAGCGCTGGCAGATCTGCTGAGCCCTGGGAGGTG 300  
DB 5240 AGGAGGCTGAGGACGAGGATCCGGGAGCGCTGGCAGATCTGCTGAGCCCTGGGAGGTG 5299  
QY 301 AGGCTACAGTAAGCAAGATCATGTCAGTATACCTTCAGCTTGGGGGACAAAGTGAAGCCG 360  
DB 5300 AGGCTACAGTAAGCAAGATCATGTCAGTATACCTTCAGCTTGGGGGACAAAGTGAAGCCG 5359  
QY 361 TAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 420  
DB 5360 TAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5419  
QY 421 GCCTAAACACCAATTAAGATTGGAGTTTATTTCTGAGGCGAGAGAACCATCAGG 480  
DB 5420 GCCTAAACACCAATTAAGATTGGAGTTTATTTCTGAGGCGAGAGAACCATCAGG 5479  
QY 481 GGGTCTTCAGCATGGGAATGG 501  
DB 5480 GGGTCTTCAGCATGGGAATGG 5500

RESULT 2  
ABS73286  
ID ABS73286 standard; DNA; 11204 BP.

XX AC ABS73286;  
XX XX ABS73286;  
XX XX ABS73286;

DT 04-DEC-2002 (first entry)  
DE DNA encoding human translocation del (12p) protein #1.  
DE Chromosome aberration; oncogenic fusion protein; cancer;  
KW Proliferative disease; cellular protein isoform; heat shock protein 90;  
KW

KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
XX Homo sapiens.  
OS WO200269900-A2.  
PN 12-SEP-2002.  
PD 01-MAR-2002; 2002WO-US006518.  
PF 01-MAR-2001; 2001US-0272751P.  
PR (CONF-) CONFORMA THERAPEUTICS CORP.  
XX Fritz LC, Burrows FU;  
XX WPI: 2002-698710/75.  
XX P-PSDB; ABG95082.

PT Treating genetically-defined disease associated with chromosomal  
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX Disclosure; Page 242-245; 389pp; English.  
XX The invention describes a method of treating genetically-defined disease  
XX associated with chromosomal aberrations yielding oncogenic fusion  
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous  
XX cell population, treating proliferative diseases associated with mutant  
XX protein or cellular protein isoforms (II) dependent on heat shock protein  
XX (HSP)-90, or selectively treating cells expressing (II) involving  
XX administering HSP90-inhibitor. The method is useful for treating  
XX genetically-defined disease with chromosomal aberration yielding  
XX oncogenic fusion protein, treating cancerous cells containing fusion  
XX protein in heterogeneous cell population, treating proliferative disease  
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
XX p53), or selectively treating cells expressing mutant protein or cellular  
XX protein isoform in a patient heterozygous for (II). The method is useful  
XX for treating a disease e.g. haematopoietic disorder such as T or B cell  
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CMML,  
XX or a disease characterised by a solid tumour such as papillary thyroid  
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
XX synovial sarcoma. The method is also useful for treating viral  
XX infections. This represents the DNA sequence of a chromosome aberration  
XX

SQ Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 U; 0 Other;  
Query Match 100.0%; Score 501; DB 6; Length 11204;  
Best Local Similarity 100.0%; Pred. No. 1.4e-113;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACATTAATAAACAGGTGTGAGCCATCGCCAGCAGGTATGCTTTATACATTAA 60  
DB 5000 ATACATTAATAAACAGGTGTGAGCCATCGCCAGCAGGTATGCTTTATACATTAA 5059  
QY 61 AAAATAGCCGTCAGTGGCTCAGCGCTGAATCCAGACACTTTGGGAGCCCAAGCGG 120  
DB 5060 AAAATAGCCGTCAGTGGCTCAGCGCTGAATCCAGACACTTTGGGAGCCCAAGCGG 5119  
QY 121 GCAGAACACCCGAGGTCTAGGAGTCCAGGCCAGCGTGGCCAAAGATGGTGAACCCCGTCT 180  
DB 5120 GCAGAACACCCGAGGTCTAGGAGTCCAGGCCAGCGTGGCCAAAGATGGTGAACCCCGTCT 5179  
QY 181 CTATTAAATAACAAACAGTCTAGGAGTCCAGGCCAGCGTGGCCAAAGATGGTGAACCCCGTCT 240  
DB 5180 CTATTAAATAACAAACAGTCTAGGAGTCCAGGCCAGCGTGGCCAAAGATGGTGAACCCCGTCT 5239

The present invention describes an activation-induced cytidine deaminase (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has cytidine activity similar to APOBEC-1. AID has anti-allergic, antianaemic, antiasthmatic, ophthalmological, anti-HIV and dermatological activities, and can be used in gene therapy. AID polynucleotides are useful in methods for identifying drugs for the treatment of B cell associated

PT Computer-aided statistical method for predicting cancer, applicable in  
PT gene therapy for evaluating cancer malignancy with data for use in drug

## RESULT 4

XX Heinrich G, Kerb R;  
XX WPI; 2003-268144/26.  
XX New use of irinotecan for preparation of compositions for treating cancer  
XX in subject having genome with variant allele comprising cytochrome p450,  
XX subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.  
XX Disclosure; SEQ ID NO 658; 86pp; English.  
XX The present invention describes the use of irinotecan (I) or its  
XX derivative for the preparation of a pharmaceutical composition for  
XX treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
XX cancer, or malignant glioma in a subject having a genome with a variant  
XX allele which comprises a cytochrome p450, subfamily IIIA (nifedipine  
XX oxidase), polypeptide 5 (CYP3A5) polynucleotide (II). (I) and (II) have  
XX cytostatic activity. The therapeutic applications of (I) is improved,  
XX since it is possible to individually treat a subject with an appropriate  
XX dosage and/or an appropriate derivative of (I). Therefore, undesirable,  
XX harmful or toxic effects are efficiently avoided. Unnecessary and  
XX potentially harmful treatment of those subjects who do not respond to the  
XX treatment with substances (nonresponders), as well as the development of  
XX drug resistances due to suboptimal drug dosing can be avoided. ACF62200  
XX to ACF62751 and ABM34912 to ABM35013 represent sequences used in the  
XX exemplification of the present invention  
XX  
XX Sequence 164702 BP; 52399 A; 32545 C; 31423 G; 48335 T; 0 U; 0 Other;  
XX  
XX Query Match 39.4%; Score 197.4; DB 7; Length 164702;  
XX Best Local Similarity 74.9%; Pred. No. 2.5e-38;  
XX Matches 269; Conservative 0; Mismatches 71; Indels 19; Gaps 1;  
XX  
XX QY 51 TATACATTAATAAATAGCCGGTGCAGTGGCTCAGCCTGTAAATCCAGCACTTTGGGAA 110  
XX DB 138901 TAAAAAGTAAAAAGGCGGGTGGTAGCCACACCTGTAAATCCTAGCACTTTGGGAG 138942  
XX QY 111 GCCAAGCGGGCAGAACACCCGAGGTCCAGGAGTCCAGGCCAGCCTGGCCCAAGATGGTGA 170  
XX DB 138841 GCAGAGGCGGGCAGATCACTCAGGTCCAGGAGTTCACAGCAGCCTGGCCCAATGGTGA 138782  
XX QY 171 AACCCGGTCTCTATTAAAAATACAAATACCTACCTGGCATGATGCGGCGCTGTATTC 230  
XX DB 138781 AACCCGGTCTCTACTAAAAATACAAATATAGTGGCGGTGGTGGCAAGCACTGTATTC 138722  
XX QY 231 CCAGCTACTCAGGAGGCTGAGGAGGAGTCCGGGAGCCTGGCGAGATCTGCCTGAGCC 290  
XX DB 138721 CCAGCTACTTGGGAGGCTGAGGAGGAGT-----TGCTTGAACC 138681  
XX QY 291 TGGAGGTTGAGGCTACAGTAAGCCAGATCATGCGAGTATCTTACGCTGGGCGACAA 350  
XX DB 138680 TGGAGGTTGAGGTTGCAAGTGGCGGAGATCGCGCCTGCACTCCAGCCTGGGCGGAG 138621  
XX QY 351 AGTGAGACCGTAAACAAAAAATAATTTAAAAAAGAAATTTAGATCAAGATCAAC 409  
XX DB 138620 AGTGAGACTCTGACTCMAAAAAAATAAGTAAAAAGAAAGAAAGAAATTAAC 138562  
XX  
XX RESULT 6  
XX ADB20845/c  
XX ID ADB20845 standard; DNA; 164702 BP.  
XX  
XX AC ADB20845;  
XX  
XX XX 20-NOV-2003 (first entry)  
XX  
XX DE MRP1 based cancer related nucleic acid SEQ ID NO:658.  
XX  
XX KW irinotecan; colorectal cancer; cervical cancer; gastric cancer;  
XX lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;  
XX variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;  
XX ds.  
XX  
XX

PT design.  
XX  
XX Disclosure; Page 84-131; 182pp; Japanese.  
XX  
XX The invention comprises a method for predicting cancer status. The method  
XX involves: measuring expression doses of genes obtained from specimens;  
XX selecting at least one gene as the gene for an assay; using the  
XX measurement results on expression doses of the selected genes for  
XX multivariate analysis; and classifying the specimens in analogous groups  
XX with results of the multivariate analysis on expression patterns of the  
XX genes. The method of the invention is useful for predicting cancer, which  
XX is applicable in gene therapy for evaluating cancer malignancy with data  
XX for use in drug design (e.g. antisense nucleic acids for use in gene  
XX therapy to treat cancer). The present DNA sequence represents a human  
XX nucleic acid of the invention  
XX  
XX Sequence 79528 BP; 19015 A; 20270 C; 20468 G; 19775 T; 0 U; 0 Other;  
XX  
XX Query Match 43.3%; Score 216.8; DB 6; Length 79528;  
XX Best Local Similarity 77.4%; Pred. No. 3.3e-43;  
XX Matches 263; Conservative 0; Mismatches 77; Indels 0; Gaps 0;  
XX  
XX QY 71 GGTGAGTGGCTCAGCCTGTAATCCAGCACTTTGGGAAGCCAGGCGGCAGAACACC 130  
XX DB 64240 GGTGCGGTGGCTATGCTTAATCTAGCACTTTGGGAGGCTGAGGTGGCGAATCACC 64181  
XX QY 131 CGAGTCCAGGATCCAGGCCAGCCTGCCAGATGGTGAACCCCGTCTCTATTAATAA 190  
XX DB 64180 TGACGTCCAGGATTCGACAGCAGCCTGCCAAGCAGGTGAACCCCGTCTCTATAAAA 64121  
XX QY 191 TACAAACATTAATCTGGGATGATGTGGCGGCTGTAAATCCAGCTACTCAGGAGGCTGA 250  
XX DB 64120 TACAAATATAGTGGCGGTGGTGGCGGCGCTGTAAATCCAGCTACGCGGAGGCTGA 64061  
XX QY 251 GCAGAGGATCCGCGGAGCCTGGCAGATCTGCTGAGCCTGGAGGTTGAGGCTACAGT 310  
XX DB 64060 GGTAGGAGAAATGCTTGAACCTAGGAGATCGCTTGAACCTGGGAGCGGAGGTTGAGT 64001  
XX QY 311 AAGCCAAAGATCATGCCAGTATATCTCAGCCTGGGCGCAAAAGTGAGACCCGTAACAAAAA 370  
XX DB 64000 GAGCCAAAGATCTGCCACTGTACTTACGCTGGGAGACAGACGAGACTCCATCTCAAA 63941  
XX QY 371 AAAAAATTTAAAAAGAAATTTAGATCAAGATCCAACT 410  
XX DB 63940 AAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 63901  
XX  
XX RESULT 5  
XX ACF62730/c  
XX ID ACF62730 standard; DNA; 164702 BP.  
XX  
XX AC ACF62730;  
XX  
XX DT 08-OCT-2003 (first entry)  
XX  
XX DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:658.  
XX  
XX KW Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;  
XX cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;  
XX cytostatic; gene; ds.  
XX  
XX OS Unidentified.  
XX  
XX XX WO2003013534-A2.  
XX  
XX PD 20-FEB-2003.  
XX  
XX PF 23-JUL-2002; 2002WO-EP008219.  
XX  
XX PR 23-JUL-2001; 2001EP-00117608.  
XX  
XX PR 24-MAY-2002; 2002EP-00011710.  
XX  
XX PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

OS Unidentified.  
XX WO2003013533-A2.  
XX 20-FEB-2003.  
XX 23-JUL-2002; 2002WO-EP008200.  
XX 23-JUL-2001; 2001EP-00117608.  
XX 24-MAY-2002; 2002EP-00011710.  
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX Heinrich G, Kerb R;  
XX WPI; 2003-354397/33.  
XX Use of irinotecan or its derivative for preparation of a pharmaceutical  
XX composition for treating cancer in a subject having a genome with a  
XX variant allele comprising a multidrug resistance protein 1  
XX polynucleotide.  
XX Disclosure; SEQ ID NO 658; 100pp; English.  
XX The present invention describes a method for the use of irinotecan (I) or  
XX its derivative for the preparation of a pharmaceutical composition for  
XX treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
XX cancer, or malignant glioma in a subject having a genome with a variant  
XX allele which comprises a multidrug resistance protein 1 (MRP1)  
XX polynucleotide (II). (I) has cytostatic activity. (I) or its derivative  
XX can be used for the preparation of a pharmaceutical composition for  
XX treating colorectal, cervical, gastric, lung, ovarian or pancreatic  
XX cancer, or malignant glioma in a subject, where the subject is a human  
XX (preferably African or Asian) or a mouse. The present sequence represents  
XX a sequence which is used in the exemplification of the present invention.  
XX Sequence 164702 BP; 52399 A; 32545 C; 31423 G; 48335 T; 0 U; 0 Other;  
XX Query Match 39.4%; Score 197.4; DB 7; Length 164702;  
XX Best Local Similarity 74.9%; Pred. No. 2.5e-38;  
XX Matches 269; Conservative 0; Mismatches 71; Indels 19; Gaps 1;  
QY 51 TATACATTAAAAATAGCCGGTGCAGTGGCTGAGCTGATATCCAGACATTGGGAA 110  
Db 138901 TAAAAAGTAAAAAGAGCGCGGTGTGGTACCCACACCTGTAATCTCTAGCACTTTGGGAG 138842  
QY 111 GCCAAGCGGGCAGAAACACCCGAGTCCAGAGTCCAGGCCAGCTGGCCAAAGATGTGA 170  
Db 138841 GCAGAGCGGGCAGATACCTGAGTTCAGAGTTCAGAGTCCAGCTGGCCAAAGATGTGA 138782  
QY 171 AACCCCGTCTCTATTAATAATACAAACATTACCTGGGCATGATGGTGGCGCCTGTAAATC 230  
Db 138781 AACCCCGTCTCTATTAATAATACAAACATTACCTGGGCATGATGGTGGCGCCTGTAAATC 138722  
QY 231 CCAGTACTCAGGAGGCTGAGCGAGGAGATCCGCGAGGCTGGCAGATCTGCTGAGCC 290  
Db 138721 CCAGTACTCAGGAGGCTGAGCGAGGAGATCCGCGAGGCTGGCAGATCTGCTGAGCC 138681  
QY 291 TGGGAGGTGGAGGTACAGTAAGCCAGATCATCCAGTATATTCAGCCTGGCGGACAA 350  
Db 138680 TGGGAGGTGGAGGTGAGTGCAGTGAGCGGAGATCCGCGAGGCTGGCAGATCTGCTGAGCC 138621  
QY 351 AGTCAGACCGTAACAAAAAAGAAATTTAAAAAAGAAATTTAGATCAAGATCCAC 409  
Db 138620 AGTCAGACCGTAACAAAAAAGAAATTTAAAAAAGAAATTTAGATCAAGATCCAC 138562

RESULT 7  
ADB87934/C  
ID ADB87934 standard; DNA; 164702 BP.  
XX  
AC ADB87934;  
XX

DT 04-DEC-2003 (first entry)  
XX Human UGT1A1 gene sequence SEQ ID NO:658.  
XX irinotecan; cancer; UGT1A1; cytostatic; topoisomerase I inhibitor;  
XX colorectal cancer; cervical cancer; gastric cancer; lung cancer;  
XX ovarian cancer; pancreatic cancer; malignant glioma;  
XX uridine diphosphate glycosyltransferase1 member A1; gene; ds.  
XX Homo sapiens.  
XX WO2003013536-A2.  
XX 20-FEB-2003.  
XX 23-JUL-2002; 2002WO-EP008217.  
XX 23-JUL-2001; 2001EP-00117608.  
XX 24-MAY-2002; 2002EP-00011710.  
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX Heinrich G, Kerb R;  
XX WPI; 2003-289896/28.  
XX Use of irinotecan to treat cancer patient by determining if patient has  
XX variant alleles of UGT1A1 gene, administering increased/decreased amounts  
XX of irinotecan based on increased/decreased levels of UGT1A1 gene product.  
XX Disclosure; SEQ ID NO 658; 107pp; English.  
XX The invention relates to the novel use of irinotecan to treat a patient  
XX suffering from cancer. This involves determining if the patient has one  
XX or more variant alleles of the UGT1A1 gene, and if the patient has one  
XX or more of such variant alleles, irinotecan is administered in an increased  
XX or decreased amount in comparison to the amount that is administered  
XX without regard to the patient's alleles in the UGT1A1 gene. The invention  
XX has cytostatic activity. A composition of the invention acts as a  
XX topoisomerase I inhibitor. The method is useful for treating a patient,  
XX an animal e.g. mouse or a human, preferably African or Asian, suffering  
XX from cancer such as colorectal, cervical, gastric cancer, lung, ovarian,  
XX pancreatic cancer or malignant glioma. The present sequence is used in  
XX the exemplification of the invention.  
XX Sequence 164702 BP; 52399 A; 32545 C; 31423 G; 48335 T; 0 U; 0 Other;  
XX Query Match 39.4%; Score 197.4; DB 9; Length 164702;  
XX Best Local Similarity 74.9%; Pred. No. 2.5e-38;  
XX Matches 269; Conservative 0; Mismatches 71; Indels 19; Gaps 1;  
QY 51 TATACATTAAAAATAGCCGGTGCAGTGGCTGAGCTGATATCCAGACATTGGGAA 110  
Db 138901 TAAAAAGTAAAAAGAGCGCGGTGTGGTACCCACACCTGTAATCTCTAGCACTTTGGGAG 138842  
QY 111 GCCAAGCGGGCAGAAACACCCGAGTCCAGAGTCCAGGCCAGCTGGCCAAAGATGTGA 170  
Db 138841 GCAGAGCGGGCAGATACCTGAGTTCAGAGTTCAGAGTCCAGCTGGCCAAAGATGTGA 138782  
QY 171 AACCCCGTCTCTATTAATAATACAAACATTACCTGGGCATGATGGTGGCGCCTGTAAATC 230  
Db 138781 AACCCCGTCTCTATTAATAATACAAACATTACCTGGGCATGATGGTGGCGCCTGTAAATC 138722  
QY 231 CCAGTACTCAGGAGGCTGAGCGAGGAGATCCGCGAGGCTGGCAGATCTGCTGAGCC 290  
Db 138721 CCAGTACTCAGGAGGCTGAGCGAGGAGATCCGCGAGGCTGGCAGATCTGCTGAGCC 138681  
QY 291 TGGGAGGTGGAGGTACAGTAAGCCAGATCATCCAGTATATTCAGCCTGGCGGACAA 350  
Db 138680 TGGGAGGTGGAGGTGAGTGCAGTGAGCGGAGATCCGCGAGGCTGGCAGATCTGCTGAGCC 138621  
QY 351 AGTCAGACCGTAACAAAAAAGAAATTTAAAAAAGAAATTTAGATCAAGATCCAC 409  
Db 138620 AGTCAGACCGTAACAAAAAAGAAATTTAAAAAAGAAATTTAGATCAAGATCCAC 138562

Db 138620 AGTCAGACTCTGACTCAAAAAAAAAAAAAAAAAAGTAAAGAAAGAAAGAAAGAAATTAAC 138562

RESULT 8

ADB96917/c

ID ADB96917 standard; DNA; 164702 BP.

XX

AC ADB96917;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human MDR1 related DNA sequence SEQ ID NO:658.

XX

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;

XX KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

XX KW multidrug resistance 1; MDR1; cytosstatic; human; CYP3A5; MRP1; MDR1;

XX KW TOP1; ds.

XX

OS Homo sapiens.

XX

PN WO2003013537-A2.

XX

PD 20-FEB-2003.

XX

PF 23-JUL-2002; 2002WO-EP008218.

XX

PR 23-JUL-2001; 2001EP-00117608.

XX

PR 24-MAY-2002; 2002EP-00011710.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

PI Heinrich G, Kerb R;

XX

DR WPI; 2003-268145/26.

XX

PT New use of irinotecan for preparation of pharmaceutical compositions for

PT PT treating cancer in subject having genome with variant allele comprising

PT PT multidrug resistance 1 polynucleotide.

XX

PS Disclosure; SEQ ID NO 658; 130pp; English.

XX

XX The invention relates to the novel use of irinotecan or its derivative

CC for the preparation of pharmaceutical compositions for treating

CC colorectal, cervical, lung, ovarian or pancreatic cancer, or

CC malignant glioma in a subject having a genome with a variant allele which

CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition

CC of the invention has cytostatic activity. The invention is useful for the

CC preparation of pharmaceutical compositions for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject (preferably human, more preferably African or Asian)

CC or a mouse. The present sequence is used in the exemplification of the

CC invention.

XX

SQ Sequence 164702 BP; 52399 A; 32545 C; 31423 G; 48335 T; 0 U; 0 Other;

Query Match 39.4%; Score 197.4; DB 9; Length 164702;

Best Local Similarity 74.9%; Pred. No. 2.5e-38;

Matches 269; Conservative 0; Mismatches 71; Indels 19; Gaps 1;

QY 51 TATACATTAAAAATAGCCGGTGCAGTGGCTCAGCTGTAATCCAGACATTGGGAA 110

Db 138901 TAAAAAGTAAAGAGCGGGGTGGTAGCCACCTGTATCTTAGCATTGGAG 138842

QY 111 GCCAAGCGGGCAGAACCCGAGGTCAAGAGTCCAGCCAGCTGGCCCAAGATGTGA 170

Db 138841 GCAGAGCGGGCAGATCACCTGAGGTCAAGAGTTCAGACCCAGCTGGCCCAATGTGA 138782

QY 171 AACCCCGTCTCTATTAAAAATACAAACATTACCTGGGCGATGCTGGGCGCTGTATC 230

Db 138781 AACCCCGTCTCTATTAAAAATACAAACATTACCTGGGCGATGCTGGGCGCTGTATC 138722

QY 231 CCAGTACTCAGGCGGTGAGCGAGGAGATCCCGGAGCCTGGCAGATCTGCTGAGCC 290

Db 138721 CCAGCTACTTGGGAGGCTGAGGCAGGAGAT-----TGCTTGAACC 138681

QY 291 TGGGAGGTTGAGGCTACAGTAAGCCAGATCATCGCAGTATCTTACGCTGGCGCAAA 350

Db 138680 TGGGAGGTTGAGGTTGAGTGCAGTGCAGCCAGATCGCCCTTGGCGCGAG 138621

QY 351 AGTCAGACCGTAAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCCAAC 409

Db 138620 AGTGAGACTCTGACTCAAAAAAAAAAAAAAAAAAGTAAAGAAAGAAAGAAATTAAC 138562

RESULT 9

ADB92108/c

ID ADB92108 standard; DNA; 164702 BP.

XX

AC ADB92108;

XX

DT 04-DEC-2003 (first entry)

XX

DE Human MDR1 related DNA sequence SEQ ID NO:658.

XX

XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;

XX KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;

XX KW multidrug resistance 1; MDR1; cytosstatic; human; UGT1A1; MRP1; TOP1; ds.

XX

OS Homo sapiens.

XX

PN WO2003013535-A2.

XX

PD 20-FEB-2003.

XX

PF 23-JUL-2002; 2002WO-EP008220.

XX

PR 23-JUL-2001; 2001EP-00117608.

XX

PR 24-MAY-2002; 2002EP-00011710.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX

PI Heinrich G, Kerb R;

XX

DR WPI; 2003-342400/32.

XX

PT New use of irinotecan for preparation of pharmaceutical compositions for

PT PT treating cancer in subject having genome with variant allele comprising

PT PT multidrug resistance 1 polynucleotide.

XX

PS Disclosure; SEQ ID NO 658; 104pp; English.

XX

XX The invention relates to a novel use of irinotecan or its derivative for

CC the preparation of a pharmaceutical composition for treating colorectal,

CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant

CC glioma in a subject having a genome with a variant allele which comprises

CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the

CC invention has cytostatic activity. The present sequence is used in the

CC exemplification of the invention.

XX

SQ Sequence 164702 BP; 52399 A; 32545 C; 31423 G; 48335 T; 0 U; 0 Other;

Query Match 39.4%; Score 197.4; DB 9; Length 164702;

Best Local Similarity 74.9%; Pred. No. 2.5e-38;

Matches 269; Conservative 0; Mismatches 71; Indels 19; Gaps 1;

QY 51 TATACATTAAAAATAGCCGGTGCAGTGGCTCAGCTGTAATCCAGACATTGGGAA 110

Db 138901 TAAAAAGTAAAGAGCGGGGTGGTAGCCACCTGTATCTTAGCATTGGGAG 138842

QY 111 GCCAAGCGGGCAGAACCCGAGGTCAAGAGTTCAGCCAGCTGGCCCAAGATGTGA 170

Db 138841 GCAGAGCGGGCAGATCACCTGAGGTCAAGAGTTCAGACCCAGCTGGCCCAATGTGA 138782

QY 171 AACCCCGTCTCTATTAAAAATACAAACATTACCTGGGCGATGCTGGGCGCTGTATC 230

Db 138781 AACCCCGTCTCTATTAAAAATACAAACATTACCTGGGCGATGCTGGGCGCTGTATC 138722

QY 231 CCAGCTACTCAGGAGGCTGAGGCGAGGAGGATCCGCGAGGCTGGCAGATCTGCTGAGCC 290  
Db 138721 CCAGCTACTTGGGAGGCTGAGGCGAGGAGAT-----TGCTTGAACC 138691  
QY 291 TGGGAGGCTTGAAGCTACAGTAAGCAAGATCATGCCAGTATCTTCCAGCTGGCGGCACAA 350  
Db 138680 TGGGAGGCTGAGGCTTGCAGTCAGCGGAGATCGCGCACTCCAGCTTGGCGGCAG 138621  
QY 351 AGTGAGACCGTAACAAAAAATTTTAAAAAAGAAATTTAGATCAAGATCCAAC 409  
Db 138620 AGTGAGACTCTGACTCAAAAAAATTTTAAAAAAGAAATTTAGATCAAGATCCAAC 138562

RESULT 10  
ABZ72040/C  
ID ABZ72040 standard; DNA; 207433 BP.

XX AC ABZ72040;  
XX DT 03-APR-2003 (first entry)  
XX DE Gene 216 H19ABAC1098L22 nucleotide sequence SEQ ID NO 5.  
XX KW Human; Gene 216; chromosome 20p13-p12; antiasthmatic; anorectic;  
XX KW obesity; inflammatory; gastrointestinal; gene therapy; vaccine; asthma;  
XX KW obesity; inflammatory bowel disease; promoter; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200178894-A2.  
XX XX 25-OCT-2001.  
XX XX 13-APR-2001; 2001WO-US012245.  
XX PR 13-APR-2000; 2000US-00548797.

XX FA (GENO-) GENOME THERAPEUTICS CORP.  
XX PI Keith T;  
XX WPI; 2001-639428/73.  
XX P-PSDB; ABR00926.

XX PT Isolated genes (Gene 216) from human chromosome 20p13-p12 and the  
XX PT proteins they encode, useful for the prevention, diagnosis and treatment  
XX PT of asthma, obesity and inflammatory bowel disease.

XX PS Example 4; Fig 7; 520pp; English.

XX CC The invention relates to isolated genes (Gene 216) from human chromosome  
XX CC 20p13-p12 and the proteins they encode. The nucleic acids and proteins  
XX CC may be used in the prevention, diagnosis and treatment of diseases  
XX CC associated with inappropriate Gene 216 expression. For example, the  
XX CC nucleic acids (or vectors) and proteins may be used to treat disorders  
XX CC associated with decreased expression by rectifying mutations or deletions  
XX CC in a patient's genome that affect the activity of gene 216 by expressing  
XX CC inactive proteins or to supplement the patients own production of Gene  
XX CC 216 proteins. Additionally, the nucleic acids may be used to produce the  
XX CC secreted gene 216 protein, by inserting the nucleic acids into a host  
XX CC cell and culturing the cell to express the protein. The nucleic acids and  
XX CC complementary sequences may also be used as DNA probes in diagnostic  
XX CC assays to detect and quantify the presence of similar nucleic acid  
XX CC sequences in samples and therefore which patients may be in need of  
XX CC restorative therapy. The Gene 216 protein may also be used as antigens in  
XX CC the production of antibodies against Gene 216 and in assays to identify  
XX CC modulators of Gene 216 expression and activity. The anti-Gene 216  
XX CC antibodies and antagonists may also be used to down regulate expression  
XX CC and activity. The anti-Gene 216 antibodies may also be used as diagnostic  
XX CC agents for detecting the presence of Gene 216 proteins in samples (e.g.  
XX CC by enzyme linked immunosorbent assay or ELISA). Disorders that may be  
XX CC prevented, diagnosed and/or treated by the above methods include, for

CC example asthma, obesity and inflammatory bowel disease. The present  
CC sequence is that of the Gene 216 genomic nucleic acid sequence, promoter  
CC or enhancer  
XX SQ Sequence 207433 BP; 52775 A; 51290 C; 51698 G; 51670 T; 0 U; 0 Other;  
Query Match 39.4%; Score 197.4; DB 5; Length 207433;  
Best Local Similarity 71.2%; Pred. No. 2.7e-38;  
Matches 284; Conservative 0; Mismatches 96; Indels 19; Gaps 1;  
QY 10 AAAACAGGTGTGAGCCACTGCGCCAGCCAGGATTTGCTCTTATACATTAAAAATAGGC 69  
Db 199036 AAAACAGGGGTAAACCCAGCCAGCGGCTAAGGTTAAATTAATCAGCAGATGAGGCC 198977  
QY 70 CGGTGTCAGTGGCTCACGCGCTGTATCCAGCACATTTGGGAAAGCCAGGCGGCGAGAACAC 129  
Db 198976 GGGCACGGTGGCTCACGCGCTGTATCCAGCACATTTGGGAGGCGGCGGCTAATCAC 198917  
QY 130 CCGAGGTGAGAGTCCAAAGGCGAGCGCTGGCCAAAGATGGTGAACCCCGTCTCTATTAAAA 189  
Db 198916 CTGAGGTGAGGCATTTCAAGACGAGCGCTGGTCAACATGGCGGAAACCCCGTCTCTACTAAAA 198857  
QY 190 ATACAAAAATTTACTCTGGGCGCATGATGGTGGGCGCGCTGTAAATCCAGCTACTCAGGAGGCTG 249  
Db 198856 ATACAAAAATTTAGCGCGCGTGGTGGTGTATTCCTGTAAACCCAGCTACTCAGGAAGCTG 198797  
QY 250 AGGCGAGGAGTCCCGGAGCGCTGGCAGATCTGCTGAGCTGGAGGCTTGGAGGTACAG 309  
Db 198796 AGGCAGGAGATC-----GCTTGAACCGGAGGTGGAGGTTCGAG 198756  
QY 310 TTAGCCCAAGATCATGCCAGTATCTTACGCTTGGGCGCAAAAGTGAGACCGCTAACAAAAA 369  
Db 198755 GGAACCAAGATCATGCCAGCGGCTTCCAGCTTGGGCAACAGATGAGATCCATTTCAAA 198696  
QY 370 AAAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAA 408  
Db 198695 AAAAAAGGAAAAAAGAAAGAAATCAGCAGATGAGTGAA 198657

RESULT 11  
ABX74891/C  
ID ABX74891 standard; DNA; 207433 BP.

XX AC ABX74891;  
XX DT 07-APR-2003 (first entry)  
XX DE BAC1098L22 DNA sequence.

XX KW Gene 216; antiasthmatic; antiinflammatory; ss; anorectic;  
XX KW chromosome 20p13-p12; single nucleotide polymorphism; SNP; gene therapy;  
XX KW respiratory disease; asthma; obesity; bronchial hyper-responsiveness;  
XX KW chronic obstructive pulmonary disease;  
XX KW adult respiratory distress syndrome; inflammatory bowel syndrome.

XX OS Synthetic.  
XX PN WO200283077-A2.  
XX PD 24-OCT-2002.  
XX PF 15-APR-2002; 2002WO-US012063.  
XX PR 13-APR-2001; 2001US-00834597.  
XX PR 13-APR-2001; 2001WO-US012245.

XX PA (SCHE ) SCHERING CORP.  
XX PA (GENO-) GENOME THERAPEUTICS CORP.  
XX PI Keith T, Little RD, Van Berdewegh P, Dupuis J, Del Maestro RG;  
XX PI Simon J, Allen K, Pandit S;  
XX XX  
XX WPI; 2003-092960/08.





QY 342 GGGCGCAAAAGTGAGACCGTAACAAAAAATTTAAAAA 385  
DB 1829 AGGCAACAGGCGCAAACTCCATCTCCAAAAAATTTAAAAA 1872

RESULT 13  
ID ADA98848 standard; DNA; 8321 BP.  
AC ADA98848;  
XX  
XX  
XX 20-NOV-2003 (first entry)  
XX Human secreted protein-related DNA sequence #441.  
XX human; secreted protein; cardiovascular disorder; arrhythmia;  
KW atherosclerosis; stroke; endocarditis; congestive heart failure;  
KW rheumatic heart disease; cardiomyopathy; hemorroids; varicose veins;  
KW migraine; thrombosis; neural disorder; immune system disorder;  
KW muscular disorder; reproductive disorder; gastrointestinal disorder;  
KW pulmonary disorder; renal disorder; proliferative disorder; cancer; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO2003004623-A2.  
XX 16-JAN-2003.  
XX  
XX 26-MAR-2002; 2002WO-US009922.  
XX 27-MAR-2001; 2001US-0278650P.  
XX 12-SEP-2001; 2001US-00950082.  
XX 12-SEP-2001; 2001US-00950083.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
XX WPI; 2003-247946/24.  
XX  
XX New human secreted polypeptide and nucleic acid molecules, useful for  
PT diagnosing, preventing, prognosticating or treating cardiovascular  
PT disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or  
PT thrombosis).  
XX  
XX Disclosure; SEQ ID NO 957; 1572pp; English.  
XX  
XX The invention comprises the amino acid and coding sequence of human  
CC secreted proteins. The DNA and protein sequences of the invention are  
CC useful in the treatment of cardiovascular disorders, such as: arrhythmia,  
CC atherosclerosis, stroke, endocarditis, congestive heart failure,  
CC rheumatic heart disease, cardiomyopathy, hemorroids, varicose veins,  
CC migraine, or thrombosis. The DNA and protein sequences may also be used  
CC for treating or preventing: neural disorders, immune system disorders,  
CC muscular disorders, reproductive disorders, gastrointestinal disorders,  
CC pulmonary disorders, renal disorders, proliferative disorders and/or  
CC cancerous diseases. The present DNA sequence is used in the  
CC exemplification of the invention. NOTE: The present sequence is shown on  
XX the WIPO website.  
XX  
XX Sequence 8321 BP; 1704 A; 2261 C; 2254 G; 2102 T; 0 U; 0 Other;  
SQ  
Query Match 39.2%; Score 196.6; DB 7; Length 8321;  
Best Local Similarity 75.2%; Pred. No. 1.7e-38;  
Matches 261; Conservative 0; Mismatches 79; Indels 7; Gaps 1;

QY 43 ATTGCTTTATACATTAATAAATAGGCGGTGAGTGCTCACGCTGTATCCAGCAC 102  
DB 2907 ATGCTTTTAAAAAATAAAGGTTGGGCGCGGTGCTCATGCTGTATCTAGCAC 2966  
QY 103 TTTGGGAACCAAGCGCGGCAACACCCAGGTGAGGATCCAGGATCCAGGCTGGGCAA 162

DB 2967 TTTGGGAGGCTGAGGTGGTGGATCACTTGAGGTGAGGATCCAGGATCCAGGCTGGGCAA 3026  
QY 163 GATGTTGAACCCCGTCTCTATTAATAAATCAACATCTCTGGCATGATGTTGGGCGC 222  
DB 3027 CATGGCGAAACCCCGTCTCTACTATAAATACAAAAATTAGCCAGGCTGTTGGGCGAAGC 3086  
QY 223 CTGTAATCCAGCTACTCAGGAGGCTGAGGAGGATCCGCGAGGCTGGCAGATCTG 282  
DB 3087 CTGTAATCCAGCTCTCAGGAGGCTGAGGAGGATCCGCGAGGCTGGCAGATCTG 3139  
QY 283 CTTGAGCCTGGGAGGTTGAGGCTACAGTACGATGAGGATCCAGGATCTGATCTGAGCTG 342  
DB 3140 CTTGAGCCTGGGAGGTTGAGGATTCAGTACGAGGATCCAGGATCTGATCTGAGCTG 3199  
QY 343 GGGCAAAAGTGAGACCGTAACAAAAAATTTAAAAAAGA 389  
DB 3200 GGGCAAGTGAGACTTTGACTCAGAAAAAATAAAGAAAGAAA 3246

RESULT 14  
ID ADA44471 standard; DNA; 8321 BP.  
XX ADA44471;  
XX  
XX 20-NOV-2003 (first entry)  
XX Human secreted protein DNA SEQ ID 664.  
XX  
XX Gene therapy; human; Antidiabetic; Anorectic; Ophthalmological;  
KW Neuroprotective; Cerebroprotective; Antianemic; ds.  
XX  
XX Homo sapiens.  
XX WO2003000865-A2.  
XX 03-JAN-2003.  
XX  
XX 26-MAR-2002; 2002WO-US009105.  
XX 27-MAR-2001; 2001US-0278650P.  
XX 12-SEP-2001; 2001US-00950082.  
XX 12-SEP-2001; 2001US-00950083.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
XX WPI; 2003-184045/18.  
XX  
XX A human secreted protein and nucleic acids useful for preparing a  
PT diagnostic or pharmaceutical composition for diagnosing or treating  
PT diabetes or conditions related to diabetes, e.g. hyperglycemia, obesity,  
PT retinopathy, neuropathy.  
XX  
XX Disclosure; SEQ ID NO 664; 701pp; English.  
XX  
XX The invention relates to novel genes and their fragments which are useful  
CC for preventing, treating or ameliorating medical conditions e.g. by  
CC protein or gene therapy. The genes are isolated from a range of human  
CC tissues disclosed in the specification. The nucleic acids and proteins  
CC are useful in the diagnosis, treatment and prevention of conditions  
CC related to diabetes, e.g. hyperglycaemia, obesity, retinopathy,  
CC polynuropathy, atherosclerosis, anaemia, stroke, gangrene, impotence,  
CC infection, cataract, renal disorders, or endocrine disorders. The present  
CC sequence was used to illustrate the invention.  
XX  
XX Sequence 8321 BP; 1704 A; 2261 C; 2254 G; 2102 T; 0 U; 0 Other;  
SQ  
Query Match 39.2%; Score 196.6; DB 7; Length 8321;  
Best Local Similarity 75.2%; Pred. No. 1.7e-38;  
Matches 261; Conservative 0; Mismatches 79; Indels 7; Gaps 1;

QY 43 ATTGCTCTTATACATTAATAAATAGGCGGTGACGTGCTCACGCCCTGTATCCAGCAC 102  
DB 2907 ATGCTTTTAAAAAAGGGTGGGCGCGTGGCTCATGCTGTATCTTAGCAC 2966  
QY 103 TTGGGAAGCCAGCGGCGAGAACACCCGAGGTGAGAGTCCAAAGCCAGCCTGGCCAA 162  
DB 2967 TTGGGAGGCTGAGTGGGTGGATCCTTTGAGGTGAGAGTTCAGACCCAGCCTGGCCAA 3026  
QY 163 CATGCTGAACCCCGTCTCTATTAAAAATACAAACATTACTCTGGCATGATGGTGGCGC 222  
DB 3027 CATGGGAACCCGCTCTCTACTTAAATAACAAAATAGCAGCGCTGGTGGCGAAGC 3086  
QY 223 CTGTAATCCAGCTACTCAGAGGCTGAGCAGGAGGATCCGCGAGCCTGGCGAGATCTG 282  
DB 3087 CTGTAATCCAGCTCTCAGAGGCTGAGGAGGCTGAGGAGGCTGAGGCTGAGGCTGAGG 3139  
QY 283 CCTGAGCTGGGAGGTTGAGGCTACAGTAAGCCAAAGATCATGCCAGTATATCTTCCAGCTG 342  
DB 3140 CTGTAATCCAGCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 3199  
QY 343 GCGCAAAAGTGAGACCGTAAACAAAAAATTTAAAAAAGA 389  
DB 3200 GCGCACAGAGTGAGACTTTGACTCAGAAAAAAGAAAAAAGAAA 3246

## RESULT 15

ADC20851  
ID ADC20851 standard; DNA; 8321 BP.  
AC  
XX  
XX  
XX  
DT 18-DEC-2003 (first entry)  
XX  
XX  
DE Human secreted protein-related DNA sequence #269.  
KW gene therapy; human; secreted protein; haemopoietic disorder;  
KW haematological disorder; anaemia; haemophilia; inflammatory disorder;  
KW inflammatory bowel disease; Crohn's disease; neoplastic disease; cancer;  
KW leukaemia; wound healing; epithelial cell proliferation disorder;  
KW immune disorder; autoimmune disorder; asthmatic disorder;  
KW cardiovascular disorder; atherosclerosis; myocarditis;  
KW infectious disease; HIV; AIDS; endocrine disorder; diabetes;  
KW gastrointestinal disorder; duodenal ulcer; gastroenteritis; gene; ds.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200292787-A2.  
XX  
XX  
PD 21-NOV-2002.  
XX  
XX  
PF 26-MAR-2002; 2002WO-US009257.  
XX  
XX  
PR 27-MAR-2001; 2001US-0278650P.  
PR 12-SEP-2001; 2001US-00950082.  
PR 12-SEP-2001; 2001US-00950083.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX  
PI Rosen CA, Ruben SM;  
XX  
XX  
DR WPI; 2003-129287/12.  
XX  
XX  
PT New human secreted proteins and nucleic acid molecules, useful for  
PT preparing a diagnostic or pharmaceutical composition for diagnosing,  
PT preventing or treating hematopoietic or hematologic disorders, e.g.  
PT anemia or hemophilia.  
XX  
XX  
PS Disclosure; SEQ ID NO 805; 1512pp; English.

CC and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease  
CC and Crohn's disease); neoplastic disease (e.g. cancer and leukaemia);  
CC wound healing and disorders of epithelial cell proliferation; immune  
CC disorders (e.g. autoimmune disorders and asthmatic disorders);  
CC cardiovascular disorders (e.g. atherosclerosis and myocarditis);  
CC infectious disease (e.g. HIV/AIDS); endocrine disorders (e.g. diabetes);  
CC and gastrointestinal disorders (e.g. duodenal ulcers and  
CC gastroenteritis). The present DNA sequence was used in the  
XX exemplification of the invention.

XX  
SQ Sequence 8321 BP; 1704 A; 2261 C; 2254 G; 2102 T; 0 U; 0 Other;

Query Match 39.2%; Score 196.6; DB 9; Length 8321;  
Best Local Similarity 75.2%; Pred. No. 1.7e-38;  
Matches 261; Conservative 0; Mismatches 79; Indels 7; Gaps 1;

QY 43 ATTGCTCTTATACATTAATAAATAGGCGGTGACGTGCTCACGCCCTGTATCCAGCAC 102  
DB 2907 ATGCTTTTAAAAAAGGGTGGGCGCGTGGCTCATGCTGTATCTTAGCAC 2966  
QY 103 TTGGGAAGCCAGCGGCGAGAACACCCGAGGTGAGAGTCCAAAGCCAGCCTGGCCAA 162  
DB 2967 TTGGGAGGCTGAGTGGGTGGATCCTTTGAGGTGAGAGTTCAGACCCAGCCTGGCCAA 3026  
QY 163 CATGCTGAACCCCGTCTCTATTAAAAATACAAACATTACTCTGGCATGATGGTGGCGC 222  
DB 3027 CATGGGAACCCGCTCTCTACTTAAATAACAAAATAGCAGCGCTGGTGGCGAAGC 3086  
QY 223 CTGTAATCCAGCTACTCAGAGGCTGAGGAGGATCCGCGAGCCTGGCGAGATCTG 282  
DB 3087 CTGTAATCCAGCTCTCAGAGGCTGAGGAGGCTGAGGAGGCTGAGGCTGAGGCTGAGG 3139  
QY 283 CCTGAGCTGGGAGGTTGAGGCTACAGTAAGCCAAAGATCATGCCAGTATATCTTCCAGCTG 342  
DB 3140 CTGTAATCCAGCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 3199  
QY 343 GCGCAAAAGTGAGACCGTAAACAAAAAATTTAAAAAAGA 389  
DB 3200 GCGCACAGAGTGAGACTTTGACTCAGAAAAAAGAAAAAAGAAA 3246

Search completed: March 4, 2004, 13:06:20  
Job time : 292.428 secs

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 13:06:29 ; Search time 55.5558 Seconds  
(without alignments)  
5004.527 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_5000\_5500

Perfect score: 501

Sequence: 1 ataccataaaacagggtgt.....ggcttcacgcatgggaatgg 501

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	195.6	39.0	98844	US-09-791-211-10	Sequence 10, Appl
C 2	194.4	38.8	87350	US-08-781-891-79	Sequence 79, Appl
C 3	194.4	38.8	87350	US-09-618-166-79	Sequence 79, Appl
C 4	194.4	38.8	87543	US-09-791-211-3	Sequence 3, Appl
C 5	192.6	38.4	111282	US-09-754-250-3	Sequence 3, Appl
C 6	192.4	38.4	70000	US-09-851-896-3	Sequence 3, Appl
C 7	189.6	37.8	55298	US-09-491-356C-1	Sequence 1, Appl
C 8	189	37.7	2841	US-09-526-133A-24	Sequence 24, Appl
C 9	189	37.7	63000	US-09-780-172-18	Sequence 18, Appl
C 10	188.8	37.7	11288	US-08-646-301A-1	Sequence 1, Appl
C 11	188.8	37.7	11288	US-08-481-968A-4	Sequence 4, Appl
C 12	188.8	37.7	11288	US-08-154-712B-4	Sequence 4, Appl
C 13	188.8	37.7	15056	US-09-474-699-10	Sequence 10, Appl
C 14	188	37.5	7676	US-08-451-777A-7	Sequence 7, Appl
C 15	188	37.5	7676	US-08-451-778A-7	Sequence 7, Appl
C 16	188	37.5	7676	US-08-598-208-7	Sequence 7, Appl
C 17	188	37.5	7676	PCT-US95-06743-7	Sequence 7, Appl
C 18	187.2	37.4	319608	US-09-539-333D-1	Sequence 1, Appl
C 19	186.6	37.2	1301	US-09-539-333D-36	Sequence 36, Appl
C 20	186.6	37.2	1386	US-09-539-333D-40	Sequence 40, Appl
C 21	186.2	37.2	112132	US-09-741-150-3	Sequence 3, Appl
C 22	186.2	37.2	112132	US-10-160-187-3	Sequence 3, Appl
C 23	186	37.1	13608	US-09-679-409-1	Sequence 1, Appl
C 24	185.4	37.0	128779	US-09-497-855A-38	Sequence 38, Appl
C 25	185.2	37.0	29629	US-09-729-995-3	Sequence 3, Appl
C 26	185.2	37.0	29629	US-10-135-689-3	Sequence 3, Appl
C 27	184.8	36.9	4823	US-08-457-254-5	Sequence 5, Appl

C 28	184.8	36.9	4823	2	US-08-484-257-20	Sequence 20, Appl
C 29	184.8	36.9	4823	3	US-08-999-927-5	Sequence 5, Appl
C 30	184.8	36.9	4823	4	US-08-461-819-5	Sequence 5, Appl
C 31	184.8	36.9	4823	5	PCT-US94-08806-28	Sequence 28, Appl
C 32	184.8	36.9	4823	5	PCT-US95-01829-5	Sequence 5, Appl
C 33	184.8	36.9	4823	5	PCT-US95-16626-5	Sequence 5, Appl
C 34	184.6	36.8	36651	4	US-09-738-894A-3	Sequence 3, Appl
C 35	184.6	36.8	36651	4	US-09-964-469-3	Sequence 3, Appl
C 36	184.6	36.8	42571	4	US-09-810-347-3	Sequence 3, Appl
C 37	184	36.7	21234	4	US-09-810-671-3	Sequence 3, Appl
C 38	184	36.7	21234	4	US-10-109-854-3	Sequence 3, Appl
C 39	183.6	36.6	1001	4	US-09-671-317-457	Sequence 457, App
C 40	183.6	36.6	1019	4	US-09-177-650-128	Sequence 128, App
C 41	183.4	36.6	55827	4	US-09-813-133A-3	Sequence 3, Appl
C 42	183.2	36.6	21968	4	US-09-851-985-3	Sequence 3, Appl
C 43	183	36.5	3694	3	US-09-232-200-46	Sequence 46, Appl
C 44	183	36.5	3694	4	US-09-232-197-46	Sequence 46, Appl
C 45	183	36.5	3694	4	US-09-232-201-45	Sequence 46, Appl

#### ALIGNMENTS

RESULT 1  
US-09-791-211-10/c  
Sequence 10, Application US/09791211  
Patent No. 6448080  
GENERAL INFORMATION:  
APPLICANT: Donna T. Ward  
TITLE OF INVENTION: ANTIGENSE MODULATION OF WRN EXPRESSION  
FILE REFERENCE: RTS-0205  
CURRENT APPLICATION NUMBER: US/09/791,211  
CURRENT FILING DATE: 2001-02-23  
NUMBER OF SEQ ID NOS: 90  
SEQ ID NO 10  
LENGTH: 98844  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: 24962  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 64383  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 65468  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 65469  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 65470  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 65471  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 87130  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 89049  
OTHER INFORMATION: unknown  
OTHER INFORMATION:  
US-09-791-211-10

Query Match 39.0%; Score 195.6; DB 4; Length 98844;  
Best Local Similarity 71.3%; Pred. No. 1.3e-42;  
Matches 281; Conservative 0; Mismatches 94; Indels 19; Gaps 1;  
QY 66 AGSCCGTGCAGTGGCTACGCTGTAAATCCAGCACTTGGGAAGCCAGCGGCGAGA 125  
||||| |

Db 95727 AGCCAGCACAGTGGCTCACGCTGTAAATCCAGCAGCTTTTGGGATGCCAAGCGGCGGGA 95668  
 QY 126 ACACCCAGGTGAGGATCCAGCCAGCTGGCAGATGGTGAAACCCCGCTCTATT 185  
 Db 95667 TTACTGAGCTGAGAAGTTGAGAGCCAGCTGGCCAAAGGTTGAAACCCCGCTCTACT 95608  
 QY 186 AAAAATACAAATTAATCTGGCATGATGGTGGCGCTGTAAATCCAGCTACTCAGGAG 245  
 Db 95607 AAAAATACAAATTTAGCAGGCGATGGTGGCATGACCTGTAAATCCAGCTACCCAGGAG 95548  
 QY 246 GCTGAGCAGGAGGATCCGGGAGCCCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGGCT 305  
 Db 95547 GCTGAGCAGGAGATC-----GCTGGAACCCAGGAGGAGGCT 95507  
 QY 306 ACAGTAAGCCAAAGATCATGCGAGTATATCTTACGCTGGGCGCACAAAGTGAGACCGTAAACA 365  
 Db 95506 GCACGAGCCAGGATCCCGCATCTACAGCTGGCGCACAGAGCAGATCCATGT 95447  
 QY 366 AAAAAAATAATTTAAAAAAGAAATTTAGATCAGATCCAACTGTAAAAAGTGGCCTA 425  
 Db 95446 CAAAAAATAAATAAATAAATAAATAAATCTTTATTTAAAAACATGTTTTCAAAGAGAAAA 95387  
 QY 426 AACACCAATTAAGAGTTTGGAGTTTATCTGC 459  
 Db 95386 AACTACTCAACAAACCTAGATATTGTAATATCC 95353

RESULT 2  
 US-08-781-891-79  
 ; Sequence 79, Application US/08781891  
 ; Patent No. 6090620  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fu, Ying-Hui  
 ; APPLICANT: Yu, Chang-En  
 ; APPLICANT: Oshima, Junko  
 ; APPLICANT: Mulligan, John T.  
 ; APPLICANT: Schellenberg, Gerald D.  
 ; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO  
 ; WERNER'S SYNDROME  
 ; NUMBER OF SEQUENCES: 209  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED AND BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/781,891  
 ; FILING DATE: 27-DEC-1996  
 ; CLASSIFICATION: 800  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: No. 6090620tenburg Ph.D., Carol  
 ; REGISTRATION NUMBER: 39,317  
 ; REFERENCE/DOCKET NUMBER: 240052.419  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 79:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 87350 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-781-891-79

Query Match 38.8%; Score 194.4; DB 3; Length 87350;  
 Best Local Similarity 75.4%; Pred. No. 2.7e-42;

Matches 263; Conservative 0; Mismatches 67; Indels 19; Gaps 1;  
 QY 57 TTAATAATAGCCGCTGCAGTGGCTCACGCTGTAAATCCAGCAGCTTTTGGGAGCCAAAG 116  
 Db 41975 TTTTAAAAAGAGCTGGGCATGGTGGCTTAAATCCAGCAGCTTTGGAGCCGAG 42034  
 QY 117 GCAGGCAACACACCCGAGGTGAGGAGTCCAGGCTCCAGGCTGGCCAGAGATGGTGAACCCC 176  
 Db 42035 GCAGGCAATCACTTGGGTGAGGTCAAGACAGCCTGGCCCAACATGATGAATCC 42094  
 QY 177 GTCTCTATTAATAATACAAATTAACCTGGGCATGATGGTGGCGCTGTAAATCCAGCT 236  
 Db 42095 GTTCTTACTTAAAGTACAAAAATTAGCTGGGCGTGGTGGGTGCTGTAAATCCAGCT 42154  
 QY 237 ACTCAGGAGGCTGAGGCGAGGAGTCCGCGAGCCTGGCAGATCTGCTGAGCCTGGGAG 296  
 Db 42155 ATTGAGGAGGCTGAGGCGAGGAGAT-----TGCTTGAACCCAGGAG 42195  
 QY 297 GTTGGGCTCAGTAAGCCAGATCATGCCAGTATATCTTACGCTGGCGCAAGAGTGAG 356  
 Db 42196 GTGGAGGTTGAGTGAGTCAAGATTTGTGCCACTGCCTTCAGCCTGGGAGACAGGCGAG 42255  
 QY 357 ACCGTAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 405  
 Db 42256 ACTCTGTCTCNAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 42304

RESULT 3  
 US-09-618-166-79  
 ; Sequence 79, Application US/09618166  
 ; Patent No. 6583112  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fu, Ying-Hui  
 ; APPLICANT: Yu, Chang-En  
 ; APPLICANT: Oshima, Junko  
 ; APPLICANT: Mulligan, John T.  
 ; APPLICANT: Schellenberg, Gerald D.  
 ; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO  
 ; WERNER'S SYNDROME  
 ; NUMBER OF SEQUENCES: 209  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed Intellectual Property Law Group  
 ; STREET: 701 Fifth Avenue, Suite 6300  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/618,166  
 ; FILING DATE: 17-Jul-2000  
 ; CLASSIFICATION: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mcmasters, David D.  
 ; REGISTRATION NUMBER: 33,963  
 ; REFERENCE/DOCKET NUMBER: 240052.419C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 79:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 87350 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-09-618-166-79

Query Match 38.8%; Score 194.4; DB 4; Length 87350;



OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 63290  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 66614  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 68660  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 68697  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 68718  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 68733  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 68739  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 69785  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 79134  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 79198  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 86336  
OTHER INFORMATION: unknown  
OTHER INFORMATION:  
US-09-791-211-3

Query Match 38.8%; Score 194.4; DB 4; Length 87543;  
Best Local Similarity 75.4%; Pred. No. 2,7e-42;  
Matches 263; Conservative 0; Mismatches 67; Indels 19; Gaps 1;  
QY 57 TTTAAAAATAGCCGGTGCAGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAAGCCAAAG 116  
Db 42168 TTTTAAAAAGCTGGCATGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAGCCGAG 42227  
QY 117 GCGGCGAGAACCCCGAGTCAAGAGTCAAGGCGAGCGCTGGCCCAAGATGTGAAACCCC 176  
Db 42228 GCAGGCGAGTCACTTCAAGTCAAGAGTTCAGACCCAGCGCTGGCCCAACATGATGAAACTCC 42287  
QY 177 GTCTCTATTAAAAATACAAACATTACCTGGGCGATGATGTGGGCGCTGTAATCCAGCT 236  
Db 42288 GTTCTTACTTAAAGTACAAAAATTAGCTGGGCGTGTGTGGTGCCCTGTAATCCAGCT 42347  
QY 237 ACTCAGGAGGCTGAGGCGAGGAGTCCGCGGAGCGCTGGCAGATCTGCTGAGCTGGGAG 296  
Db 42348 ATTCAGGAGGCTGAGGCGAGGAGT-----TGCTTGAACCCAGGAG 42388  
QY 297 GTTGGAGTACAGTAAAGCAAGATCATGCCAGTATCTCAGCTGGGCGGCAAGAGTGGAG 356  
Db 42389 GTGGAGGTGGAGTGAAGTCAAGATTTGCCCTCAGCTTCCAGCTGGGAGACAGAGCGAG 42448  
QY 357 ACCGTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 405  
Db 42449 ACTCTGTCTCNAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 42497

RESULT 5  
US-09-754-250-3/c  
Sequence 3, Application US/09754250  
Patent No. 6376225  
GENERAL INFORMATION:  
APPLICANT: WEI, Ming-Hui et al  
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN  
TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF  
FILE REFERENCE: CL001063  
CURRENT APPLICATION NUMBER: US/09/754,250  
CURRENT FILING DATE: 2001-01-05  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 111282  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)\_(111282)  
OTHER INFORMATION: n = A, T, C or G  
US-09-754-250-3

Query Match 38.4%; Score 192.6; DB 4; Length 111282;  
Best Local Similarity 76.7%; Pred. No. 8.9e-42;  
Matches 257; Conservative 0; Mismatches 59; Indels 19; Gaps 1;  
QY 67 GCGCGTGCAGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAAGCCAAAGCGGCGAGAA 126  
Db 18615 GCCAGGTGCAGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAGGTCAAGCGCGCAGAT 18556  
QY 127 CACCCGAGTCAAGAGTCCAAAGCCAGCGCTGGCCCAAGATGTGAAACCCCGTCTCTATTA 186  
Db 18555 CACCTGAGGCGAGGAGTTCGAGACCAGCGCTGGCCCAATATGTGAAACCCCGTCTCTACCA 18496  
QY 187 AATAACAAACATTACCTGGGCGATGATGGTGGGCGCTGTAATCCAGCTACTCAGGAGG 246  
Db 18495 AAGTACAAAAATTAGCGGCGCATGCTGGCAGTGCCTGTGATCCAGCTACTTGGGAGG 18436  
QY 247 CTGAGGCGAGGATCCGCGGAGCGCTGGCAGATCTGCCGTGGAGCTTGGAGGTTGAGGCTA 306  
Db 18435 CTGAGGCGAGCAATC-----ACTTGAACCCAGGAGTGGAGGTTG 18395  
QY 307 CAGTAAGCCAGATCATGCCAGTATCTCAGCTGGGCGCAAAAGTGAACCGTAAACAA 366  
Db 18394 CAGTGAGAAGATGCACCTCAGCTCCAGCTGGGCGACAGAGCAAGACTGTCTCAA 18335  
QY 367 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 401  
Db 18334 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 18300

RESULT 6  
US-09-851-896-3/c  
Sequence 3, Application US/09851896  
Patent No. 6410325  
GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett  
APPLICANT: Susan M. Freier  
APPLICANT: Andrew T. Watt  
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPE)  
TITLE OF INVENTION: EXPRESSION  
FILE REFERENCE: RTS-0220  
CURRENT APPLICATION NUMBER: US/09/851,896  
CURRENT FILING DATE: 2001-05-08  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 3  
LENGTH: 70000  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
US-09-851-896-3

Query Match 38.4%; Score 192.4; DB 4; Length 70000;  
Best Local Similarity 77.3%; Pred. No. 8.4e-42;  
Matches 255; Conservative 0; Mismatches 56; Indels 19; Gaps 1;  
QY 67 GCGCGTGCAGTGGCTCAGCGCTGTAATCCAGACACTTTGGGAAGCCAAAGCGGCGAGAA 126



Db 1407 TTAAGACTGAACACAGGCGCTAGTGGCTCAGCGCTGTAAATCCAGCAGCTTTGGGA 1348  
QY 110 AGCCAGGCGGCGAGAACACCCGAGGTCAGAGTCCAGGCGCAGCTGGCCAGATGGTG 169  
Db 1347 GCGGAGGCGGCTGATCACCTGAGTCAAGAAATCCAGACAGCTAGCCACACGCG 1288  
QY 170 AAACCCCTCTCTATTAATAATACAAATTAACCTGGGCGATGAGTGGGCGCTGTAAAT 229  
Db 1287 AAACCCCTCTCTATTAATAATACAAATTAACCTGGGCGATGAGTGGGCGCTGTAAAT 1228  
QY 230 CCAGCTACTCAGGAGGCTGAGGCGAGGAGTCCGCGGAGCTGGCAGATCTGCTGAGC 289  
Db 1227 CCAGCTACTCAGGAGGCTGAGGCGAGGAGTCCGCGGAGCTGGCAGATCTGCTGAGC 1187  
QY 290 CTGGAGGTTGAGGCTCAGTAAAGCAAGTATCCAGTATCTTCAAGCTGGCGGACCA 349  
Db 1186 CTGGAGGTTGAGGCTCAGTAAAGCAAGTATCCAGTATCTTCAAGCTGGCGGACCA 1127  
QY 350 AAGTCAGACCGTAAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCC 406  
Db 1126 GAGCAGACTCCGCTCAGAAAAAATTAACAAAAAATTAACAAAAAATTAACAAAAA 1070

RESULT 9  
US-09-780-172-18/c  
; Sequence 18, Application US/09780172  
; Patent No. 6607916  
; GENERAL INFORMATION:  
; APPLICANT: Robert McKay  
; APPLICANT: Susan M. Freier  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION  
; FILE REFERENCE: RTS-0159  
; CURRENT APPLICATION NUMBER: US/09/780,172  
; CURRENT FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 96  
; SEQ ID NO 18  
; LENGTH: 63000  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-09-780-172-18

Query Match 37.7%; Score 189; DB 4; Length 63000;  
Best Local Similarity 74.1%; Pred. No. 6.7e-41;  
Matches 275; Conservative 0; Mismatches 75; Indels 21; Gaps 2;  
QY 52 ATACATTAATAATAGGCGGTCAGTGGCTCAGCGCTGTAAATCCAGCAGCTTTGGGAAG 111  
Db 19563 AAATTTTAAATCGGCTGGCGCAGTGGCTCAGCGCTGTAAATCCAGCAGCTGTGGAGG 19504  
QY 112 CCAAGCGGCGAGAACACCGGAGTCCAGAGTCCAGGCGAGCTGGCCAGATGGTGA 171  
Db 19503 CTGAGCGGCGGATCA--CGAGTCAAGATCGAGCCAGCTGGCTTAAATGGTGA 19446  
QY 172 ACCCGTCTCTATTAAAAATACAAATTAACCTGGGCGATGAGTGGGCGCTGTAATCC 231  
Db 19445 ACCCGTCTCTATTAAAAATACAAATTAAGTGGGCGCTGGGCGCTGTAATCC 19386  
QY 232 CAGCTACTCAGGAGGCTGAGGCGAGGATCCGCGAGCTGGCAGATCTGCTGAGCT 291  
Db 19385 CAGCTACTCAGGAGGCTGAGGCGAGGAT--GGCGTGAACCC 19345  
QY 292 GCGAGGTTGAGGCTACAGTAAAGCAAGATCATGCCAGTATCTTCAAGCTGGCGGACAA 351  
Db 19344 GCGAGGCGAGGCTTGGCTGAGCGGAGATCGTCCACTGCTCAGCTGGCGGACAGA 19285  
QY 352 GTGAGCCGTAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCACTG 411  
Db 19284 GCGAGCTCCATCTCAAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCACTG 19225  
QY 412 TAAAGTGGC 422

Db 19224 TCACAGTGGC 19214  
RESULT 10  
US-08-646-301A-1  
; Sequence 1, Application US/08646301A  
; Patent No. 6194211  
; GENERAL INFORMATION:  
; APPLICANT: Richards, Cynthia Ann  
; APPLICANT: Huber, Brian E.  
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic  
; Patent No. 6194211  
; TITLE OF INVENTION: Antigen for Expression Targeting  
; FILE REFERENCE: PB1508USW  
; CURRENT APPLICATION NUMBER: US/08/646,301A  
; CURRENT FILING DATE: 1996-05-16  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 11288  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-08-646-301A-1

Query Match 37.7%; Score 188.8; DB 3; Length 11288;  
Best Local Similarity 73.0%; Pred. No. 3.9e-41;  
Matches 279; Conservative 0; Mismatches 82; Indels 21; Gaps 2;  
QY 60 AAAATAGGCGGTCAGTGGCTCAGCGCTGTAAATCCAGCAGCTTTGGGAAGCCAGGCG 119  
Db 529 AAATCAGCGCGCGGCTGGCTCAGCGCTGTAAATCCAGCAGCTTTAGAAAGCTGAGGTG 588  
QY 120 GGAGAACACCCGAGTCCAGGAGTCCAGGCGAGCTGGCAGATGGTGAACCCCGTC 179  
Db 589 GGCAGATTAATCTGAGTCCAGGAGTTCAGACCCCTGGCCCAATATGGTGAACCCCGTC 648  
QY 180 TCTATTAAAAATACAAATTAACCTGGGCGATGATGGGCGCTGTAAATCCAGCTACT 239  
Db 649 TCTATTAAAAATACAAATTAACCTGGGCGATGATGGGCGCTGTAAATCCAGCTACT 708  
QY 240 CAGGAGCTCAGGCGAGGATCCGCGAGCTGGCAGATCTGCTGAGCTGGGAGTT 299  
Db 709 CCGGAGGCTCAGGCTGGCAAT-----TGCCTGGACCCAGGAAGCA 749  
QY 300 GAGGCTACATAGCCAGGATCATGCGAGTATCTTCAAGCTGGGCGACAAAGTGA-- 357  
Db 750 GAGGCTCAGTGGCGAGGATTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 809  
QY 358 CCCTAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCACTGTGTAATAA 417  
Db 810 CTGTAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCACTGTGTAATAA 869  
QY 418 GTGCGCTAAACACCACTTAA 439  
Db 870 ATCTCTTTGGGTTAACAAAAA 891

RESULT 11  
US-08-481-968A-4  
; Sequence 4, Application US/08481968A  
; Patent No. 6300490  
; GENERAL INFORMATION:  
; APPLICANT: Huber, Brian  
; APPLICANT: Richards, Cynthia  
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (C  
; FILE REFERENCE: PB1087US4  
; CURRENT APPLICATION NUMBER: US/08/481,968A  
; CURRENT FILING DATE: 1998-06-07  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 11288



; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-08-481-968A-4

Query Match 37.7%; Score 188.8; DB 4; Length 11288;  
 Best Local Similarity 73.0%; Pred. No. 3.9e-41;  
 Matches 279; Conservative 0; Mismatches 82; Indels 21; Gaps 2;

QY	60	AAAAATAGCGCGGTGCAAGTGGCTCACGCCCTGTAAATCCAGACACTTTGGGAAGCCCAAGCGC	119
DB	529	AAAATCAGCCGGCGCGGTGGCTCACGCCCTGTAAATCCAGACACTTTAGAAAGGCTGAGGTG	588
QY	120	GGCAGAAACACCCGAGGTTCAGAGTCCAAAGCCAGCCCTGGCCCAAGATGGTGAACCCCGTC	179
DB	589	GGCAGATTACTTGAGGTTCAGAGTTCAAGACCCCTGGCCCAATATGGTGAACCCCGGC	648
QY	180	TCATNTAAAAATACAAACATTACTCTGGGCATGATGTGTGGCGCTGTAATCCCAGCTACT	239
DB	649	TCTACTAAAAATACAAAAATAGCTGGGCATGTGTGTGGCGCTGTAATCCCAGCTACT	708
QY	240	CAGGAGCTCAGCAGCAGAGATCCGGGAGCCTGGCAGATCTGCCTAGCCTGGGAGTT	299
DB	709	CGGAGGCTCAGGCTGGACAAAT-----TGCCTGGACCCAGGAAGCA	749
QY	300	GAGGCTACAGTAAAGCCAAAGATCATGCCCAGTATACTTCAGGCTGGCGGCACAAAGTGAGA--	357
DB	750	GAGGTTCAGTGAGCCAAAGATGTGCCACTGCCTCCAGCTTGGGCAACAGAGCCAGACT	809
QY	358	CCGTACAAAAAATAAAAAATTTTAAAAAAGAAATTTAGATCAAGATCCAACCTGTAAAAA	417
DB	810	CTCTAAAAAATAAAAAAATAAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGTATATAA	869
QY	418	GTGGCCTAAACACCCACATTTAA 439	
DB	870	ATCTCTTGGTTAAACAAAAA 891	

RESULT 12  
 US-08-154-712B-4  
 ; Sequence 4, Application US/08154712B  
 ; Patent No. 6337209  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Huber, Brian  
 ; APPLICANT: Richards, Cynthia  
 ; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen Reg  
 ; TITLE OF INVENTION: Sequence  
 ; FILE REFERENCE: PB1087US3  
 ; CURRENT APPLICATION NUMBER: US/08/154,712B  
 ; CURRENT FILING DATE: 1993-11-19  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 11288  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-08-154-712B-4

Query Match 37.7%; Score 188.8; DB 4; Length 11288;  
 Best Local Similarity 73.0%; Pred. No. 3.9e-41;  
 Matches 279; Conservative 0; Mismatches 82; Indels 21; Gaps 2;

QY	60	AAAAATAGCGCGGTGCAAGTGGCTCACGCCCTGTAAATCCAGACACTTTGGGAAGCCCAAGCGC	119
DB	529	AAAATCAGCCGGCGCGGTGGCTCACGCCCTGTAAATCCAGACACTTTAGAAAGGCTGAGGTG	588
QY	120	GGCAGAAACACCCGAGGTTCAGAGTCCAAAGCCAGCCCTGGCCCAAGATGGTGAACCCCGTC	179
DB	589	GGCAGATTACTTGAGGTTCAGAGTTCAAGACCCCTGGCCCAATATGGTGAACCCCGGC	648
QY	180	TCATNTAAAAATACAAACATTACTCTGGGCATGATGTGTGGCGCTGTAATCCCAGCTACT	239
DB	649	TCTACTAAAAATACAAAAATAGCTGGGCATGTGTGTGGCGCTGTAATCCCAGCTACT	708



Search completed: March 4, 2004, 16:42:01  
Job time : 59.5558 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 15:00:30 ; Search time 244.179 Seconds  
(without alignments)  
7504.213 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_5000\_5500  
Perfect score: 501  
Sequence: 1 ataccataaaacagggtgt.....ggtcttcagcatgggaatgg 501

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: /cgn2\_6/ptodata/2/pubna/US07\_PUBCOMB.seq.\*
  - 2: /cgn2\_6/ptodata/2/pubna/PCT\_NEW\_PUB.seq.\*
  - 3: /cgn2\_6/ptodata/2/pubna/US06\_NEW\_PUB.seq.\*
  - 4: /cgn2\_6/ptodata/2/pubna/US06\_PUBCOMB.seq.\*
  - 5: /cgn2\_6/ptodata/2/pubna/US07\_NEW\_PUB.seq.\*
  - 6: /cgn2\_6/ptodata/2/pubna/PCTUS\_PUBCOMB.seq.\*
  - 7: /cgn2\_6/ptodata/2/pubna/US08\_NEW\_PUB.seq.\*
  - 8: /cgn2\_6/ptodata/2/pubna/US08\_PUBCOMB.seq.\*
  - 9: /cgn2\_6/ptodata/2/pubna/US09A\_PUBCOMB.seq.\*
  - 10: /cgn2\_6/ptodata/2/pubna/US09B\_PUBCOMB.seq.\*
  - 11: /cgn2\_6/ptodata/2/pubna/US09C\_PUBCOMB.seq.\*
  - 12: /cgn2\_6/ptodata/2/pubna/US09\_NEW\_PUB.seq.\*
  - 13: /cgn2\_6/ptodata/2/pubna/US10A\_PUBCOMB.seq.\*
  - 14: /cgn2\_6/ptodata/2/pubna/US10B\_PUBCOMB.seq.\*
  - 15: /cgn2\_6/ptodata/2/pubna/US10C\_PUBCOMB.seq.\*
  - 16: /cgn2\_6/ptodata/2/pubna/US10\_NEW\_PUB.seq.\*
  - 17: /cgn2\_6/ptodata/2/pubna/US60\_NEW\_PUB.seq.\*
  - 18: /cgn2\_6/ptodata/2/pubna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	11204	9	US-09-966-880A-35 Sequence 35, Appl
2	283.4	56.6	6564	9	US-09-966-880A-10 Sequence 10, Appl
3	204.4	40.8	3010	15	US-10-108-260A-1125 Sequence 1125, Ap
c 4	198.8	39.7	669	15	US-10-027-632-284984 Sequence 284984,
c 5	197.4	39.4	207433	15	US-10-277-216-5 Sequence 5, Appli
c 6	197.4	39.4	207433	16	US-10-126-022-5 Sequence 5, Appli
7	197	39.3	1138	15	US-10-027-632-119235 Sequence 119235,
8	197	39.3	1138	15	US-10-027-632-119236 Sequence 119236,
9	197	39.3	1138	15	US-10-027-632-119237 Sequence 119237,
10	196.2	39.2	1746	15	US-10-027-632-187984 Sequence 187984,
c 11	196.2	39.2	1746	10	US-09-764-891-6056 Sequence 6056, Ap
c 12	196.2	39.2	1746	10	US-09-764-891-6057 Sequence 6057, Ap
c 13	196.2	39.2	250000	14	US-10-225-810-26 Sequence 26, Appl
c 14	195.2	39.0	70000	16	US-10-210-723-13 Sequence 13, Appl
15	195	38.9	821	15	US-10-027-632-169387 Sequence 169387,

ALIGNMENTS

RESULT 1

US-09-966-880A-35  
; Sequence 35, Application US/09966880A  
; Patent No. US20020164743A1  
; GENERAL INFORMATION:  
; APPLICANT: Honjo, Tasuku  
; APPLICANT: Muramatsu, Masamichi  
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE  
; FILE REFERENCE: 06501-088001  
; CURRENT APPLICATION NUMBER: US/09966,880A  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: PCT/JP00/01918  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: JP 11-371382  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: JP 11-178999  
; PRIOR FILING DATE: 1999-06-24  
; PRIOR APPLICATION NUMBER: JP 11-87192  
; PRIOR FILING DATE: 1999-03-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 11204  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-966-880A-35

Query Match 100.0%; Score 501; DB 9; Length 11204;  
Best Local Similarity 100.0%; Pred. No. 1.9e-122;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ATACATTAATAAACAGGTGTGAGCCACTGCGCCAGCAGGTATTGCTCTTATACATTAA 60  
Db 5000 ATACATTAATAAACAGGTGTGAGCCACTGCGCCAGCAGGTATTGCTCTTATACATTAA 5059  
  
Qy 61 AAAATAGCGCGTTCAGTGTCTCAGCCTTAATCCAGACACTTTGGGAAGCAAGCGG 120  
Db 5060 AAAATAGCGCGTTCAGTGTCTCAGCCTTAATCCAGACACTTTGGGAAGCAAGCGG 5119

Result No.	Score	Query Match	Length	ID	Description
1	501	100.0	11204	9	US-09-966-880A-35 Sequence 35, Appl
2	283.4	56.6	6564	9	US-09-966-880A-10 Sequence 10, Appl
3	204.4	40.8	3010	15	US-10-108-260A-1125 Sequence 1125, Ap
c 4	198.8	39.7	669	15	US-10-027-632-284984 Sequence 284984,
c 5	197.4	39.4	207433	15	US-10-277-216-5 Sequence 5, Appli
c 6	197.4	39.4	207433	16	US-10-126-022-5 Sequence 5, Appli
7	197	39.3	1138	15	US-10-027-632-119235 Sequence 119235,
8	197	39.3	1138	15	US-10-027-632-119236 Sequence 119236,
9	197	39.3	1138	15	US-10-027-632-119237 Sequence 119237,
10	196.2	39.2	1746	15	US-10-027-632-187984 Sequence 187984,
c 11	196.2	39.2	1746	10	US-09-764-891-6056 Sequence 6056, Ap
c 12	196.2	39.2	1746	10	US-09-764-891-6057 Sequence 6057, Ap
c 13	196.2	39.2	250000	14	US-10-225-810-26 Sequence 26, Appl
c 14	195.2	39.0	70000	16	US-10-210-723-13 Sequence 13, Appl
15	195	38.9	821	15	US-10-027-632-169387 Sequence 169387,

QY 121 GCAGAACACCCGAGGTCCAGAGTCCAGGCCAGCCTGGCCCAAGATGGTGAACCCCGTCT 180  
 Db 5120 GCAGAACACCCGAGGTCCAGAGTCCAGGCCAGCCTGGCCCAAGATGGTGAACCCCGTCT 5179  
 QY 181 CTATTAAATACAAACATTACTGGCATGTGGCGCTGTATCCAGTACTC 240  
 Db 5180 CTATTAAATACAAACATTACTGGCATGTGGCGCTGTATCCAGTACTC 5239  
 QY 241 AGGAGCTCAGGCGAGGATCCGGGAGCCTGGCAGATCTGCTGAGCCTGGGAGGTTG 300  
 Db 5240 AGGAGCTCAGGCGAGGATCCGGGAGCCTGGCAGATCTGCTGAGCCTGGGAGGTTG 5299  
 QY 301 AGGCTACAGTACCAAGATCATGCCAGTACTTCCAGTCTGGGCGACAAAGTGAGCCG 360  
 Db 5300 AGGCTACAGTACCAAGATCATGCCAGTACTTCCAGTCTGGGCGACAAAGTGAGCCG 5359  
 QY 361 TAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 420  
 Db 5360 TAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5419  
 QY 421 GCTTAAACACCAATTAAAGATTTGGAGTTTGGAGTTTATTTCTGAGGCGAAGAACCATCAGG 480  
 Db 5420 GCTTAAACACCAATTAAAGATTTGGAGTTTATTTCTGAGGCGAAGAACCATCAGG 5479  
 QY 481 GGGTCTTCAGCATGGGAATGG 501  
 Db 5480 GGGTCTTCAGCATGGGAATGG 5500

RESULT 2

US-09-966-880A-10  
 ; Sequence 10, Application US/09966880A  
 ; Patent No. US2002016473A1

; GENERAL INFORMATION:

; APPLICANT: Honjo, Tasuku  
 ; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE  
 ; FILE REFERENCE: 06501-088001  
 ; CURRENT APPLICATION NUMBER: US/09/966,880A  
 ; CURRENT FILING DATE: 2001-09-28  
 ; PRIOR APPLICATION NUMBER: PCT/JP00/01918  
 ; PRIOR FILING DATE: 2000-03-28  
 ; PRIOR APPLICATION NUMBER: JP 11-371382  
 ; PRIOR FILING DATE: 1999-12-27  
 ; PRIOR APPLICATION NUMBER: JP 11-178999  
 ; PRIOR FILING DATE: 1999-06-24  
 ; PRIOR APPLICATION NUMBER: JP 11-87192  
 ; PRIOR FILING DATE: 1999-03-29  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 6564  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-966-880A-10

Query Match 56.6%; Score 283.4; DB 9; Length 6564;  
 Best Local Similarity 99.6%; Pred. No. 8.9e-85;  
 Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 217 GGGGCGCTGTAATCCCACTACTCAGGAGGCTCAGGAGGATCCGGGAGCCTGGCA 276  
 Db 1 GGGGCGCTGTAATCCCACTACTCAGGAGGCTCAGGAGGATCCGGGAGCCTGGCA 60  
 QY 277 GATCTGCTGAGCCTGGGAGGTTGAGGCTACAGTACGATCCAGATCATGCCAGTATCTTC 336  
 Db 61 GATCTGCTGAGCCTGGGAGGTTGAGGCTACAGTACGATCCAGATCATGCCAGTATCTTC 120  
 QY 337 AGCTTGGCGCAAGTGAAGCCGTACAAAAAATAAATAAATAAATAAATAAATAAATAA 396  
 Db 121 AGCTTGGCGCAAGTGAAGCCGTACAAAAAATAAATAAATAAATAAATAAATAAATAA 180

QY 397 ATCAAGATCAACTGTAAAAAGTGGCTTAAACACACACATTAAGAGTTTGGAGTTATTC 456  
 Db 181 ATCAAGATCAACTGTAAAAAGTGGCTTAAACACACATTAAGAGTTTGGAGTTATTC 240  
 QY 457 TGCAGGCAGAGAGAACCACTCAGGGGCTCTTCAGCATGGGAATGG 501  
 Db 241 TGCAGGCAGAGAGAACCACTCAGGGGCTCTTCAGCATGGGAATGG 285

RESULT 3

US-10-108-260A-1125  
 ; Sequence 1125, Application US/10108260A  
 ; Publication No. US20040005560A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE  
 ; TITLE OF INVENTION: No. US20040005560A1s1 full length cDNA  
 ; FILE REFERENCE: HI-A0106  
 ; CURRENT APPLICATION NUMBER: US/10/108,260A  
 ; CURRENT FILING DATE: 2002-03-27  
 ; NUMBER OF SEQ ID NOS: 5458  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1125  
 ; LENGTH: 3010  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-108-260A-1125

Query Match 40.8%; Score 204.4; DB 15; Length 3010;  
 Best Local Similarity 75.3%; Pred. No. 6e-44;  
 Matches 274; Conservative 0; Mismatches 76; Indels 14; Gaps 1;

QY 41 GTATTGCTCTTATACATTAATAAATAAGGCGGTGAGTGGCTCAGCCTGTATCCAGC 100  
 Db 1749 GTTTCTGTCTTAAACGAAAGATTTCGCCAGGTGCGAGTGGCTCATGCCGTATCCAGC 1808  
 QY 101 ACTTTGGGAAGCCAGGCGGCGAGAACACCCGAGGTCCAGAGTCCAAAGCCAGCCTGGCC 160  
 Db 1809 ACTTTGGGAGCGCGAGCGAGTCACTGAGTCCAGAGTTCGAGACCCAGCCTGGCC 1868  
 QY 161 AAGATGTGAAACCCCGTCTCTATTAATAAATAAATAAATAAATAAATAAATAAATAA 220  
 Db 1869 AACATGTGAAACTCCGCTCTCTACTAAAAATAAAAAATAGCTGGGTATGGTGGCAGGT 1928  
 QY 221 GCCTGTAATCCAGTACTCAGGAGGCTGAGGCGAGGATCCGCGAGGCTCGCAGATC 280  
 Db 1929 GCCTGTAATCCAGTACTCAGGAGGCTGAGGCGAGGATAGCTTGAACACGGAG-- 1985  
 QY 281 TGCCTGAGCCTGGGAGGTTGAGGCTACAGTAAGCCAGATCATGCCAGTATATCTCAGCC 340  
 Db 1986 -----GCGAGCGGAGGTTGCGAGTGGCCGAGATAGGCCACTGCACCTCCAGCC 2034  
 QY 341 TGGCGGACAAAGTGAAGCCCTTAAACAAAAAATAAATAAATAAATAAATAAATAAATAA 400  
 Db 2035 TGAGCAACAGAGTGAGACTCCATCTAAAAATAAATAAATAAATAAATAAATAAATAA 2094  
 QY 401 AGAT 404  
 Db 2095 AAAT 2098

RESULT 4

US-10-027-632-284984/c  
 ; Sequence 284984, Application US/10027632  
 ; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 284984  
LENGTH: 669  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-284984

Query Match 39.7%; Score 198.8; DB 15; Length 669;  
Best Local Similarity 76.0%; Pred. No. 9.5e-43;  
Matches 260; Conservative 0; Mismatches 77; Indels 5; Gaps 1;

QY 79 GCTCAGCCTGTATCCAGCACTTTGGGAAGCCAGCGGGGCGAAGACCCCGAGGTCA 138  
DB 464 GCTCAGCCTGTATCCAGCACTTTGGGAAGCCAGCGGGGCGAAGACCCCGAGGTCA 405  
QY 139 GGAGTCCAAAGCGCAGCTGGCCCAAGATGGTGAACCCCGTCTCTATTAAAAATCAAAACA 198  
DB 404 GGAGTTTGAGACCAAGCTGGCCCAACATGGTGAACCCCGTCTCTATTAAAAATCAAAACA 345  
QY 199 TTACTGGCGATGATGGTGGGCGCTGTAAATCCCAAGTACTCAGAGGCTGAGCGAGAG 258  
DB 344 TGAGCGAGCATGGTGGGCGGCGGCGGCTAGTCCAGCTACTCGGAAGTCTGAGGCGAG 285  
QY 259 GATCGCGAGGCTGGCAGAG-----TCTGCTTGGAGCTGGAGGTTGAGGCTACAGTAAG 313  
DB 284 ATCTTGTCTGCTGGTGAAGCCCGAGCCCTGAACCCAGGAGCGGAGGTTGAGTAAG 225  
QY 314 CCAAGATCATGCGATATCTTACGCTGGGCGCAAAAGTGAAGCCGTAACAAAAA 373  
DB 224 CCAAGATCTGCGCACTGCACTCCAGCTGGGAGCAAAAGTGAAGTCAAGTCTCAAAAAA 165  
QY 374 AAAATTTAAAAAAGAAATTTAGATCAAGATCCCACTGTAA 415  
DB 164 AAAAAAAGAAAAAAGAAAGAAATTTATTTATGTGTAA 123

RESULT 5  
US-10-277-216-5/c  
Sequence 5, Application US/10277216  
Publication No. US20040002470A1  
GENERAL INFORMATION:  
APPLICANT: KEITH, TIM  
TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,  
TITLE OF INVENTION: OBESITY, AND INFLAMMATORY BOWEL DISEASE  
FILE REFERENCE: 2976-4051  
CURRENT APPLICATION NUMBER: US/10/277,216  
CURRENT FILING DATE: 2002-10-17  
PRIOR APPLICATION NUMBER: 10/126,022  
PRIOR FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: 09/834,597  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 09/548,797  
PRIOR FILING DATE: 2000-04-13  
NUMBER OF SEQ ID NOS: 420  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 207433  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-277-216-5

Query Match 39.4%; Score 197.4; DB 15; Length 207433;  
Best Local Similarity 71.2%; Pred. No. 2.7e-41;  
Matches 284; Conservative 0; Mismatches 96; Indels 19; Gaps 1;

QY 10 AAAACAGGTGTGAGCCACTGCGCCAGCCAGGATTTGCTCTTATATCAATTAAAAATAGGC 69  
DB 199036 AAAACAGGGGTAAACACACCGCACCGGCTAAGGTTAAACATTTAAATCAGCATGAGGC 198977  
QY 70 CGGTGCAAGTGGCTCAGCGCTGTAAATCCAGCACTTTGGGAAGCCAGGCGGCGAGAACAC 129  
DB 198976 GGGCAGCGGTGGCTCAGCGCTGTAAATCCAGCACTTTGGGAAGCCAGGCGGCGGCTAATCAC 198917  
QY 130 CCGAGGTCAAGGATCCAAAGCCAGCGCTGGCCCAAGATGGTGAACCCCGTCTCTATTAAAA 189  
DB 198916 CTGAGGTCAAGCATTCAGACCAAGCGCTGGTCAACATGGCGAAACCCCGTCTCTACTAAAA 198857  
QY 190 ATACAAACATTTACCTGGGCGATGATGGTGGGCGGCTGTAAATCCAGTACTCAGGAGGCTG 249  
DB 198856 ATACAAAAATTTAGCGGGCGTGGTGGTGAATTCCTGTAAACCCAGCTACTCAGGAAGCTG 198797  
QY 250 AGGCGAGGATCCGCGGAGCGCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGGCTACAG 309  
DB 198796 AGGCGAGGATC-----GCTTGAACCCGCGGAGGTTGAGGTTGCGAG 198756  
QY 310 TAAGCAAGATCATGCGCACTATCTTACGCTGGGCGCAAAAGTGAAGCCGTAACAAAAA 369  
DB 198755 GGAACCAAGATCATGCGCACTTCCAGCTGGGCAACAGAGTGAAGTCCATTTTCAAA 198696  
QY 370 AAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAA 408  
DB 198695 AAAAAAGAAAAAAGAAAGAAATTCAGCATGAGTGAA 198657

RESULT 6  
US-10-126-022-5/c  
Sequence 5, Application US/10126022  
Publication No. US20040023215A1  
GENERAL INFORMATION:  
APPLICANT: KEITH, TIM  
TITLE OF INVENTION: NOVEL HUMAN GENE RELATING TO RESPIRATORY DISEASES,  
TITLE OF INVENTION: OBESITY, AND INFLAMMATORY BOWEL DISEASE  
FILE REFERENCE: 2976-4039US2  
CURRENT APPLICATION NUMBER: US/10/126,022  
CURRENT FILING DATE: 2002-04-19  
PRIOR APPLICATION NUMBER: 09/834,597  
PRIOR FILING DATE: 2001-04-13  
PRIOR APPLICATION NUMBER: 09/548,797  
PRIOR FILING DATE: 2000-04-13  
NUMBER OF SEQ ID NOS: 420  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 207433  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-126-022-5

Query Match 39.4%; Score 197.4; DB 16; Length 207433;  
Best Local Similarity 71.2%; Pred. No. 2.7e-41;  
Matches 284; Conservative 0; Mismatches 96; Indels 19; Gaps 1;

QY 10 AAAACAGGTGTGAGCCACTGCGCCAGCCAGGATTTGCTCTTATATCAATTAAAAATAGGC 69  
DB 199036 AAAACAGGGGTAAACACACCGCACCGGCTAAGGTTAAACATTTAAATCAGCATGAGGC 198977  
QY 70 CGGTGCAAGTGGCTCAGCGCTGTAAATCCAGCACTTTGGGAAGCCAGGCGGCGAGAACAC 129  
DB 198976 GGGCAGCGGTGGCTCAGCGCTGTAAATCCAGCACTTTGGGAAGCCAGGCGGCGGCTAATCAC 198917  
QY 130 CCGAGGTCAAGGATCCAAAGCCAGCGCTGGCCCAAGATGGTGAACCCCGTCTCTATTAAAA 189  
DB 198916 CTGAGGTCAAGCATTCAGACCAAGCGCTGGTCAACATGGCGAAACCCCGTCTCTACTAAAA 198857

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RESULT 7
US-10-027-632-119235
/ Sequence 119235, Application US/10027632
/ Publication NO. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827,129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: PastSeq for Windows Version 4.0
/ SEQ ID NO 119235
/ LENGTH: 1138
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-119235

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QY 354 GAGACCGTGTACAAAAAATTTTAAAAAAGAAATTT 394
DB   |||||
DB 510 GAGACTCCATCTCAAAAAAATTTTAAAAAAGAAATTT 550
      |||||

RESULT 8
US-10-027-632-119236
; Sequence 119236, Application US/10027632
; Publication No. US20030204075A5
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 119236
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-119236

Query Match          39.3%; Score 197; DB 15; Length 1138;
Best Local Similarity 76.8%; Pred. No. 3.6e-42;
Matches 262; Conservative 0; Mismatches 60; Indels 19; Gaps 1;

QY 54 ACATTAAAAAATAGGCGGTGCAGTGGCTCACCGCTGTATCCAGCACCTTTGGGAGCC 113
DB 229 ACTCAAGATTTTGGCGCGCACAGTGGCTCACACCTGTATCCTGCACCTTTGGGAGGCC 288

QY 114 AAGCGGGCAGAACACCCGAGGTTCAGAGTCCAAAGCCAGCTTGGCCAAAGATGGTGAAC 173
DB 289 GAGGCGAGGTGGATATACCCGAGGTTCAGAGTTCAAACACCCAGCTTGGCCAAAGATGAAT 348

QY 174 CCGCTCTCTATTTAAAAATACAAACATTACCTGGGCATGATGGTGGGCGCCTGTAAATCCCA 233
DB 349 CCCTCTCTACTTAAATAACAAAATTTAGCTGGGCATGGTGGCAGACACCTGTAAATCCCA 408

QY 234 GCTACTCAGAGGCTGAGGAGGAGGATCCGGAGCGCTGGCAGATCTGCTGAGCCTGG 293
DB 409 GCTACTCAGAGGCTGAGGAGGAGAT-----TGCTTGAACCCGG 449

QY 294 GAGGTTGAGGCTACAGTAAGCCAAAGATCATGCGAGTATCTTTCAGCCTGGGCGCAAAAGT 353
DB 450 GAGTTGAGGTTGAGTGCAGTGCAGCCAGATCATGCCATTCGACTCCAGCCTGGGCGACAGG 509

QY 354 GAGACCGGTACAAAAAATTTTAAAAAAGAAATTT 394
DB   |||||
DB 510 GAGACTCCATCTCAAAAAAATTTTAAAAAAGAAATTT 550
      |||||

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119237
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-119237

Query Match      39.3%; Score 197; DB 15; Length 1138;
Best Local Similarity 76.8%; Pred. No. 3.6e-42;
Matches 262; Conservative 0; Mismatches 60; Indels 19; Gaps 1;

QY 54 ACATTAAATAAGCGCGTGCAGTGGCTCAGCGCTGTAATCCAGCAGCTTTGGAGGCC 113
DB 229 ACTCAAGAAATTTGGCGGCACAGTGGCTCAGCGCTGTAATCCCTGCACTTTGGAGGCC 288
QY 114 AAGCGGGGAGAACACCCAGGCTCAGGAGTCAAGCGGCAGCGCTGGCCAAAGTGGTGAAC 173
DB 289 GAGGAGGCTGGATTACCGAGGTCAGGAGTTCACACAGCTGGCCAAACATGATGAAT 348
QY 174 CCGCTCTCTATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 233
DB 349 CCGCTCTCTATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 408
QY 234 GCTACTCAGGAGGCTGAGGAGGAGGATCCGGGAGGCTGGCAGATCTGCTGAGCGTGG 293
DB 409 GCTACTCAGGAGGCTGAGGAGGAGGAT-----TGCTTGAACCCCG 449
QY 294 GAGGTTGAGGCTACAGTAAAGCAAGATCATGCCAGTATATCTTCCAGCTGGGCGACAAAGT 353
DB 450 GAGTTGAGGCTTGCAGTGAAGCGGAGATCATGCCATTCAGCTCCAGCTGGGCGACAGAGG 509
QY 354 GAGACGCTAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 394
DB 510 GAGACTCCATCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 550

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RESULT 10
US-10-027-632-187984
; Sequence 187984, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483

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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187984
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-187984

Query Match      39.2%; Score 196.2; DB 15; Length 676;
Best Local Similarity 73.7%; Pred. No. 4.7e-42;
Matches 272; Conservative 0; Mismatches 78; Indels 19; Gaps 1;

QY 35 AGCCAGGATTTGCTTTATATACATTAAATAAATAAAGCGGTCAGTGGCTCATGCTGTAAT 94
DB 168 AGCCAGGATTTGCTTTATATACATTAAATAAATAAAGCGGTCAGTGGCTCATGCTGTAAT 227
QY 95 CCCAGCATTGGGAAGCCAGCGGCGAGACACCCAGGTCAGGAGTCCAGGCCAGC 154
DB 228 CTGAGCATTGGGAGCGAGAGCGGTCAGTGGCTCATGAGGTCAGGAGTCCAGGCCAGC 287
QY 155 CTGCGCAAGATGGTGAACCCCGCTCTCTATTAAATAAATAAATAAATAAATAAATAAATAA 214
DB 288 CTGCGCAACATGGCGAAACCCCTGCTCTACTAAATAAATAAATAAATAAATAAATAAATAA 347
QY 215 GTGGGCGCTGTAATCCAGCTACTCAGGAGGTCAGGAGGTCAGGAGGTCAGGAGGTCAGGAG 274
DB 348 GTGGGCGCTGTAATCCAGCTACTCAGGAGGTCAGGAGGTCAGGAGGTCAGGAGGTCAGGAG 388
QY 275 CAGATCTGCTGAGCTGGGAGGTTGAGGCTACAGTAAAGCAAGATCATGCCAGTATATCT 334
DB 389 GAGATTTGCTTGACCCAGGAGTAGAGGTTGAGTAAAGTCCAGACTGTGCCACTGCAT 448
QY 335 TCAGCTGGGCGCAAGAGTGAAGCCGTAAACAAAAAATAAATAAATAAATAAATAAATAAATAA 394
DB 449 TCAGCTGGGCGCAAGAGTGAAGCTGTCTGTAATAAATAAATAAATAAATAAATAAATAAATAA 508
QY 395 AGATCAAGA 403
DB 509 TGTAAGA 517

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RESULT 11
US-09-764-891-6056/c
; Sequence 6056, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6056
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-6056

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Query Match      39.2%; Score 196.2; DB 10; Length 1743;
Best Local Similarity 75.4%; Pred. No. 7.1e-42;
Matches 266; Conservative 0; Mismatches 68; Indels 19; Gaps 1;

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Qy 405 CCAACTGTAAAA 417  
Db 502 ATATATATATATA 514

Search completed: March 4, 2004, 19:00:17  
Job time : 248.513 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:54:45 ; Search time 1959.09 Seconds  
(without alignments)  
7636.686 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_5000\_5500  
Perfect score: 501  
Sequence: 1 atacattataaacaggtgt.....ggtcttcagcatgggaatgg 501

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pin:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_mus:\*
- 23: em\_gss\_pro:\*
- 24: em\_gss\_rod:\*
- 25: em\_gss\_rpg:\*
- 26: em\_gss\_vri:\*
- 27: em\_gss1:\*
- 28: gb\_gss1:\*
- 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	203.6	40.6	666	28	B88182
C 2	201.6	40.2	678	28	AQ387027
C 3	200.2	40.0	3.4	9	AA828637
C 4	198.2	39.6	736	13	BUS54403

C 5	196.6	39.2	445	12	BQ023922
C 6	196.6	39.2	607	28	AQ554450
C 7	195.6	39.0	495	28	AQ336857
C 8	195.6	39.0	530	13	BUT52902
C 9	195.4	39.0	370	13	EX485214
10	194.8	38.9	374	28	AQ021361
11	194.6	38.8	607	28	BZ603705
12	192.4	38.4	393	10	BF805088
C 13	192.4	38.4	393	10	BF805088
C 14	192	38.3	617	28	AQ383054
C 15	192	38.3	895	12	BM452899
C 16	190.8	38.1	501	9	AA722505
C 17	190.8	38.1	603	28	AQ381919
C 18	190.8	38.1	945	13	BUT17036
C 19	190.2	38.0	879	13	BQ708582
C 20	190.2	38.0	493	13	EX486751
C 21	190.2	38.0	602	13	EX480725
C 22	190.2	38.0	664	28	AQ581318
C 23	190	37.9	452	14	T74524
C 24	189.8	37.9	462	28	AQ504564
C 25	189.6	37.8	342	13	BX484854
C 26	189.6	37.8	589	13	EX46260
C 27	189.6	37.8	642	28	B59854
C 28	189.6	37.8	648	28	BZ611349
C 29	189.4	37.8	711	28	AQ415030
C 30	189.4	37.8	1389	11	BC019872
C 31	189.2	37.8	619	12	B1870387
C 32	189.2	37.8	687	29	AG085195
C 33	189.2	37.8	688	29	AG118939
C 34	188.8	37.7	689	13	BU661880
C 35	188.8	37.7	814	28	AQ780979
C 36	188.8	37.7	1538	10	BG036370
C 37	188.6	37.6	703	28	AQ035234
C 38	188.6	37.6	711	13	EX4645025
C 39	188.4	37.6	411	9	A1590458
C 40	188.4	37.6	673	29	AG046383
C 41	188.4	37.6	4125	11	BC028413
C 42	188.2	37.6	739	28	AQ035003
C 43	188	37.5	601	13	BX506204
C 44	188	37.5	623	28	AQ055264
C 45	187.8	37.5	432	12	B1496637

ALIGNMENTS

RESULT 1  
B88182/c  
LOCUS B88182  
DEFINITION B88182 666 bp DNA linear GSS 09-APR-1999  
genomic survey sequence.  
ACCESSION B88182.1 GI:2929314  
VERSION GSS.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 666)  
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)  
JOURNAL Unpublished (1998)  
COMMENT Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 0208  
Email: mda@adams@igir.org  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

BQ023922 UT-1-BB1p  
AQ554450 RPCI-11-4  
AQ336857 RPCI11-71  
BUT52902 UT-1-BB1  
EX485214 DXF2P686E  
AQ021361 CIT-HSP-2  
BZ603705 WFADP21TR  
BF805088 ILS-CI015  
AQ383054 RPCI11-13  
BM452899 AGENCOURT  
AA722505 zh31g08.8  
AQ381919 RPCI11-13  
BUT17036 AGENCOURT  
BQ708582 AGENCOURT  
EX486751 DXF2P686E  
EX480725 DXF2P686O  
AQ581318 RPCI-11-4  
T74524 YC83c08.r1  
AQ545454 RPCI-11-2  
BZ773416 mcv69a07.  
BX484854 DXF2P686L  
BX46260 DXF2P781E  
B59854 CIT-HSP-345  
BZ611349 WHAAO01TR  
AQ415030 RPCI-11-2  
BC019872 Homo sapi  
B1870387 60335633  
AG085195 Pan trogl  
AG118939 Pan trogl  
BU661880 cl78b10.z  
AQ780979 HS 3138.B  
BG036370 602326675  
AQ035234 CIT-HSP-2  
EX4645025 DXF2P781E  
A1590458 tt76h09.x  
AG046383 Pan trogl  
BC028413 Homo sapi  
AQ035003 CIT-HSP-2  
BX506204 DXF2P686A  
AQ055264 CIT-HSP-2  
B1496637 df126h05.

(pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page: [http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html)  
Seq primer: SP6  
Class: BAC ends.

FEATURES source

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Location/Qualifiers
1. .666
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:750877"
/db_xref="taxon:9606"
/clone="RPC1-11-23L"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPC1-11"
/notes="Vector: pBACRPC11 Human Male BAC"

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## ORIGIN

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Query Match      40.6%; Score 203.6; DB 28; Length 666;
Best Local Similarity 72.7%; Pred. No. 1.8e-24;
Matches 263; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

  QY      65  TAGGCCGGTGAGTGGCTCAGCCTGTAATCCACAGCACTTTGGGAAGCCCAAGCGGGGGCAG 124
  DB      362  TGGCCAGGCAAGTGTCTCACCTGTAAATCAGACACTTTGAGAGGCCCAAGCCAGCGCG 303

  QY      125  AACACCCGAGGTCCAGGAGTCCAAAGCCGAGCTGGCCCAAGATGGTGAAACCCCGTCTCTAT 184
  DB      302  ATCACTGAGTCCAGGAGTTCGAGACCCAGCCTGACCAACATGCGCAAACTCGTCTCTAC 243

  QY      185  TAAAAATACAACATTTACCTGGGCATCATGGTGGGGCCCTGTAAATCCCACTACTTCAGGA 244
  DB      242  TAAAAATACA AAAATTTAGCCAGGCATGGTGGTGGGTGCCTGTAAATCTCAGCTACTCAGGA 183

  QY      245  GCCTCAGGCAGGAGGATCCGGGAGCCTGGCCAGATCTGCCTCAGCCTCGGGAGTTTGAGGC 304
  DB      182  GCCTCAGCGAGGAAATCAATTTGACGACGAGAGAATCAATTTGAACCCAGGAGCGAGAGT 123

  QY      305  TACAGTAGCCAGAGTCAATGCCAGTATATCTTCAAGCTGGCGCAAAAGTAGAGACCGTAAC 364
  DB      122  TGCAGTAGCCAAAGATGGCCCACTGTATTTCAAGCTGGGCAACAGTAGTGAGACTCTGTCTC 63

  QY      365  AAAAAA AAAAAATTTTAAAAAAGAAATTTAGATCAAGATCCAACATGTAAAAAGTGGCT 424
  DB      62  AAAAAA AAAAAA AAAAAA CCAAAAAACATTAATTTCTTCCCAATATGAGGCCAGATGGACT 3

  QY      425  AA 426
  DB      2  CA 1

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[illegible]

ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 678)
AUTHORS	Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J. C.
TITLE	Use of PAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL	Unpublished (1997)
COMMENT	Other GSSs: RPCI11-153C12.TV Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbs@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/>) or from Research Genetics ([info@resgen.com](http://info@resgen.com)). BAC end search page: [http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html)  
Seq primer: SP6  
Class: BAC ends.

Location/Qualifiers

1. .678

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="GDB:7558427"

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/clone="RPCI-11-153C12"

/sex="Male"

/cell\_type="Lymphocytes"

/clone\_lib="RPCI-11"

/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; pPC11 Human Male BAC Library"

**FEATURES**  
**SOURCE**

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7558427"
/db_xref="taxon:9606"
/clone="RPCI-11-153C12"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note=vector: pBACe3.6;
RPCI11 Human Male BAC Li
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## ORIGIN

Query Match	40.2%;	Score	201.6;	DB	28;	Length	678;	
Best Local Similarity	73.2%;	Pred.	No. 3.8e-24;					
Matches	281;	Conservative	0;	Mismatches	84;	Indels	19; Gaps	1;
Qy	22	AGCCACTGCGCCAGCCAGCGTAATGTCTTATACATTAAAAAATAGCGCGGTGACGTGGC	81					
Db	38	AGCTGSGTGACACAGACGACACCATCTCTAAAAATAAAAATAAGCGCGCGGTGGC	97					
Qy	82	TCACGCTGTAAATCCCAAGCACTTTGGGAAGCCAGCGGGCAGAACACCCAGGTTCAGGA	141					
Db	98	TCACGCTGTAAATCCCAAGCACTTTGGGAGGCTAAGCGGGCAGATCACCTGAGGTTCAGGA	157					
Qy	142	GTCCAAAGCCAGCGCTGCCCAAGATGTTGAACCCCGTCTCTATTTAAAAATACAAACATT	201					
Db	158	GTTGAGACCAAGCTGCCCAACATGTTGTAACCCCATCTCTACTAAAAATAAAAAATTA	217					
Qy	202	CCTGGGCATGATGGTGGGCGCCTGTAAATCCCAAGCTACTCAGGAGCTCAGGCAGAGAT	261					
Db	218	GCCGGGCATGGTGGTGGTGCTGTAAATCCCAAGCTACATGGGAGGCTGAGGCAGAGAT	277					
Qy	262	CCGCGGAGCCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGGCTACAGTTAAGCCAAATC	321					
Db	278	-----TGCTTGAACTCTGGGAGCGGAGGTTGAGTGAGCCGAGATC	318					
Qy	322	ATGCCAGTATACTTTCAGCTCGGGCGCAAAAGTGAGACCGCTAACAAAAAATAAAAAATTTA	381					
Db	319	GTGCCATTGCTACTCCAGCTTGGGACAGAGCAAGACTCTGTCTGAAAAATAAATAATAA	378					
Qy	392	AAAAAGAAATTTAGATCAAGATC	405					
Db	379	ATAAAAAATCTCTCTCATCATC	402					

RESULT 3  
AA828637/C

AA828637	314 bp	mRNA	linear	EST 07-APR-1998
cd79d11.s1	NCI_CGAP_Ov2	Homo sapiens	cdNA clone	IMAGE1374185
similar to contains Alu repetitive element; mRNA sequence.				
AA828637				
AA828637.1	GI:2901736			
EST.				
Homo sapiens (human)				
Homo sapiens				
Eukaryota; Metazoa;				
Eukaryota; Chordata;				
Mammalia; Eutheria;				
Primates;				
Catarrhini; Hominoidea;				
Homo.				

REFERENCE 1 (bases 1 to 314)  
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: David B. Krizman, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Insert Length: 405 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham.

## FEATURES

Location/Qualifiers  
 1..314  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clones="IMAGE:1374165"  
 /sex="female"  
 /tissue\_type="ovary"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CCAP Ov2"  
 /note="Vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

## ORIGIN

Query Match 40.0%; Score 200.2; DB 9; Length 314;  
 Best Local Similarity 79.1%; Pred. No. 8.7e-24;  
 Matches 238; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
 QY 77 GTGGCTCAGCGCTGTAATCCAGACATTTGGAGCCAGCGGCGGAGACACCCGAGGT 136  
 Db 301 GTACTATACCTGTAATCTTAGACATTTGGAGCCAGCGGCGGAGATCACTGAGGT 242  
 QY 137 CAGGAGTCCAAAGCGCCTGGCCAGATGTTGAAACCCCGTCTCTATTAAATACAAA 196  
 Db 241 TCGGAGTTCAGGACCGCCTGGCCAAATGTTGAAACCCCATCTCTACTAAATACAAA 182  
 QY 197 CATTAAGTGGCGATGATGGCGCTGTAATCCAGCTACTCAGGAGGCTGAGCGAG 256  
 Db 181 AATCAGCTGGGTATGGTGGTGGCGCTCTAATCTTAGCTACTTGGGAGGCTTAGGCGG 122  
 QY 257 AGGATCCGCGAGCGCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGGCTACAGTAAAGCCA 316  
 Db 121 AGAATCACTTCAACGCGAGGAGATCACTTTGAACCCAGGAGGCTTGCAGTGAGCGG 62  
 QY 317 AGATCATGCCAGTATATTGAGCTGGCGGCAAGTGAACCTGAGACCTAACAAAAA 376  
 Db 61 AGATCATGCCAGTATATTGAGCTGGCGGCAAGTGAACCTGAGACCTAACAAAAA 2  
 QY 377 A 377  
 Db 1 A 1

## RESULT 4

BUS54403/c  
 LOCUS BUS54403  
 DEFINITION AGENCOURT\_10410045 NIH\_MGC\_82 Homo sapiens cDNA clone IMAGE:6621672  
 5', mRNA sequence.  
 ACCESSION BUS54403  
 VERSION BUS54403.1 GI:24039369  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 736)  
 NIH-MGC <http://mgi.nci.nih.gov/>.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: CLONTECH  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LCM2873 row: 1 column: 24  
 High quality sequence stop: 517.

## FEATURES

Location/Qualifiers  
 1..736  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clones="IMAGE:6621672"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH MGC 82"  
 /note="Organ: testis; Vector: pDNR-LJB (Clontech); Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCGGAGTGT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

## ORIGIN

Query Match 39.6%; Score 198.2; DB 13; Length 736;  
 Best Local Similarity 76.4%; Pred. No. 1.3e-23;  
 Matches 256; Conservative 0; Mismatches 78; Indels 1; Gaps 1;  
 QY 67 GCGCGGTGAGTGGCTCAGCGCTGTAATCCAGACATTTGGAGCCAGCGGCGGAGAA 126  
 Db 548 GCGCGGTATGGTGGCTCAGCGCTGTAATCCAGACATTTGGAGCCAGCGGCGGAGAA 489  
 QY 127 CACCCGAGTCAAGGAGTCCAAAGGCGGCTGGCCAGATGCTGAAACCCCGTCTCTATTA 186  
 Db 488 AACCTGAGTCAAGGAGTCTGAGACAGCGCTGGCCATGCTGTAACCCCGTATCTACTA 429  
 QY 187 AAATAACAAACATTACCTGGGCGATGATGGGCGCTGTAAATCCAGCTACTCAGGAGG 246  
 Db 428 AAATGCAAAAATTAGCTGGGCGATGGTGGGCGACCTGTAAATCCAGCTACTCAGGAGG 369  
 QY 247 CTGAGCGAGGAGTCCGC-GGAGCGCTGGCAGATCTGCTGAGCCTGGGAGGTTGAGGCT 305  
 Db 368 CTGAGGTAGGAGATTTGCTCAAGCAATTCCTTGGCTTGAACCCAGAGGGGAGGCT 309  
 QY 306 ACAGTAAGCCCAAGATCATGCCAGTATATTGAGCCTGGGCGGACAAAGTGAGACCGTAACA 365  
 Db 308 GCAGTGAGCCAAAGATTGCAACCACTGCACTCCAGTATGGGTGACAGAGCGAGACTCCGTCT 249  
 QY 366 AAAAAAATTTTAAAAAAGAAATTTAGATCA 400  
 Db 248 CAAAAAATAAATAACAAAAATGCAAAATTTTAAACA 214

## RESULT 5

BQ023922/c  
 LOCUS BQ023922  
 DEFINITION UI-1-BBip-aun-b-07-0-UI.sl NCI-CCAP\_P16 Homo sapiens cDNA clone  
 UI-1-BBip-aun-b-07-0-UI 3', mRNA sequence.  
 ACCESSION BQ023922  
 VERSION BQ023922.1 GI:19759201

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 445)
JOURNAL NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Steven Brown
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 11-307, xLUJ (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..445
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-1-BB1p-aun-b-07-0-UI"
/tissue_type="Placenta"
/dev_stage="Full Term"
/clone_lib="NCI CGAP Pl6"
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with
a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Pl6 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are GA, AGGAA. For
additional information, contact: Bento Soares,
bento-soares@uiowa.edu
TAG TISSUE=placenta human full term
TAG LIB=UI-1-BB1p
TAG_SEQ=AGGAA"

ORIGIN
Query Match 39.2%; Score 196.6; DB 12; Length 445;
Best Local Similarity 77.2%; Pred. No. 3e-23;
Matches 257; Conservative 0; Mismatches 64; Indels 12; Gaps 1;

QY 52 ATACATTAAAAATAGCGCGGTGACGTGCTCAGCGCTGTATCCAGCACTTTGGGAGG 111
DB 321 ATATCTATATTTGGCTGGGTGACGTGCTCATGCTGTATCCAGCACTTCGGAGG 262

QY 112 CCAAGCGGGCGAGAACACCCGAGGTCAGAGTCCAGGCCAGCTGGCCAGATGGTGA 171
DB 261 CCGAGGCGAGGAGATCACTGAGGTCAGGAGTTTAAAGACCAAGCTGGCCAACTGGTGA 202

QY 172 ACCCGCTCTCTATTAATAACAACATTACTCGGCGATGATGGTGGCGCTCTATCC 231
DB 201 ATCCCGTCTCTACTAAATAACAATAAAGCCGGGATGGTGGAGCGCTGTATCC 142

QY 232 CAGCTACTCAGGAGGCTGAGGCGAGGATCCGGAGCCCTGGCAGATCTGCTGAGCCCT 291
DB 141 CAGCTACTTGGAGGCTGAGGCGAGGAGATCACTTGAAC-----CCAGAACCT 94

QY 292 GGGAGGTTGAGCTACAGTAAAGCAAGATCATGCCAGTACTTCAAGCTGGGCGAGAA 351

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DB 93 GGGAGGCGAGAGGTTGACGTGAGCCGAGATTGTGCCACTGTACTCCATCCTCGGTGACAGA 34
QY 352 GTGAGACCGCTAACCAAAAAAATTTTAAAA 384
DB 33 GGGAGACTTCGTGCGCAAAAAAATTTTAAAA 1

RESULT 6
AQ554450/c
LOCUS
DEFINITION
ACCESSION AQ554450
VERSION AQ554450.1
KEYWORDS GI:4913627
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 607)
Zhao,S.; Adams,M.D.; Niernan,W., Malek,J., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other GSSs: RPCI-11-422120.TV
Contact: Shaying Zhao, William Niernan, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbs@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pister@dejong.med.buffalo.edu). Clones may be purchased from
BACRAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7661875"
/db_xref="taxon:9606"
/clone="RPCI-11-422120"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
RPCI11 Human Male BAC Library"

ORIGIN
Query Match 39.2%; Score 196.6; DB 28; Length 607;
Best Local Similarity 74.6%; Pred. No. 2.7e-23;
Matches 247; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 65 TAGCGCGGTGACGTGCTCAGCGCTGTAATCCAGCACTTTGGGAGCGAGCGGCGAG 124
DB 337 TGCCCGGCGACAGTGTCTCACACCTGTATCACAGCACTTTGAGAGGCGCAGCGCG 278

QY 125 AACACCGGAGGTGAGGAGTCCAGGCTGGCCAGAGATGGTGAACCCCGCTCTCTAT 184
DB 277 ATCACTGAGGTGAGGAGTTCGAGACCAAGCTGACCAACATGGCGACCTGCTCTAC 218

QY 185 TAAATAACAACATTACTCGGCGATGATGGTGGCGCTGTATCCAGCTACTCAGGA 244
DB 217 TAAATAACAACAAATAGCCAGGCATGGTGGTGGCTGTATCTCAGCTACTCAGGA 158

QY 245 GCGTGGAGGAGGAGGATCCGCGAGCTGCGAGATCTGCGTGGAGGTTGAGGC 304

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DB 157 GGCTGACGAGGAGATCATTTGGACGAGGAGATCATTTGAACCCAGGAGGAGAGGT 98  
 QY 305 TACAGTAAGCCAGATCATGTCAGTATATCTTTCAGCTGGGCGACAAAGTGAGACCGTAAC 364  
 DB 97 TGCAGTGAGCCAGAGTATGCTCCACTGTATTTTCAGCTGGGCGACAAAGTGAGACTCTGTCTC 38  
 QY 365 AAAAAAAAAAATTTAAAAAGAAATTTA 395  
 DB 37 AAGAGAAACAAACCAACCAACCAACCAATTA 7

RESULT 7  
 A0236857/c  
 LOCUS A0236857 495 bp DNA linear GSS 21-APR-1999  
 DEFINITION RPII11-71K16.TJ RPII-11 Homo sapiens genomic clone RPII-11-71K16,  
 genomic survey sequence.  
 ACCESSION A0236857  
 VERSION A0236857  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,  
 Berry,K., Granger,D., Suh,B., Wible,C., de Jong,P. and Venter,J.C.  
 TITLE Use of human BAC End Sequences for Sequence-Ready Map Building  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mdadams@tigr.org

Clones are derived from the human BAC library RPII-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@jmg.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
 Research Genetics (info@resgen.com). BAC end search page:  
 http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html  
 Seq primer: SP6  
 Class: BAC ends.

FEATURES  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="GDB:7527135"  
 /db\_xref="taxon:9606"  
 /clone="RPII-11-71K16"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /clone\_lib="RPII-11"  
 /note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 RPII11 Human Male BAC Library"

ORIGIN  
 Query Match 39.0%; Score 195.6; DB 28; Length 495;  
 Best Local Similarity 71.3%; Pred. No. 4.2e-23;  
 Matches 258; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 65 TAGGCGGTCAGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAAGCGCAAGCGGGCAG 124  
 DB 403 TGGCAGGACACAGTGTCTACACCTGAATCAGACACTTTGAGAGCCAGGACGAGCG 344  
 QY 125 AACACCCGAGGTTCAGAGTTCAGGCGAGCTGGGCGACAGATGGTGAACCCCGTCTTAT 184  
 DB 343 ATCACCTGAGGTTCAGAGTTCAGGCGAGCTGGGCGACAGATGGTGAACCCCGTCTTAT 284  
 QY 185 TAAATAACAACATTTACCTGGGCGATGATGGGCGCTGTAAATCCAGCTACTTCAGGA 244  
 DB 283 TAAATAACAACATTTAGCAGCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 224

QY 245 GGCTGAGGAGGAGATCCGCGAGCTGGCAGATCTGCTGAGCTGGGAGGTGAGGC 304  
 DB 223 GGCTGAGGAGGAGATCATTTTGGACGAGGAGATCATTTTGAACCCAGGAGGAGGT 164  
 QY 305 TACAGTAAGCCAGATCATGTCAGTATATCTTTCAGCTGGGCGACAAAGTGAGACCGTAAC 364  
 DB 163 TGCAGTGAGCCAGAGTATGCTCCACTGTATTTTCAGCTGGGCGACAAAGTGAGACTCTGTCTC 104  
 QY 365 AAAAAAAAAAATTTAAAAAGAAATTTAGATCAAGATCCCACTGTAAAGTGGCT 424  
 DB 103 AAGAAAAAAGAAAAAACCACCAACCAACCAATTTCTCTCAATATGAAGCGACAGTGGACT 44  
 QY 425 AA 426  
 DB 43 CA 42

RESULT 8  
 BU752902/c  
 LOCUS BU752902 530 bp mRNA linear EST 10-OCT-2002  
 DEFINITION UI-1-BB1-aic-b-04-0-UI.a1 NCI CGAP P15 Homo sapiens cDNA clone  
 UI-1-BB1-aic-b-04-0-UI 3', mRNA sequence.

ACCESSION BU752902  
 VERSION BU752902.1 GI:23710587  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Dr. Steven Brown  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 The following repetitive elements were found in this cDNA  
 sequence: 10-306, >ALU (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 Location/Qualifiers  
 1..530  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-1-BB1-aic-b-04-0-UI"  
 /tissue\_type="Placenta"  
 /dev\_stage="Full Term"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP P15"  
 /note="Organ: Placenta; Vector: pTT3-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: EcoRI; Site\_2: Not I;  
 NCI-CGAP P15 is a subtracted cDNA library constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoRI adaptor, digested  
 with Not I, and cloned directionally into pTT3-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for this library are GA, AGGAA. For  
 additional information, contact: Bento Soares,  
 bento-soares@uiowa.edu  
 TAG TISSUE=placenta human full term  
 TAG\_LIB=UI-1-BB1  
 TAG\_SEQ=AGGAA"



```
ORIGIN
Query Match      39.0%; Score 195.6; DB 13; Length 530;
Best Local Similarity 77.1%; Pred. No. 4.1e-23;
Matches 256; Conservative 0; Mismatches 64; Indels 12; Gaps 1;

QY 52 ATACATTAATAAATAGCGCGTGCAGTGCCTCAGCCCTGTAATCCACGACACTTTGGGAAG 111
DB 320 ATATACTATATTTGGCTGGGTGCAGTGGCTCATGCCCTGTAATCCACGACACTTCGGGAGG 261
QY 112 CCAGGGCGGCGAGACACCCGAGGTCAGGAGTCCAGGCCAGCTGCCAGATGGTGA 171
DB 260 CCGAGGCGAGGAGATCAGCTCAGGTCAGGAGTTTAAGACCAAGCTTGCACCAATGGTGA 201
QY 172 ACCCGCTCTCTATTAATAAATACAAACATTAACCTGGGCATGATGGTGGCGCTGTATATCC 231
DB 200 ATCCCGCTCTCTACTAAAAATACAAAAATAAGCGGCGATGGTGGTGAACGCGCTGTATATCC 141
QY 232 CAGCTACTCAGGAGGCTCAGCGAGGAGGATCCGGGAGCTGGCGAGATCTGCCCTGAGCCT 291
DB 140 CAGCTACTTGGGAGGCTCAGCGAGGAGATCAGTTGAAC-----CCAGAACCT 93
QY 292 GGGAGGTTGAGGCTACAGTAAGCAACGATCATGCCAGTATATCTTTCAGCTGGGCGACAAA 351
DB 92 GGGAGGCGAGGTTGCACTGAGCGAGAGTTGTCACCTGACTCCTCCTGGGTGACAGA 33
QY 352 GTGAGACCGTACAAAAAATAAATAAATTTAA 383
DB 32 GGGAGACTTCGTCGCAAAAAAATAAATAAATAA 1

RESULT 9
BX485214      370 bp mRNA linear EST 04-SEP-2003
LOCUS DKEZp686E14246 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKEZp686E14246 5', mRNA sequence.
ACCESSION BX485214
VERSION BX485214
KEYWORDS BX485214.1 GI:31947745
SOURCE EST.
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 370)
Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
Fobbo, G., Han, M. and Wiemann, S.
EST (Koehler, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by BPFZ (Biomedical Research Center at the Heinrich-
Heine-University, Duesseeldorf/Germany) within the cDNA sequencing
consortium of the German Genome Project. No sl sequence available.
This clone (DKEZp686E14246) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
Location/Qualifiers
1..370
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKEZp686E14246"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: SflIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match      39.0%; Score 195.4; DB 13; Length 370;
Best Local Similarity 75.6%; Pred. No. 5.1e-23;
Matches 264; Conservative 0; Mismatches 66; Indels 19; Gaps 1;

QY 69 CCGGTGCGAGTGCTCAGCCCTGTAATCCAGCACTTTGGGAAGCCAGCGGGGAGACA 128
DB 2 CCGGTGCGAGTGCTCAGCCCTGTAATCCAGCACTTTGGGAAGCGGAGGTGGGTGATCA 61
QY 129 CCGGAGGTCAGGAGTCCCAAGCCAGCTGGCGCAAGATGGTGAACCCCGCTCTTATTAAA 188
DB 62 CCAGAGGTCAGGAGTTCGAGACCCAGCTAGCAACATGCAAAACCCCGCTCTACTAAA 121
QY 189 AATACAAACATTAACCTGGGCATGATGGTGGGGCCCTGTAAATCCAGCTACTCTCAGGAGCT 248
DB 122 AATACAAAACTAGCCGGGCATCGTGGCGGGCGCCCTGCAATCCCGAGCTACTCAGGAGCT 181
QY 249 GAGGCGAGGAGGATCCCGGAGGCTGGCAGATCTGCTCAGCTGGGAGGTTGAGGCTACA 308
DB 182 GAGGCGAGGAGT-----AGCTTGAGCCCGGAGGTGGAGGTGCGA 222
QY 309 GTAAGCAGAGTCATGCCAGTATATCTCAGCTGGGCGACAAAGTGAGACCGTAACAAA 368
DB 223 GTGAGCTGAGATCAGGTCAGCGCACTCCAACTGGGCGACAGAGCAAGACTGTCTCAAAA 282
QY 369 AAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAACTGTAAAAA 417
DB 283 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 331

RESULT 10
AQ021361      374 bp DNA linear GSS 09-JUN-1998
LOCUS CIT-HSP-2307K5 TF CIT-HSP Homo sapiens genomic clone 2307K5,
DEFINITION genomic survey sequence.
ACCESSION AQ021361
VERSION AQ021361.1 GI:3200097
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 374)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other-GSSs: CIT-HSP-2307K5.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: maddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
Location/Qualifiers
1..374
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2307K5"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII"

ORIGIN
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Query Match 38.9%; Score 194.8; DB 28; Length 374;  
 Best Local Similarity 76.3%; Pred. No. 6.4e-23;  
 Matches 261; Conservative 0; Mismatches 62; Indels 19; Gaps 1;

QY 67 GSCCGGTGAGGCTGAGCTGTAATCCAGCACTTTGGAGCCAGCGGCGAGAA 126  
 Db 4 GCCAGGTGGGCTCATGCTGTAATCCAGCACTATGGAGCCAGGAGGAGGAT 63  
 QY 127 CACCCGAGGTGAGGAGTCCAGGCCAGCGCTGCGCCAAAGATGGTGAACCCCGCTCTATT 186  
 Db 64 CTCAGAGGTGAGGAGTTCGAGACCAGCGCTGCGCCAAAGATGGTGAACCCCGCTCTATT 123  
 QY 187 AAAATACAAACATTAACCTGGGATGATGGTGGGCGCTGTAATCCAGCTACTCAGAGG 246  
 Db 124 AAAATACAAACATTAACCTGGGATGATGGGCGGACCTGTAATCCAGCTACTCAGAGG 183  
 QY 247 CTGAGCGAGGAGTCCGCGAGCGCTGCGCAGATCTGCGCTGAGCGCTGGGAGGTTGAGGCTA 306  
 Db 184 CTGAGCGAGGAGT-----TGCTTGAAGTGGGAGGCGAGGTTG 224  
 QY 307 CAGTAAGCCAGATCATGCGAGTATCTTACGCTTGGGCGGACAAAGTGAGCCGTACAA 366  
 Db 225 CAGTGAGCAAGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284  
 QY 367 AAAAAAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAA 408  
 Db 285 AAAAAAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCAA 326

RESULT 11  
 BZ603705  
 LOCUS WHAP21TR Human MCF7 breast cancer cell line library (MCF7\_1) Homo sapiens genomic clone MCF7\_1-22D18, genomic survey sequence.  
 DEFINITION BZ603705.1 GI:31512167  
 ACCESSION BZ603705  
 VERSION GSS.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 607)  
 AUTHORS Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P., Gray, J.W. and Collins, C.  
 TITLE End-sequence profiling: Sequence-based analysis of aberrant genomes  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)  
 MEDLINE 22709111  
 PUBMED 12788976  
 COMMENT Contact: Volik SV  
 Colin Collins' lab  
 UCSF Comprehensive Cancer Center  
 UCSF Box 0808, San Francisco, CA 94143-0808, USA  
 Tel: 415 502 7066  
 Fax: 415 502 5665  
 Email: svolik@cc.ucsf.edu  
 This clone is available from Amplicon Express  
 http://www.genomex.com  
 Class: BAC ends.

FEATURES  
 source  
 1..607  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="MCF7\_1-22D18"  
 /sex="female"  
 /clone\_lib="Human MCF7 breast cancer cell line library (MCF7\_1)"  
 /note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

ORIGIN

Query Match 38.8%; Score 194.6; DB 28; Length 607;  
 Best Local Similarity 70.6%; Pred. No. 5.7e-23;  
 Matches 283; Conservative 0; Mismatches 99; Indels 19; Gaps 1;

QY 48 TCTTATACATTTAAAAATAGGCGGTGAGTGGCTCACCCCTGTATATCCAGCACTTTGG 107  
 Db 131 TGTCAAAAAAGTAAATTTGAAGCTGGGCACTGGCTCACACCTGTATATCCAGCACTTTGG 190  
 QY 108 GAAGCCAAAGCGGGGAGAACACCCGAGGTGAGAGTCCAGAGTCCAGCCAGCTGGCCAGATGG 167  
 Db 191 GAGGCTGAGTGGGAGATCACTGAGGTGAGAGTTCAGAGCCAGCTGGCCAGATGG 250  
 QY 168 TGAACCCCGTCTCTATTAAAAATACAAACATTAACCTGGGCGATGATGGTGGCGCTGTA 227  
 Db 251 TGAACCCCGTCTCTCACTAAAAATACAAACATTAACCTGGGCGATGATGGTGGCGCTGTA 310  
 QY 228 ATCCCACTGCTACTCAGGAGCTGAGGAGGAGGATCCGCGAGCTGGCAGATCTGCTCA 287  
 Db 311 ATCCCACTGCTACTCGGAGGCTGAGGAGGAGT-----TGCTTCA 351  
 QY 288 GCTGGGAGGTTGAGGCTACAGTAAGCCAGATCATGCGAGTATATCTTACGCTGGGCGA 347  
 Db 352 ACCTGGGAGGCGAGGTTGAGTGGAGCCGAGATCACACCTGTACTCCAGCTGGGCGA 411  
 QY 348 CAAAGTGAGACCTGAACAAAAAATTTAAAAAAGAAATTTAGATCAAGATCCA 407  
 Db 412 CAGGTGAGAGTGTTCGTAAACAAACAAATTAATTAATGTAATGTAATGTAATGTAATGTA 471  
 QY 408 ACTGTAAAAAGTGGCTTAAACACCACTTAAAGAGTTTGG 448  
 Db 472 TCTCAGAAAAATACAAATTAACCTACAACTTAATATTAAGTA 512

RESULT 12  
 BZ605088  
 LOCUS IL15-C10150-061100-225-e12 C10150 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BZ605088  
 ACCESSION BZ605088.1 GI:12134077  
 VERSION ZST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 393)  
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 MEDLINE 20202663  
 PUBMED 10737800  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-C10150-061100-225-e12&t3=2000-11-06&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 389.  
 Location/Qualifiers

FEATURES

source  
1. 393  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/dev\_stage="Adult"  
/clone\_lib="C10150"  
/note="Organ: colon, ins; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
ORIGIN  
Query Match 38.4%; Score 192.4; DB 10; Length 393;  
Best Local Similarity 75.0%; Pred. No. 1.6e-22;  
Matches 261; Conservative 0; Mismatches 68; Indels 19; Gaps 1;  
QY 44 TTGCTCTTATACATATAAATAGCCGGTCCAGTGGCTCAGCTGTGTAATCCAGCACT 103  
DB 54 TGGGTGTTAAACNTTAAGGATGCGCGCGCGTGGCTCAGCGCTGTATCCAGCACT 123  
QY 104 TTGGGAACCAAGGGGCGGAGAACACCGAGGTGAGAGTCCAGGCCAGCTGGCCAG 163  
DB 124 TTGGGAGCCGAGGCGAGACGATCACTGAGATTAGGATTTCCAGACCGCTGGCTAAC 183  
QY 164 ATGGTGAACCCCGCTCTTATATAAATAACAAACATTACCTGGGCATGATGGTGGGGCC 223  
DB 184 ATGGTGAACCCCGCTCTTACCAAAATACAAATTAAGCGGCGATGGTGGCGGCC 243  
QY 224 TGTATCCAGCTACTCAGAGGCTGAGCGAGGAGTCCCGGAGCGCTGCAGATCTGC 283  
DB 244 TGTATCCAGCTACTCAGAGGCTGAGCGAGGAGTCCCGGAGCGCTGCAGATCTGC 284  
QY 284 CTGACCTGGGAGGTTGAGGCTTACAGTAAGCCAGATCATGCCAGTATCTTACGCTGG 343  
DB 285 TTGAACCCGGAGGTTGAGGTTGAGTGGCGAGATCAGCCACTGCATCCAGCTGG 344  
QY 344 GCGACAAAGTGAGACCGGTAACAAAAAATTTAAAAAAGAAA 391  
DB 345 GTGACAGGTTGAGACTCCATCTCTCANAAGAAAAAACAACAAACANA 392

RESULT 13  
AQ383054/c  
LOCUS  
DEFINITION  
RPCI11-139K16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-139K16,  
genomic survey sequence.  
ACCESSION  
AQ383054.1 GI:4354077  
VERSION  
GSS.  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 617)  
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and  
Venter, J. C  
Map Building  
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
Map Building  
Unpublished (1997)  
Other GSSs: RPCI11-139K16.TV  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeet@ig.orsg  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/>) or from  
Research Genetics (<http://info@resgen.com>). BAC end search page:  
[http://www.tigr.org/tldb/hungen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html)  
Seq primer: SP6  
Class: BAC ends.

#### FEATURES

Location/Qualifiers  
1. 617  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="GDB:7533247"  
/db\_xref="taxon:9606"  
/clone="RPCI-11-139K16"  
/sex="Male"  
/cell\_type="Lymphocytes"  
/clone\_lib="RPCI-11"  
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
RPCI11 Human Male BAC Library"

#### ORIGIN

Query Match 38.3%; Score 192; DB 28; Length 617;  
Best Local Similarity 74.1%; Pred. No. 1.5e-22;  
Matches 243; Conservative 0; Mismatches 85; Indels 0; Gaps 0;  
QY 90 GTAATCCAGCACTTTGGAGAGCCAGCGGCGGAGACACCCGAGTCCAGAGTCCAGG 149  
DB 617 GTAATCCTAGCACTTTGGGGGCCAAAGACGGCGGATCACCTAAGTCCAGAGTTAAGG 558  
QY 150 CCAGCTGCGCCAGAGTGTGAAACCCCGTCTCTATTAATAATACAAACATTACCTGGGCA 209  
DB 557 CCAGCTGCGCCAAACACGGTGAACCCCTCTCTACTATAAATACAAAATTTAGTCAGCGC 498  
QY 210 TGATGTGGCGGCCCTGTAATCCAGCTACTCAGAGGCTGAGGAGGAGGATCCGCGAG 269  
DB 497 TGGTGGCGGCGACCTGTATTCCAGCTACTGGGGAGGCTGAGGCGAGGAGATCGCTTGA 438  
QY 270 CCTGGCAGATCTGCTGAGCGCTGGGAGGTTGAGGCTACAGTAAGCCAAAGATCATGCCAGT 329  
DB 437 CGCAGGAGATCGCTTGAACCCAGGCGGAGGTTGCAAGTGAAGTGAATCAGACCACT 378  
QY 330 ATACTTCAGCTGGCGGCAAAAGTGAGACCGTGAACAAAAAATTTAAAAAAGA 389  
DB 377 GCATCCAGCTGGGTGACAGGTCAGACTCCATCTCAAAAAAAGAAAAAAGA 318  
QY 390 AATTTAGATCAAGATCCAACTGTAATA 417  
DB 317 AAAGAAAAAGAAAGAGTGAAGAGA 290

#### RESULT 14

BM452899  
LOCUS  
DEFINITION  
BM452899.1 GI:18501939  
ACCESSION  
BM452899  
VERSION  
EST.  
KEYWORDS  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 895)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clones are derived from the human BAC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LLAM12203 row: n column: 03

High quality sequence stop: 657.

## FEATURES

Location/Qualifiers  
1. .895  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5527874"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 72"  
/notes="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 38.3%; Score 192; DB 12; Length 895;  
Best Local Similarity 75.1%; Pred. No. 1.3e-22;  
Matches 257; Conservative 0; Mismatches 75; Indels 10; Gaps 1;  
QY 48 TCCTATACATTAATAAGCGGTGCAGTGGCTCACGGCTGTATCCAGCAGCTTGG 107  
Db 421 TCTAAGAAAATAAGCGTGGCCAGGTGAGTAGGTACGCGCTGTATCCAGCAGCTTTAG 480  
QY 108 GAAGCCAAAGCGGCGCAGAACACCCGAGGTCCAGAGTCCAAAGCCAGCCTGGCCAGATGG 167  
Db 481 GAGGCCAAGGTGGTGTGATCACTGAGGTTCAGACCCAGCTGGCCACATGG 540  
QY 168 TGAACCCCGTCTCTATTAATAATACAAATACCTGGGCATGATGGGGCGCTGTA 227  
Db 541 TGAACCCCGTCTGTAATAATAATACAAATATAGTGGGCATGATGGGGCGCTGTA 600  
QY 228 ATCCCACTACTCAGGAGGTGAGGAGGAGGATCCGCGAGGCTGGCAGATCTGCTCA 287  
Db 501 ATCTAGTACTCAGAGGCTGAGGCGGAGATCGTTGAACCCGGGA-----A 650  
QY 288 GCCTGGAGGTTAGGCTACAGTAAGCAAGATCATGCCAGTATATTCAGCTGGGCGA 347  
Db 651 GCCCAGGAGGAGGTTGAGTGAGTGAGATGGCCATTGCACTCCGGCGCTGGGCAA 710  
QY 348 CAAGTCAGACCGGTAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 389  
Db 711 CTGAGCAAACTCCATCTCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 752

## RESULT 15

AA722505/c  
LOCUS AA722505 501 bp mRNA linear EST 02-JAN-1998  
DEFINITION z131908.81 Soares\_pineal\_gland.N3HPG Homo sapiens cDNA clone  
IMAGE:413726 3' similar to contains Alu repetitive element;; mRNA  
sequence.

AA722505.1 GI:2740212

AA722505

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 501)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,

Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Willson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 478.

## FEATURES

Location/Qualifiers  
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1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5' TGTTACCAATCTGAAGTGGAGCGGCGGTTTTTTTTTTTTTTTTTT  
3'], double-stranded cDNA was size selected, ligated to  
Eco RI adapters (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of a modified pT7T3  
vector (Pharmacia). Library constructed by Bento Soares  
and M.Fatima Bonaldo."

## ORIGIN

Query Match 38.1%; Score 190.8; DB 9; Length 501;  
Best Local Similarity 71.9%; Pred. No. 2.6e-22;  
Matches 266; Conservative 0; Mismatches 97; Indels 7; Gaps 1;  
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Search completed: March 4, 2004, 16:38:38

Job time : 1964.09 secs

Does not  
encounter sid 15

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:50:45 ; Search time 2291.28 Seconds  
(without alignments)  
9552.848 Million cell updates/sec

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Sequence: 1 gaaacttgatgcacact.....ggaccattcaatggagaaa 505

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
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15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
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19: em\_mu.\*  
20: em\_on.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
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34: em\_hg\_pln.\*  
35: em\_hg\_rtd.\*  
36: em\_hg\_nam.\*  
37: em\_hg\_vit.\*  
38: em\_sy.\*  
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41: em\_hgo\_other.\*

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4	505	100.0	71132	9	AC092184	AC092184 Homo sapi
5	429.4	85.0	2818	6	BD016833	BD016833 Novel cyt
6	428	84.8	2172	6	BD016840	BD016840 Novel cyt
7	428	84.8	2791	9	AB040431	AB040431 Homo sapi
8	79	15.6	166447	2	BX323824	BX323824 Danio rer
9	73.2	14.5	3000	6	AX822415	AX822415 Sequence
10	73.2	14.5	3000	6	AX825612	AX825612 Sequence
11	73.2	14.5	3000	6	AX826055	AX826055 Sequence
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14	71.6	14.2	3000	6	AX822287	AX822287 Sequence
15	71.6	14.2	3000	6	AX825602	AX825602 Sequence
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ALIGNMENTS

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LOCUS BD016835  
DEFINITION Novel cytidine deaminase.  
ACCESSION BD016835  
VERSION BD016835.1 GI:22558011  
KEYWORDS JP 2001245669-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Honjo, T. and Muramatsu, M.  
TITLE Novel cytidine deaminase  
JOURNAL Patent: JP 2001245669-A 8 11-SEP-2001;

BD016835 Novel cytidine deaminase. 564 bp DNA linear PAT 27-AUG-2002

Pred. No. is the number of results predicted by chance to have a

JAPAN TOBACCO INC, TASUKU HONJO  
 OS Homo sapiens (human)  
 PN JP 2001245669-A/8  
 PD 11-SEP-2001  
 PF 28-MAR-2000 JP 2000092981  
 PI TASUKU HONJO, MASAMICHI MURAMATSU  
 PC C12N15/09, A61K39/395, A61K39/395, A61P1/00, A61P11/06, A61P13/12,  
 PC A61P17/00,  
 PC A61P27/02, A61P27/16, A61P37/02, A61P37/08, C07K16/18, C12N1/19, PC  
 C12N1/21,  
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 ACCESSION BD016860  
 VERSION BD016860.1 GI:22558036  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 11204)

Honjo, T. and Muramatsu, M.  
 Novel cytidine deaminase  
 Patent: JP 2001245669-A 33 11-SEP-2001;  
 JOURNAL JAPAN TOBACCO INC, TASUKU HONJO  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001245669-A/33  
 PD 11-SEP-2001  
 PF 28-MAR-2000 JP 2000092981  
 PI TASUKU HONJO, MASAMICHI MURAMATSU  
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ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,  
Alsbrooks, S.L., Amaral, H.C., Are, J.R., Ayele, M., Banks, T.,  
Barbaria, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,  
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,  
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Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Din, H.H.,  
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,  
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Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P.,  
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Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,  
Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P.,  
Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M.,  
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Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y.,  
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Leal, B., Lee, B., Lewis, D.C., Lewis, L., Li, J., Li, Z., Lichtarge, O.,  
Lieu, C., Liu, J., Liu, W., Louleghed, H., Lozano, R.J., Lu, X.,  
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Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,  
Rivas, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,  
Scherer, S., Scott, G., Shen, H., Shim, C., Shooshitari, N., Sisson, I.,  
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,  
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Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,  
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Wu, C., Wu, Y.F., Zhou, J., Zorrilla, S., Zorrilla, S., Kuchelapati, R.,  
Weinstock, G. and Gibbs, R.  
Direct Submission  
Unpublished  
2 (bases 1 to 71132)

TITLE  
JOURNAL  
REFERENCE

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (sites)  
Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.  
Isolation, tissue distribution, and chromosomal localization of the  
human activation-induced cytidine deaminase (AID) gene  
Genomics 68 (1), 85-88 (2000)  
20408890  
MEDLINE  
PUBMED 10950930  
REFERENCE  
AUTHORS  
Muto, T., Muto, T., Levy, Y., Geissmann, F., Plebani, A., Sanal, O.,  
Catalan, N., Porveille, M., Dufourcq-Lageouse, R., Gennery, A.,  
Tescan, I., Ersoy, F., Kayserili, H., Ugazio, A.G., Brousse, N.,  
Muramatsu, M., Notarangelo, L.D., Kinoshita, K., Honjo, T., Fischer, A.  
and Durandy, A.  
Activation-induced cytidine deaminase (AID) deficiency causes the  
autosomal recessive form of the Hyper-IgM syndrome (HIGM2)  
Cell 102 (5), 565-575 (2000)  
20460541  
MEDLINE  
PUBMED 11007475  
REFERENCE  
AUTHORS  
Muto, T., Muramatsu, M., Taniwaki, M., Kinoshita, K. and Honjo, T.  
Direct Submission  
Submitted (18-MAR-2000) Tasuku Honjo, Kyoto University, Department  
of Medical Chemistry, Faculty of Medicine, Yoshida, Sakyo-ku,  
Kyoto, Kyoto 606-8501, Japan (E-mail: honjo@four.med.kyoto-u.ac.jp,  
Tel: 81-75-753-4371 (ext. 4371), Fax: 81-75-753-4388)  
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DFGIRNKGCHVELLEFYSMDLPGRCYRVFTSPICDCAHVDLFRNP  
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ORIGIN  
Query Match 100.0%; Score 505; DB 9; Length 11204;  
Best Local Similarity 100.0%; Pred. No. 1.4e-64;  
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAACCTGAATGCACAACTCTTATTTAACTTATTTGACATAAGTTTGTAAAGAG 60  
Db 10700 GAAAACTGAATGCACAACTCTTATTTAACTTATTTGACATAAGTTTGTAAAGAG 10759  
Qy 61 TTTAAATGTACTTCATGATTCATTTATTTATTTATTTTCGCTCTAATGTTT 120  
Db 10760 TTTAAATGTACTTCATGATTCATTTATTTATTTATTTTCGCTCTAATGTTT 10819  
Qy 121 TTTTAAATCATGATTTCTTTTCGATATATTTGAAATGGAGTCTCAAGGCTTCATAAAT 180  
Db 10820 TTTTAAATCATGATTTCTTTTCGATATATTTGAAATGGAGTCTCAAGGCTTCATAAAT 10879  
Qy 181 TATACTTTAGAAATGATTCATAAACAAGTATGTAATTTGACATTCAGTAATGGTG 240  
Db 10880 TATACTTTAGAAATGATTCATAAACAAGTATGTAATTTGACATTCAGTAATGGTG 10939  
Qy 241 CTACGAAGCCATTTCTCTTGATTTTGTAGTAACTTTTATGACGCAAAATTTGCTTCGGC 300  
Db 10940 CTACGAAGCCATTTCTCTTGATTTTGTAGTAACTTTTATGACGCAAAATTTGCTTCGGC 10999  
Qy 301 TCACCTTTCAATCAGTAAATATAATGATATAATTTTGGAGCTGTGAGATAAAATACC 360

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Best Local Similarity 100.0%; Pred. No. 8.6e-65;
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 TTAATAATTTGATCTTCATGTAATTCATTTATTTATTTATTTTTCGCTCAATGATTT 120
Db 45303 TTAATAATTTGATCTTCATGTAATTCATTTATTTATTTATTTTTCGCTCAATGATTT 45362
QY 121 TTTTATTAACATGATTTCTTTCTGATATATTGAAATGGAGTCTCAAAGCTTCATAAAT 180
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QY 181 TATTAACCTTTAGAAATGATTTCTAATAACAGTATGTAATTTGTAACATTCAGTAATGGTG 240
Db 45423 TATTAACCTTTAGAAATGATTTCTAATAACAGTATGTAATTTGTAACATTCAGTAATGGTG 45482
QY 241 CTACGAAGCCATTTCTCTTGATTTTCTAGTAACTTTTATGACAGCAAAATTTGCTTCGGC 300
Db 45483 CTACGAAGCCATTTCTCTTGATTTTCTAGTAACTTTTATGACAGCAAAATTTGCTTCGGC 45542
QY 301 TCACCTTCAATCAGTTAAATGATATAATTTTGGAAAGCTGTGAAGATAAAATACC 360
Db 45543 TCACCTTCAATCAGTTAAATGATATAATTTTGGAAAGCTGTGAAGATAAAATACC 45602
QY 361 AAATAAAATAATATAAAGTATGATTTATGAGTTTAAATATAAATAACAGTATGATGAA 420
Db 45603 AAATAAAATAATATAAAGTATGATTTATGAGTTTAAATATAAATAACAGTATGATGAA 45662
QY 421 TAAACTTGAGAGTCCAGAGTTATCCCATACATCTGTAATCAACTAATTTCTCAAGAGG 480
Db 45663 TAAACTTGAGAGTCCAGAGTTATCCCATACATCTGTAATCAACTAATTTCTCAAGAGG 45722
QY 481 TGTAAGGACCATTCATGAGGAAA 505
Db 45723 TGTAAGGACCATTCATGAGGAAA 45747

RESULT 5
BD016833 2818 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Novel cytidine deaminase.
ACCESSION BD016833
VERSION BD016833.1 GI:22558009
KEYWORDS JP 2001245669-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Honjo, T. and Muramatsu, M.
TITLE Novel cytidine deaminase
JOURNAL Patent: JP 2001245669-A 6 11-SEP-2001;
JAPAN TOBACCO INC. TASUKU HONJO
COMMENT
OS Homo sapiens (human)
PN JP 2001245669-A/6
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO, MASAMICHI MURAMATSU
PC C12N15/09, A61K39/395, A61P1/00, A61P11/06, A61P13/12,
PC A61P17/00.
PC A61P27/02, A61P27/16, A61P37/08, C07K16/18, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12N9/78, C12P21/02, C12P21/08, C12N1/21, C12R1/19, PC
(C12N5/10, C12R1/91), C12N15/00, C12N5/00, C12N5/00, C12R1/91) CC
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FT CDS (80) .. (676)
FT 3'UTR (677) .. (2818).
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Best Local Similarity 99.8%; Pred. No. 1.8e-53;
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2367 GAAACCTGGAATGACCAACTGCTCTTATTTAAATCTTATTTGACATAAGTTTGTAAAGAG 2426
QY 61 TTAATAATTTGATCTTCATGTAATTCATTTATTTATTTTTCGCTCAATGATTT 120
Db 2427 TTAATAATTTGATCTTCATGTAATTCATTTATTTATTTTTCGCTCAATGATTT 2486
QY 121 TTTTATTAACATGATTTCTTTCTGATATATTGAAATGGAGTCTCAAAGCTTCATAAAT 180
Db 2487 TTTTATTAACATGATTTCTTTCTGATATATTGAAATGGAGTCTCAAAGCTTCATAAAT 2546
QY 181 TATAACTTTAGAAATGATTTCTAATAACAGTATGTAATTTGTAACATTCAGTAATGGTG 240
Db 2547 TATAACTTTAGAAATGATTTCTAATAACAGTATGTAATTTGTAACATTCAGTAATGGTG 2606
QY 241 CTACGAAGCCATTTCTCTTGATTTTCTAGTAACTTTTATGACAGCAAAATTTGCTTCGGC 300
Db 2607 CTACGAAGCCATTTCTCTTGATTTTCTAGTAACTTTTATGACAGCAAAATTTGCTTCGGC 2666
QY 301 TCACCTTCAATCAGTTAAATGATATAATTTTGGAAAGCTGTGAAGATAAAATACC 360
Db 2667 TCACCTTCAATCAGTTAAATGATATAATTTTGGAAAGCTGTGAAGATAAAATACC 2726
QY 361 AAATAAAATAATATAAAGTATGATTTATGAGTTTAAATATAAATAACAGTATGATGAA 420
Db 2727 AAATAAAATAATATAAAGTATGATTTATGAGTTTAAATATAAATAACAGTATGATGAA 2786
QY 421 TAAACTTGAGA 431
Db 2787 TAAACTTGAGA 2797

RESULT 6
BD016840 2172 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Novel cytidine deaminase.
ACCESSION BD016840
VERSION BD016840.1 GI:22558016
KEYWORDS JP 2001245669-A/13.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Honjo, T. and Muramatsu, M.
TITLE Novel cytidine deaminase
JOURNAL Patent: JP 2001245669-A 13 11-SEP-2001;
JAPAN TOBACCO INC. TASUKU HONJO
COMMENT
OS Homo sapiens (human)
PN JP 2001245669-A/13
PD 11-SEP-2001
PF 28-MAR-2000 JP 2000092981
PI TASUKU HONJO, MASAMICHI MURAMATSU
PC C12N15/09, A61K39/395, A61P1/00, A61P11/06, A61P13/12,
PC A61P17/00.
PC A61P27/02, A61P27/16, A61P37/08, C07K16/18, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12N9/78, C12P21/02, C12P21/08, C12N1/21, C12R1/19, PC
(C12N5/10, C12R1/91), C12N15/00, C12N5/00, C12N5/00, C12R1/91) CC
FH Key Location/Qualifiers
FT 5'UTR (1) .. (79)
FT CDS (80) .. (676)
FT 3'UTR (677) .. (2818).
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Query Match 84.8%; Score 428; DB 6; Length 2172;  
Best Local Similarity 100.0%; Pred. No. 3.1e-53;  
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAACTTGAATGCACTGCTTATTTAACTTATGATATGATATTTTGGTCTCAATGATTT 120  
DB 1745 GAAACTTGAATGCACTGCTTATTTAACTTATGATATGATATTTTGGTCTCAATGATTT 1804  
QY 61 TTAATAAATGTTACTTCAATGATATGATATTTTAACTTATGATATTTTGGTCTCAATGATTT 120  
DB 1805 TTAATAAATGTTACTTCAATGATATGATATTTTAACTTATGATATTTTGGTCTCAATGATTT 1854  
QY 121 TTTATTAAATGATTTTCTTTTCTGATATTTGAAATGAGTCTCAAGCTTCATAAAT 180  
DB 1865 TTTATTAAATGATTTTCTTTTCTGATATTTGAAATGAGTCTCAAGCTTCATAAAT 1924  
QY 181 TATAACTTTAGAAATGATTTCTAATAACACGATGATTTTAACTTGAACATTCGATGATGGT 240  
DB 1925 TATAACTTTAGAAATGATTTCTAATAACACGATGATTTTAACTTGAACATTCGATGATGGT 1984  
QY 241 CTACGAAGCAATTTCTTTGATTTTATGATTTTAACTTTTATGACAGCAAAATTTGCTTCTGGC 300  
DB 1985 CTACGAAGCAATTTCTTTGATTTTATGATTTTAACTTTTATGACAGCAAAATTTGCTTCTGGC 2044  
QY 301 TCACATTTCAATCAGTAAATGATTAATGATTAATTTTGGACCTGTGAAGTAAATATACC 360  
DB 2045 TCACATTTCAATCAGTAAATGATTAATGATTAATTTTGGACCTGTGAAGTAAATATACC 2104  
QY 361 AAATAAATAATATATAAAGTATTTTATGATTTTAACTTTAAATATAAATCAGTATGATGAA 420  
DB 2105 AAATAAATAATATATAAAGTATTTTATGATTTTAACTTTAAATATAAATCAGTATGATGAA 2164  
QY 421 TAAACTTG 428  
DB 2165 TAAACTTG 2172

RESULT 7  
LOCUS AB040431 2791 bp mRNA linear PRI 03-OCT-2000  
DEFINITION Homo sapiens AID mRNA for activation-induced cytidine deaminase, complete CDS.  
ACCESSION AB040431  
VERSION AB040431.1 GI:9988409  
KEYWORDS AID; activation-induced cytidine deaminase; Human AID.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.  
TITLE Isolation, tissue distribution, and chromosomal localization of the human activation-induced cytidine deaminase (AID) gene  
JOURNAL Genomics 68 (1), 85-88 (2000)  
MEDLINE 20408890  
PUBMED 10950930  
REFERENCE 2 (sites)  
AUTHORS Revy,P., Muto,T., Levy,Y., Geissmann,F., Plebani,A., Sanal,O., Catalan,N., Forveille,M., Dufourcq-Lageleouse,R., Gennery,A., Tezcan,I., Ersoy,F., Kayserili,H., Ugazio,A.G., Brouse,N., Muramatsu,M., Notarangelo,L.D., Kinoshita,K., Honjo,T., Fischer,A. and Durandy,A.  
TITLE Activation-induced cytidine deaminase (AID) deficiency causes the autosomal recessive form of the Hyper-IgM syndrome (HIGM2)  
JOURNAL Cell 102 (5), 565-575 (2000)  
MEDLINE 20460541  
PUBMED 11007475  
REFERENCE 3 (bases 1 to 2791)  
AUTHORS Muto,T., Muramatsu,M., Taniwaki,M., Kinoshita,K. and Honjo,T.

TITLE Direct Submission  
JOURNAL Submitted (18-MAR-2000) Tasaku Honjo, Kyoto University, Department of Medical Chemistry, Faculty of Medicine, Yoshida, Sakyo-ku, Kyoto, Kyoto 606-8501, Japan (E-mail:honjo@four.med.kyoto-u.ac.jp, Tel:81-75-753-4371(ex.4371), Fax:81-75-753-4388)  
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ORIGIN

Query Match 84.8%; Score 428; DB 9; Length 2791;  
Best Local Similarity 100.0%; Pred. No. 2.9e-53;  
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAACTTGAATGCACTGCTTATTTAACTTATGATATTTTGGTCTCAATGATTT 60  
DB 2364 GAAACTTGAATGCACTGCTTATTTAACTTATGATATTTTGGTCTCAATGATTT 2423  
QY 61 TTAATAAATGTTACTTCAATGATTTTCAATTTATATTTTATATTTTGGTCTCAATGATTT 120  
DB 2424 TTAATAAATGTTACTTCAATGATTTTCAATTTATATTTTGGTCTCAATGATTT 2483  
QY 121 TTTATTAAATGATTTTCTTTTCTGATATTTGAAATGAGTCTCAAGCTTCATAAAT 180  
DB 2484 TTTATTAAATGATTTTCTTTTCTGATATTTGAAATGAGTCTCAAGCTTCATAAAT 2543  
QY 181 TATAACTTTAGAATGATTTCTAATAACACGATGATTTGAAATGAGTCTCAAGTATGGTG 240  
DB 2544 TATAACTTTAGAATGATTTCTAATAACACGATGATTTGAAATGAGTCTCAAGTATGGTG 2603  
QY 241 CTACGAAGCAATTTCTTTGATTTTATGATTTTAACTTTTATGACAGCAAAATTTGCTTCTGGC 300  
DB 2604 CTACGAAGCAATTTCTTTGATTTTATGATTTTAACTTTTATGACAGCAAAATTTGCTTCTGGC 2663  
QY 301 TCACATTTCAATCAGTAAATGATTAATGATTAATTTTGGACCTGTGAAGTAAATATACC 360  
DB 2664 TCACATTTCAATCAGTAAATGATTAATGATTAATTTTGGACCTGTGAAGTAAATATACC 2723  
QY 361 AAATAAATAATATAAAGTATTTATGATTTTAACTTTAAATATAAATCAGTATGATGAA 420  
DB 2724 AAATAAATAATATAAAGTATTTATGATTTTAACTTTAAATATAAATCAGTATGATGAA 2783  
QY 421 TAAACTTG 428  
DB 2784 TAAACTTG 2791

RESULT 8  
LOCUS BX323824/c 166447 bp DNA linear HTG 21-OCT-2003  
DEFINITION Danio rerio clone DKEY-37F18, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 19 unordered pieces.  
ACCESSION BX323824  
VERSION BX323824.4 GI:37805603  
KEYWORDS HTG; HTGS PHASE1.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 166447)  
Sims, S.  
Direct Submission  
Submitted (20-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Oct 21, 2003 this sequence version replaced gi:30026999.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: zfish-help@sanger.ac.uk  
----- Project Information  
Center project name: zK37P18  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Chemistry: Dye-terminator; 100% of reads  
Consensus quality: 15874 bases at least Q40  
Consensus quality: 15843 bases at least Q30  
Consensus quality: 160876 bases at least Q20  
Insert size: 164647; sum-of-contigs  
Insert size: 181199; 3.2% error; agarose-fp  
Quality coverage: 6.51x in Q20 bases; sum-of-contigs Quality  
coverage: 6.15x in Q20 bases; agarose-fp  
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COMMENT

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 19 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 22674: contig of 22674 bp in length  
22675 22774: gap of 100 bp  
22775 31865: contig of 9091 bp in length  
31866 31965: gap of 100 bp  
31966 38466: contig of 6500 bp in length  
38467 42826: contig of 4261 bp in length  
42827 42927: gap of 100 bp  
42928 48541: contig of 5615 bp in length  
48542 48642: gap of 100 bp  
48643 56767: contig of 8126 bp in length  
56768 56867: gap of 100 bp  
56868 76763: contig of 19796 bp in length  
76764 88853: contig of 12090 bp in length  
88854 95380: gap of 100 bp  
95381 95481: contig of 6427 bp in length  
95482 101276: contig of 5796 bp in length  
101277 101377: gap of 100 bp  
101378 116856: contig of 15480 bp in length  
116857 116956: gap of 100 bp  
116957 125237: contig of 8281 bp in length  
125238 125337: gap of 100 bp  
125338 131209: contig of 5872 bp in length  
131210 131309: gap of 100 bp  
131310 134536: contig of 3227 bp in length  
134537 134636: gap of 100 bp  
134637 138678: contig of 4042 bp in length  
138679 138778: gap of 100 bp  
138779 149409: contig of 10531 bp in length  
149410 149510: gap of 100 bp  
149511 152111: contig of 2702 bp in length  
152112 152311: gap of 100 bp  
152312 163792: contig of 11481 bp in length  
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Best Local Similarity 48.1%; Pred. NO. 0.004;  
Matches 202; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

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Qy 101 TATTTTGGCTAATGATTTTATTAATGAATGATTTTCCCTTTCTGATATATGAATGA 160  
Db 152792 AATTTATTTAT 152733

QY 161 GTCTCAAGCTTCAPAAATTTATACCTTTAGAAATGATCTTAATAACAACGCTATGTAAT 220  
 Db 152732 TTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 152673  
 QY 221 GTAACATTCGAGTATGCTGACGAGCCATTTCTCTGATTTTCTAGTAACTTTTATG 280  
 Db 152672 AATAATATGTTTAAATTAATTAATTAATTAATTTTNTTTTATTTTAAATAATTTATTT 152613  
 QY 281 ACAGCAAAATTTGCTTCTGCTCAGCTTCCATTCAGTTAAATTAATTAATTAATTTTGA 340  
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 QY 341 ACCTGTGAGATTAATACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 400  
 Db 152552 ATTAATTAATTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 152493  
 QY 401 AAAAAATCAGTATGATGAATAAATTCGAGAGTCCAGAGTTATCCCATACATCTGTAAT 460  
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RESULT 9  
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 LOCUS AX822415 3000 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 307 from Patent EP1340818  
 ACCESSION AX822415  
 VERSION AX822415.1 GI:39749043  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Adorjan,P., Burger,M., Maier,S., Nimmrich,I., Becker,E., Lesche,R.,  
 Rujan,T. and Schmitt,A.  
 TITLE Method and nucleic acids for the analysis of a colon cell  
 JOURNAL proliferative disorder  
 PATENT: EP 1340818-A 307 03-SEP-2003;  
 FEATURES Epigenomics AG (DE)  
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 Best Local Similarity 48.6%; Pred. No. 0.078;  
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QY 2 AAAACTTGAATGCACAACTGCTCTTATTTAACTTTATTTGTCATATAGTTTGTAAAGAGT 61  
 Db 164 AAAATTTGAGTTTTAGTTTTTTTATATGTGAAATGGAGAAATAAATTTGTAAATTA 223

QY 62 TAAAAATTTGTTACTTCATGTATTCATTTATATTTTATATTTTATTTTTCGCTCTAATGATTT 121  
 Db 224 TTAATTTGTTTATTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 283

QY 122 TTATTAACATGATTTCCCTTTCTGATATATTTGAATGGAGTCTCAAGCTTCATAAATTT 181  
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QY 182 ATAACTTTAGAATGATTTCTTAATAACAACGATGTAATTTGTAACATTCAGTAATGGTGC 241  
 Db 344 TTTTATTTTTCAGAAATTTAGAAAGGAATATATTTGTTGGTAATGTTTATTTTATTTTAA 403

QY 242 TAGGAAGCCATTTCTCTGATTTTATTTAGTAACTTTTATGACAGCAAAATTTGCTCTGGCT 301  
 Db 404 AATAAATTTTGTAGGAAGAATATTTTAGTAAGTGAATGAGAGTAGTAATGATTTGTTTTATT 463

QY 302 CACTTTCAATCAGTTTAAATTAATTAATTAATTTTGAAGCTGTGAAGATAAAATACCA 361  
 Db 464 ATTTTAAATTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 523

QY 362 AATAAATTAATAAAGTATTTATGAGCTTAAATTAATTAATTAATTAATTAATTAATTAATTA 415  
 Db 524 TTTATTAATAAATAAATTTGTAATTTAATTAAGTATTTAGGGTTGATATTTGTTTTTGA 577

RESULT 11  
 AX826055  
 LOCUS AX826055 3000 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 307 from Patent WO03072821.  
 ACCESSION AX826055  
 VERSION AX826055.1 GI:39751569  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

QY 362 AATAAATAATATAAAGTATTTATATCAAGTTAAATTAATAAATAAATCAGTATGA 415  
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RESULT 10  
 AX825612  
 LOCUS AX825612 3000 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 20 from Patent WO03072820.  
 ACCESSION AX825612  
 VERSION AX825612.1 GI:39751139  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Adorjan,P., Burger,M., Maier,S., Lesche,R., Cottrell,S. and  
 Mooney,S.  
 TITLE Method and nucleic acids for the analysis of colon cell  
 JOURNAL proliferative disorders  
 PATENT: WO 03072820-A 20 04-SEP-2003;  
 FEATURES Epigenomics AG (DE)  
 source Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="chemically treated genomic DNA (Homo sapiens)"

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Query Match 14.5%; Score 73.2; DB 6; Length 3000;  
 Best Local Similarity 48.6%; Pred. No. 0.078;  
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QY 2 AAAACTTGAATGCACAACTGCTCTTATTTAACTTTATTTGTCATATAGTTTGTAAAGAGT 61  
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QY 62 TAAAAATTTGTTACTTCATGTATTCATTTATATTTTATATTTTATTTTTCGCTCTAATGATTT 121  
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QY 182 ATAACTTTAGAATGATTTCTTAATAACAACGATGTAATTTGTAACATTCAGTAATGGTGC 241  
 Db 344 TTTTATTTTTCAGAAATTTAGAAAGGAATATATTTGTTGGTAATGTTTATTTTATTTTAA 403

QY 242 TAGGAAGCCATTTCTCTGATTTTATTTAGTAACTTTTATGACAGCAAAATTTGCTCTGGCT 301  
 Db 404 AATAAATTTTGTAGGAAGAATATTTTAGTAAGTGAATGAGAGTAGTAATGATTTGTTTTATT 463

QY 302 CACTTTCAATCAGTTTAAATTAATTAATTAATTTTGAAGCTGTGAAGATAAAATACCA 361  
 Db 464 ATTTTAAATTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 523

QY 362 AATAAATTAATAAAGTATTTATGAGCTTAAATTAATTAATTAATTAATTAATTAATTAATTA 415  
 Db 524 TTTATTAATAAATAAATTTGTAATTTAATTAAGTATTTAGGGTTGATATTTGTTTTTGA 577

RESULT 11  
 AX826055  
 LOCUS AX826055 3000 bp DNA linear PAT 11-DEC-2003  
 DEFINITION Sequence 307 from Patent WO03072821.  
 ACCESSION AX826055  
 VERSION AX826055.1 GI:39751569  
 KEYWORDS synthetic construct  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.



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Matches 231; Conservative 0; Mismatches 227; Indels 3; Gaps 2;
QY 8 TGAATGCACAACTGCTCTTATTTAACTTATGTACATAAGTTTGTAAAGAGTTAAAAA 67
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QY 128 ACATGATTTCTTTTCTGATATATGAAATGGAGCTCAAGCTCCATAAATTTAACT 187
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Db 27121 ATATAATATATGTTT-TATGTATTTATATAAATAATATATGTTTATGTTATTTATA 27063
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QY 308 CAATCAGTTAAATAAATGATAATAATTTTGGAGCTGTGAAGATAAATAACCAATAAA 367
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QY 368 AT--AATATAAAGTATTTATATGAGTTAAATAAATAAATAACAGTATGAGTAATAAC 425
Db 26942 ATTATATAAATAATATATATTTTATATAATAATAATAATATATTTTATTTATATA 26883
QY 426 TTGAGAGTCCAGAGTTATCCCATACATCTGTTATCAACTA 466
Db 26882 ACTATATATATAATATATATTTATTTATTTATATATTA 26842

RESULT 14
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LOCUS AX822287 3000 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 179 from Patent EP1340818.
ACCESSION AX822287
VERSION AX822287.1 GI:39748915
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: EP 1340818-A 179 03-SEP-2003;
EpiGenomics AG (DE)
FEATURES
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1. 3000
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN
Query Match 14.2%; Score 71.6; DB 6; Length 3000;
Best Local Similarity 48.3%; Pred. No. 0.13;
Matches 200; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
QY 2 AAACCTTGAATGCACAACTGCTTATTTTAACTTATTTGTACATAAGTTTGTAAAGAGT 61
Db 164 AAATTTGAGTCTTTTATGTTTATATGTAATGGAATGGAATAAATAATTTGTAATAAT 223
QY 62 TAAATATGTTACTTCATGTTATTTATTTATTTTATTTTTCGCTCTAATGATTTT 121
Db 224 TTAATTTGTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 283
QY 122 TTATTAACATGATTTTCTTTTCTGATATATTGAATGAGTCTCAAGCTTCATAAATTT 181
Db 284 TTAGATGTTTATTTTAAATATGTTTAAATTCGTTTGTGTTTATTTTATTTTATTT 343
QY 182 ATAACTTTAGAAATGATTTCTTAATACACAGTATGTAATTTGTAACATTGCAAGTAA 241
Db 344 TTTTATTTTGAAGAAATAGAAAGAAATATTTATGTTTGGTAAATGTTTATTTTAA 403
QY 242 TACGAAGCCATTTCTCTTGAATTTTATGTAATTTTATGACAGCAAAATTTGCTTCTGCT 301
Db 404 AATAAATTTGTAGGAAGAAATATTTTAGTAAGTGAAGTAGTAACGATTTGTTTATTT 463
QY 302 CACTTTCAATCAGTTAAATAATGATAAATTTTGGAGCTGTGAAGATAAATAACCA 361
Db 464 ATTTTAAATTTATATATTTATTTTATGAGTTTATTTTAAAGTATTTGATATAATTTT 523
QY 362 AATAAATAATATAAAGTATTTATATGAAAGTTTAAATAAATAAATAACAGTATGA 415
Db 524 TTTATTAATAAATAAATTTGTAATTAAGTATTTAGGGTTCATATTTGTTTGA 577

RESULT 15
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LOCUS AX825602 3000 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 10 from Patent WO03072820.
ACCESSION AX825602
VERSION AX825602.1 GI:39751129
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Lesche, R., Cottrell, S. and
Mooney, S.
TITLE Method and nucleic acids for the analysis of colon cell
JOURNAL proliferative disorders
Patent: WO 03072820-A 10 04-SEP-2003;
EpiGenomics AG (DE)
FEATURES
source
1. 3000
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
ORIGIN
Query Match 14.2%; Score 71.6; DB 6; Length 3000;
Best Local Similarity 48.3%; Pred. No. 0.13;
Matches 200; Conservative 0; Mismatches 214; Indels 0; Gaps 0;
QY 2 AAACCTTGAATGCACAACTGCTTATTTTAACTTATTTGTACATAAGTTTGTAAAGAGT 61
Db 164 AAATTTGAGTCTTTTATGTTTATATGTAATGGAATGGAATAAATAATTTGTAATAAT 223
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Qy 362 AATAAATATATATAAAGTGATTTATATGAAGTTAAAAATAAAAAATCAGTATGA 415  
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Job time : 2295.28 secs

GenCore version 5.1.6  
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Sequence: 1 gaaacttgatgacacact.....ggaccattcaatggagaaaa 505

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: Geneseqn1990s:\*  
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4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505	100.0	6564	3 AAC55314	AAC55314 Human act
2	505	100.0	11204	3 AAC55339	AAC55339 Human act
3	505	100.0	11204	6 ABS73286	ABS73286 DNA encod
4	429.4	85.0	2818	3 AAC55312	AAC55312 Human act
5	428	84.8	2172	3 AAC55319	AAC55319 Human act
6	428	84.8	2791	6 ABS73287	ABS73287 DNA encod
7	428	84.8	2791	6 ABS73288	ABS73288 DNA encod
8	418	82.8	574	4 AAK81089	AAK81089 Human imm
9	73.2	14.5	3000	9 ADB54251	ADB54251 Pretreate
10	73.2	14.5	3000	9 ADB37774	ADB37774 Human che
11	73.2	14.5	29993	9 ADB37662	ADB37662 Human che
12	71.6	14.2	3000	9 ADB54123	ADB54123 Pretreate
13	71.6	14.2	3000	9 ADB37764	ADB37764 Human che
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16	71.6	14.2	38342	4 AAS46745	AAS46745 Tumour su
17	71.6	14.2	38342	6 ABL31506	ABL31506 Signal tr
18	67.8	13.4	8056	7 ABL10100	ABL10100 Haematopo
19	66.4	13.1	240000	7 ACD13446	ACD13446 Human DNA
20	64.6	12.8	8056	7 ABL10246	ABL10246 Haematopo
21	64.2	12.7	6370	6 ABL31349	ABL31349 Signal tr
22	64.2	12.7	6370	6 ABL70568	ABL70568 Chemical
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ALIGNMENTS

RESULT 1

AAC55314  
ID AAC55314 standard; DNA; 6564 BP.

XX AAC55314;

XX 05-FEB-2001 (first entry)

XX Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:10.

XX Activation-induced cytidine deaminase; AID; cytidine deaminase;  
XX Immune related disease; allergy; allergic disease; antiallergic;  
XX Antianaemic; antidiabetic; ophthalmologic; anti-HIV; dermatological;  
XX gene therapy; B cell associated immune system disorder; food allergy;  
XX immunodeficiency disease; immunoglobulin A deficiency disease; asthma;  
XX IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;  
XX drug allergy; allergic rhinitis; Rosen disease; Digeorge disease; AIDS;  
XX ataxia telangiectasia; common variable immunodeficiency disorder;  
XX major histocompatibility class II deficiency disease;  
XX auto immunodeficiency syndrome; Igg subclass selection disorder; ds.

XX Homo sapiens.

XX WO200058480-A1.

XX 05-OCT-2000.

XX 28-MAR-2000; 2000WO-JF001918.

XX 29-MAR-1999; 99JP-00087192.

XX 24-JUN-1999; 99JP-00178999.

XX 27-DEC-1999; 99JP-00371382.

XX (NISR) JAPAN TOBACCO INC.

XX (HONJ/) HONJO T.

XX Honjo T, Muramatsu M;

XX WPI; 2000-611715/58.

XX Nucleic acid encoding activation induced cytidine deaminase, useful as a target for drug development for immune-related diseases including allergies.

XX Claim 17; Page 145-150; 174pp; Japanese.



CC The present invention describes an activation-induced cytidine deaminase  
CC (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has  
CC cytidine activity similar to APOBEC-1. AID has anti-allergic, antianaemic,  
CC antiasthmatic, ophthalmological, anti-HIV and dermatological activities,  
CC and can be used in gene therapy. AID polynucleotides are useful in  
CC methods for identifying drugs for the treatment of B cell associated  
CC immune system disorders, immunodeficiency diseases and allergies, such as  
CC immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-  
CC globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy,  
CC drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia  
CC telangiectasia, common variable immunodeficiency disorder, MHC (major  
CC histocompatibility class II deficiency disease, AIDS (auto  
CC immunodeficiency syndrome), elevated IGE disorder, and IGC subclass  
CC selection disorder. The DNA sequences encoding AID may be used for gene  
CC therapy and the antibodies to the AID protein may be used for diagnosis  
CC and treatment of these disorders. The present sequence represents a  
CC genomic DNA sequence of human AID  
XX  
SQ Sequence 6564 BP; 1909 A; 1358 C; 1383 G; 1914 T; 0 U; 0 Other;  
Query Match 100.0%; Score 505; DB 3; Length 6564;  
Best Local Similarity 100.0%; Pred. No. 8e-72;  
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAACTTGAATGCACAACTGCTTATTTAATCTTATGTCATAGTTGTAAAGAG 60  
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QY 301 TCACCTTTCAATCAGTTAAATGATTAATTAATTTTGAAGCTGTGAAGATAAATACC 360  
Db 5785 TCACCTTTCAATCAGTTAAATGATTAATTAATTTTGAAGCTGTGAAGATAAATACC 5844  
QY 361 AAATAAAATATATAAAGTGATTTATATGAAGTTAAATAAATAAATCAGTATGATGAA 420  
Db 5845 AAATAAAATATATAAAGTGATTTATATGAAGTTAAATAAATAAATCAGTATGATGAA 5904  
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Db 5905 TAACTTTGAGTCCAGAGGTTATCCATACATCTGTATCACTAATTTCTCAAGGG 5964  
QY 481 TGTAAAGGACCATTCATGAGAGAAA 505  
Db 5965 TGTAAAGGACCATTCATGAGAGAAA 5989  
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ID AAC55339 standard; DNA; 11204 BP.  
XX  
AC AAC55339;  
AC AAC55339;  
XX  
DT 05-FEB-2001 (first entry)  
XX  
DE Human activation-induced cytidine deaminase genomic DNA SEQ ID NO:35.  
XX  
KW Activation-induced cytidine deaminase; AID; cytidine deaminase;  
KW immune related disease; allergy; allergic disease; antiallergic;

KW antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;  
KW gene therapy; B cell associated immune system disorder; food allergy;  
KW immunodeficiency disease; immunoglobulin A deficiency disease; asthma;  
KW IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;  
KW drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;  
KW ataxia telangiectasia; common variable immunodeficiency disorder;  
KW major histocompatibility class II deficiency disease;  
KW auto immunodeficiency syndrome; IGC subclass selection disorder; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200058480-A1.  
XX  
XX 05-OCT-2000.  
XX  
XX 28-MAR-2000; 2000WO-JP001918.  
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XX 29-MAR-1999; 99JP-00087192.  
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XX 24-JUN-1999; 99JP-00178999.  
XX  
XX 27-DEC-1999; 99JP-00371382.  
XX  
XX (NISR) JAPAN TOBACCO INC.  
XX  
XX (HONJ/) HONJO T.  
XX  
XX Honjo T, Muramatsu M;  
XX  
XX WPI; 2000-611715/58.  
XX  
XX Nucleic acid encoding activation induced cytidine deaminase, useful as a  
XX target for drug development for immune-related diseases including  
XX allergies.  
XX  
XX Claim 17; Page 163-170; 174pp; Japanese.  
XX  
XX The present invention describes an activation-induced cytidine deaminase  
XX (AID). AID structurally relates to an RNA editing enzyme APOBEC-1 and has  
XX cytidine activity similar to APOBEC-1. AID has anti-allergic, antianaemic,  
XX antiasthmatic, ophthalmological, anti-HIV and dermatological activities,  
XX and can be used in gene therapy. AID polynucleotides are useful in  
XX methods for identifying drugs for the treatment of B cell associated  
XX immune system disorders, immunodeficiency diseases and allergies, such as  
XX immunoglobulin A (IGA) deficiency disease, IGA nephritis, gamma-  
XX globulinaemia, atopic dermatitis, allergic colitis, asthma, food allergy,  
XX drug allergy, allergic rhinitis, Rosen disease, DiGeorge disease, ataxia  
XX telangiectasia, common variable immunodeficiency disorder, MHC (major  
XX histocompatibility class II deficiency disease, AIDS (auto  
XX immunodeficiency syndrome), elevated IGE disorder, and IGC subclass  
XX selection disorder. The DNA sequences encoding AID may be used for gene  
XX therapy and the antibodies to the AID protein may be used for diagnosis  
XX and treatment of these disorders. The present sequence represents a  
XX genomic DNA sequence of human AID  
XX  
SQ Sequence 11204 BP; 3305 A; 2273 C; 2373 G; 3253 T; 0 U; 0 Other;  
Query Match 100.0%; Score 505; DB 3; Length 11204;  
Best Local Similarity 100.0%; Pred. No. 7.7e-72;  
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAACTTGAATGCACAACTGCTTATTTAATCTTATGTCATAGTTGTAAAGAG 60  
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QY 61 TTAATAATTTGTTACTTCATGATTCATTTATATTTATTTATTTGCGTCTAATGATT 120  
Db 10760 TTAATAATTTGTTACTTCATGATTCATTTATATTTATTTATTTGCGTCTAATGATT 10819  
QY 121 TTTATTAACATGATTTCCCTTTCTGATATATTTGAATGGAGTCTCAAGCTTCATAAAT 180  
Db 10820 TTTATTAACATGATTTCCCTTTCTGATATATTTGAATGGAGTCTCAAGCTTCATAAAT 10879  
QY 181 TATAACTTTAGAAATGATTTCTAATAACACGATGTAATTTGAATGATGATGATGGTG 240  
Db 10880 TATAACTTTAGAAATGATTTCTAATAACACGATGTAATTTGAATGATGATGATGGTG 10939



Query Match	85.0%	Score 429.4	DB 3	Length 2818
Best Local Similarity	99.8%	Pred. No. 8.7e-60		
Matches 430	Conservative	0	Mismatches 1	Indels 0
			Gaps	0

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QY	301	TCACTTTCAATCAGTTAAATAAATGATAAATAATTTTGGAGCTGTGAAGATAAAATACC	360
Db	2667	TCACTTTCAATCAGTTAAATAAATGATAAATAATTTTGGAGCTGTGAAGATAAAATACC	2726
QY	361	AAATATAATAATATAAAAGTATTTATATGAGTTTAAATAAAAAATCAGTATGATGAA	420
Db	2727	AAATATAATAATATAAAAGTATTTATATGAGTTTAAATAAAAAATCAGTATGATGAA	2786
QY	421	TAAACTTGAGA	431
Db	2787	TAAACTTGAAA	2797
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QY	AAC55319		
XX	ID	AAC55319 standard; DNA; 2172 BP.	
XX	AC	AAC55319;	
XX	DT	05-FEB-2001 (first entry)	
XX	Human	Human activation-induced cytidine deaminase exon 5 SEQ ID NO:15.	
XX	Activation-induced	Activation-induced cytidine deaminase; AID; cytidine deaminase;	
XX	immune related	immune related disease; allergy; allergic disease; antiallergic;	
XX	antianaemic;	antianaemic; antiasthmatic; ophthalmological; anti-HIV; dermatological;	
XX	gene therapy;	gene therapy; B cell associated immune system disorder; food allergy;	
XX	immunodeficiency	immunodeficiency disease; immunoglobulin A deficiency disease; asthma;	
XX	IGA nephritis;	IGA nephritis; gamma-globulinaemia; atopic dermatitis; allergic colitis;	
XX	drug allergy;	drug allergy; allergic rhinitis; Rosen disease; DiGeorge disease; AIDS;	
XX	ataxia telangiectasia;	ataxia telangiectasia; common variable immunodeficiency disorder;	
XX	major histocompatibility	major histocompatibility class II deficiency disease;	
XX	auto immunodeficiency	auto immunodeficiency syndrome; IqG subclass selection disorder; ds.	
XX	Homo sapiens.		
XX	WC2000059480-A1.		
XX	05-OCT-2000.		
XX	28-MAR-2000;	2000WO-JP001918.	
XX	29-MAR-1999;	99JP-00087192.	
XX	24-JUN-1999;	99JP-00178999.	
XX	27-DEC-1999;	99JP-00371382.	
XX	(NISR ) JAPAN TOBACCO INC.		
XX	(HONJ/ ) HONJO T.		
XX	Honjo T, Muramatsu M;		
XX	WPI;	2000-611715/58.	
XX	Nucleic acid encoding	activation induced cytidine deaminase, useful as a	
XX	target for drug development	for immune-related diseases including	
XX	allergies.		
XX	Claim 18;	Page 152-153; 174pp; Japanese.	
XX	The present invention	describes an activation-induced cytidine deaminase	
XX	(AID). AID	structurally relates to an RNA editing enzyme APOBEC-1 and has	
XX	cytidine activity	similar to APOBEC-1. AID has antiallergic, antianaemic,	
XX	antiasthmatic;	ophthalmological, anti-HIV and dermatological activities,	
XX	and can be used	in gene therapy. AID polynucleotides are useful in	
XX	methods for identifying	drugs for the treatment of B cell associated	
XX	immune system disorders,	immunodeficiency diseases and allergies, such as	
XX	immunoglobulin A (IGA)	deficiency disease, IGA nephritis, gamma-	
XX	globulinaemia, atopic	dermatitis, allergic colitis, asthma, food allergy,	
XX	drug allergy, allergic	rhinitis, Rosen disease, DiGeorge disease, ataxia	



Db		2784 TAAACTTG 2791	
RESULT 7			
ABS73288			
ID	ABS73288 standard; DNA; 2791 BP.		
XX			
AC	ABS73288;		
XX			
DT	04-DEC-2002 (first entry)		
DE	DNA encoding human translocation del(12p) protein #3.		
XX			
KW	Chromosome aberration; oncogenic fusion protein; cancer;		
KW	proliferative disease; cellular protein isoform; heat shock protein 90;		
KW	HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;		
KW	T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;		
KW	acute myeloid leukaemia; AML; Chronic myelomonocytic leukaemia; CMWL;		
KW	acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;		
KW	papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;		
KW	rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.		
OS	Homo sapiens.		
XX			
PN	WO200269900-A2.		
XX			
PD	12-SEP-2002.		
XX			
PF	01-MAR-2002; 2002WO-US006518.		
XX			
PR	01-MAR-2001; 2001US-0272751P.		
XX			
PA	(CONF-) CONFORMA THERAPEUTICS CORP.		
PI	Fritz LC, Burrows FJ;		
DR	WPI; 2002-698710/75.		
DR	P-PSDB; ABG95084.		
XX			
PT	Treating genetically-defined disease associated with chromosomal		
PT	aberrations yielding oncogenic fusion proteins, e.g. cell proliferative		
PT	diseases, involves administering an inhibitor of heat shock protein 90.		
PS	Disclosure; Page 248-249; 389pp; English.		
CC	The invention describes a method of treating genetically-defined disease		
CC	associated with chromosomal aberrations yielding oncogenic fusion		
CC	proteins (I), treating cancerous cells containing (I) in a heterogeneous		
CC	cell population, treating proliferative diseases associated with mutant		
CC	protein or cellular protein isoforms (II) dependent on heat shock protein		
CC	(HSP)-90, or selectively treating cells expressing (II) involving		
CC	administering HSP90-inhibitor. The method is useful for treating		
CC	genetically-defined disease with chromosomal aberration yielding		
CC	oncogenic fusion protein, treating cancerous cells containing fusion		
CC	protein in heterogeneous cell population, treating proliferative disease		
CC	(e.g. rheumatoid arthritis or cancer) associated with mutant protein or		
CC	cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.		
CC	p53), or selectively treating cells expressing mutant protein or cellular		
CC	protein isoform in a patient heterozygous for (II). The method is useful		
CC	for treating a disease, e.g. haematopoietic disorder such as T or B cell		
CC	lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,		
CC	or a disease characterised by a solid tumour such as papillary thyroid		
CC	carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and		
CC	synovial sarcoma. The method is also useful for treating viral		
CC	infections. This represents the DNA sequence of a chromosome aberration		
XX	Sequence 2791 BP; 842 A; 548 C; 625 G; 776 T; 0 U; 0 Other;		
SQ			
Query Match	84.8%; Score 428; DB 6; Length 2791;		
Best Local Similarity	100.0%; Pred. No. 1.4e-59;		
Matches 428; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 GAAAAGTTGAATGCACAAGTCTTATTATTTTAATCTTATGTACATAAGTTGTAAAAAGAG 60		
Db	2364 GAAAAGTTGAATGCACAAGTCTTATTATTTTAATCTTATGTACATAAGTTGTAAAAAGAG 2423		
QY	61 TTAAAAATTTGTTACTTCATGTATTCAITTTATATTTTTTATATTTTGGCGTCTAATGATTT 120		
Db	2424 TTAAAAATTTGTTACTTCATGTATTCAITTTATATTTTTTATATTTTGGCGTCTAATGATTT 2483		
QY	121 TTTTATTAAACATGATTTCCITTTCTGATATTTGAAATGGAGTCTCAAAGCTTCATAAATT 180		
Db	2484 TTTTATTAAACATGATTTCCITTTCTGATATTTGAAATGGAGTCTCAAAGCTTCATAAATT 2543		
QY	181 TATAACTTTAGAATGATTTCTTAATAACAACGATGTAATTTGAACATTCAGTAATGGTG 240		
Db	2544 TATAACTTTAGAATGATTTCTTAATAACAACGATGTAATTTGAACATTCAGTAATGGTG 2603		
QY	241 CTACGAAGCCATTTCTCTCATTTTGTAGTAAACCTTTTAGACAGCAAAATTTGCTTCTGGC 300		
Db	2604 CTACGAAGCCATTTCTCTCATTTTGTAGTAAACCTTTTAGACAGCAAAATTTGCTTCTGGC 2663		
QY	301 TCACCTTCAATCAGTTAAATAAATGATAAATAAATTTTGAAGCTGTGAAGATAAAAATACC 360		
Db	2664 TCACCTTCAATCAGTTAAATAAATGATAAATAAATTTTGAAGCTGTGAAGATAAAAATACC 2723		
QY	361 AAATAAAATATATAAAAGTGATTTATGAACTTAAATATAAATAAATAAATCAGTATGATGGAA 420		
Db	2724 AAATAAAATATATAAAAGTGATTTATGAACTTAAATATAAATAAATAAATCAGTATGATGGAA 2783		
QY	421 TAAACTTG 428		
Db	2784 TAAACTTG 2791		
RESULT 8			
AAX81089			
ID	AAX81089 standard; DNA; 574 BP.		
XX			
AC	AAX81089;		
XX			
DT	07-NOV-2001 (first entry)		
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35901.		
XX			
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cystostatic; gene therapy; vaccine; metastasis; db.		
OS	Homo sapiens.		
XX			
PN	WO200157182-A2.		
XX			
PD	09-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US001354.		
XX			
PR	31-JAN-2000; 2000US-0179065P.		
PR	04-FEB-2000; 2000US-0180628P.		
PR	24-FEB-2000; 2000US-0184664P.		
PR	02-MAR-2000; 2000US-0186350P.		
PR	16-MAR-2000; 2000US-0189874P.		
PR	17-MAR-2000; 2000US-0190076		

PR	14-AUG-2000;	2000US-0225213P.	PR	08-NOV-2000;	2000US-0246523P.
PR	14-AUG-2000;	2000US-0225214P.	PR	08-NOV-2000;	2000US-0246524P.
PR	14-AUG-2000;	2000US-0225266P.	PR	08-NOV-2000;	2000US-0246525P.
PR	14-AUG-2000;	2000US-0225267P.	PR	08-NOV-2000;	2000US-0246526P.
PR	14-AUG-2000;	2000US-0225269P.	PR	08-NOV-2000;	2000US-0246527P.
PR	14-AUG-2000;	2000US-0225270P.	PR	08-NOV-2000;	2000US-0246528P.
PR	14-AUG-2000;	2000US-0225447P.	PR	08-NOV-2000;	2000US-0246532P.
PR	14-AUG-2000;	2000US-0225757P.	PR	08-NOV-2000;	2000US-0246609P.
PR	14-AUG-2000;	2000US-0225759P.	PR	08-NOV-2000;	2000US-0246610P.
PR	14-AUG-2000;	2000US-0225759P.	PR	08-NOV-2000;	2000US-0246611P.
PR	18-AUG-2000;	2000US-0226279P.	PR	08-NOV-2000;	2000US-0246613P.
PR	22-AUG-2000;	2000US-0226681P.	PR	17-NOV-2000;	2000US-0249207P.
PR	22-AUG-2000;	2000US-0226868P.	PR	17-NOV-2000;	2000US-0249208P.
PR	22-AUG-2000;	2000US-0227182P.	PR	17-NOV-2000;	2000US-0249209P.
PR	23-AUG-2000;	2000US-0227009P.	PR	17-NOV-2000;	2000US-0249210P.
PR	30-AUG-2000;	2000US-0228924P.	PR	17-NOV-2000;	2000US-0249211P.
PR	01-SEP-2000;	2000US-0228287P.	PR	17-NOV-2000;	2000US-0249212P.
PR	01-SEP-2000;	2000US-0228343P.	PR	17-NOV-2000;	2000US-0249213P.
PR	01-SEP-2000;	2000US-0228344P.	PR	17-NOV-2000;	2000US-0249214P.
PR	01-SEP-2000;	2000US-0228345P.	PR	17-NOV-2000;	2000US-0249215P.
PR	05-SEP-2000;	2000US-0228509P.	PR	17-NOV-2000;	2000US-0249216P.
PR	05-SEP-2000;	2000US-0229511P.	PR	17-NOV-2000;	2000US-0249217P.
PR	06-SEP-2000;	2000US-0230437P.	PR	17-NOV-2000;	2000US-0249218P.
PR	06-SEP-2000;	2000US-0230438P.	PR	17-NOV-2000;	2000US-0249244P.
PR	08-SEP-2000;	2000US-0231242P.	PR	17-NOV-2000;	2000US-0249245P.
PR	08-SEP-2000;	2000US-0231243P.	PR	17-NOV-2000;	2000US-0249284P.
PR	08-SEP-2000;	2000US-0231244P.	PR	17-NOV-2000;	2000US-0249285P.
PR	08-SEP-2000;	2000US-0231411P.	PR	17-NOV-2000;	2000US-0249297P.
PR	08-SEP-2000;	2000US-0231414P.	PR	17-NOV-2000;	2000US-0249299P.
PR	08-SEP-2000;	2000US-0232080P.	PR	17-NOV-2000;	2000US-0249300P.
PR	08-SEP-2000;	2000US-0232081P.	PR	01-DEC-2000;	2000US-0250160P.
PR	12-SEP-2000;	2000US-0232196P.	PR	05-DEC-2000;	2000US-0250391P.
PR	14-SEP-2000;	2000US-0232397P.	PR	05-DEC-2000;	2000US-0251030P.
PR	14-SEP-2000;	2000US-0232398P.	PR	05-DEC-2000;	2000US-0251988P.
PR	14-SEP-2000;	2000US-0232399P.	PR	06-DEC-2000;	2000US-0256719P.
PR	14-SEP-2000;	2000US-0233400P.	PR	06-DEC-2000;	2000US-0251479P.
PR	14-SEP-2000;	2000US-0233401P.	PR	08-DEC-2000;	2000US-0251856P.
PR	14-SEP-2000;	2000US-0233063P.	PR	08-DEC-2000;	2000US-0251868P.
PR	14-SEP-2000;	2000US-0233064P.	PR	08-DEC-2000;	2000US-0251869P.
PR	14-SEP-2000;	2000US-0233065P.	PR	08-DEC-2000;	2000US-0251989P.
PR	21-SEP-2000;	2000US-0234223P.	PR	08-DEC-2000;	2000US-0251990P.
PR	21-SEP-2000;	2000US-0234274P.	PR	11-DEC-2000;	2000US-0254097P.
PR	25-SEP-2000;	2000US-0234997P.	PR	05-JAN-2001;	2001US-0259678P.
PR	25-SEP-2000;	2000US-0234998P.			
PR	26-SEP-2000;	2000US-0234998P.			
PR	27-SEP-2000;	2000US-0235484P.			
PR	27-SEP-2000;	2000US-0235834P.			
PR	27-SEP-2000;	2000US-0235836P.			
PR	29-SEP-2000;	2000US-0236327P.			
PR	29-SEP-2000;	2000US-0236327P.			
PR	29-SEP-2000;	2000US-0236367P.			
PR	29-SEP-2000;	2000US-0236368P.			
PR	29-SEP-2000;	2000US-0236369P.			

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SQ Sequence 574 BP; 201 A; 80 C; 85 G; 208 T; 0 U; 0 Other;
Query Match 82.8%; Score 418; DB 4; Length 574;
Best Local Similarity 100.0%; Pred. No. 6.3e-58;
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAACTTGAATGCAACTGCTTATTTTAACTTATTTGACATAAAGTTTGTAAAGAG 60
DB 157 GAAACTTGAATGCAACTGCTTATTTTAACTTATTTGACATAAAGTTTGTAAAGAG 216
QY 61 TTAAAAATTTTACTTCATGATTCATTTATATTTTATATTTTGGCTCTAATGATTT 120
DB 217 TTAAAAATTTTACTTCATGATTCATTTATATTTTATATTTTGGCTCTAATGATTT 276
QY 121 TTATTAACATGATTTCTTTCTGATATTTGAAATGGAGTCTCAAAGCTTCTATAAAT 180
DB 277 TTATTAACATGATTTCTTTCTGATATTTGAAATGGAGTCTCAAAGCTTCTATAAAT 336
QY 181 TATAACTTTGAATGATTTCTTAATAACACGATGATTAATTTGAACATTCGATGATGG 240
DB 337 TATAACTTTGAATGATTTCTTAATAACACGATGATTAATTTGAACATTCGATGATGG 396
QY 241 CTACGAAGCCATTTCTCTGATTTTATGTAATTTTATGACAGCAAAATTTGCTTCTGGC 300
DB 397 CTACGAAGCCATTTCTCTGATTTTATGTAATTTTATGACAGCAAAATTTGCTTCTGGC 456
QY 301 TCACCTTCATGATTTTAAATGAATGATAATTTTGGAGCTGTGAAGATAAATATACC 360
DB 457 TCACCTTCATGATTTTAAATGAATGATAATTTTGGAGCTGTGAAGATAAATATACC 516
QY 361 AAATAAAATAATAAAGTGATTTATATGAAGTTTAAATAAATAAATCAGTATGATGG 418
DB 517 AAATAAAATAATAAAGTGATTTATATGAAGTTTAAATAAATAAATCAGTATGATGG 574

RESULT 9
ADB54251
ID ADB54251 standard; DNA; 3000 BP.
XX
AC ADB54251;
XX
DT 04-DEC-2003 (first entry)
XX
DE Pretreated genomic DNA region 175.
XX
KW colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytosstatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
XX
OS Unidentified.
XX
PN WO2003072821-A2.
XX
PD 04-SEP-2003.
XX
PF 27-FEB-2003; 2003WO-EP002035.
XX
PR 27-FEB-2002; 2002EP-00004551.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
PI Rujan T, Schmitt A;
XX
XX WPI; 2003-731620/69.
XX
PT Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
XX Claim 32; SEQ ID NO 307; 74pp; English.
XX
XX The invention relates to a novel method for detecting and differentiating
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CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytosstatic activity whilst the method may be useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the pretreated genomic DNA
CC region of the invention. This sequence is not shown within the
CC specification but is taken from Wipoweb.
XX
SQ Sequence 3000 BP; 679 A; 0 C; 788 G; 1533 T; 0 U; 0 Other;
Query Match 14.5%; Score 73.2; DB 9; Length 3000;
Best Local Similarity 48.6%; Pred. No. 0.0031;
Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;
QY 2 AAAAAGTGAATGCAACTGCTTATTTTAACTTATTTGACATAAAGTTTGTAAAGAGT 61
DB 164 AAAATTTGAGTTTATTTTATGTAATGGAGAAATAAATTTGTAAATTTAA 223
QY 62 TAAAAATTTGACTTCATGATTTTATTTATTTTATTTTTCGGCTCTAATGATTTT 121
DB 224 TTAATTTGTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 283
QY 122 TTATTAACATGATTTCTCTGATTTTATGTAATTTTAAATGGAGTCTCAAAGCTTCAATAATTT 181
DB 284 TTAGAATGCTTTTAAATTTATGTTTAAATTTTGTGTTTAAATTTTATTTTATTTT 343
QY 182 ATAACCTTTGAATGATTTCTTAATAACAAGTATGTAATTTGTAACATTCGAGTAATCGTGC 241
DB 344 TTTTATTTTGAATTTAGAAAGGAATTTATGTTTGGTATTTATTTATTTTATTTTAA 403
QY 242 TAGCAAGCCATTTCTCTGATTTTATGTAACATTTTATGACAGCAAAATTTGCTTCTGGCT 301
DB 404 AATAAATTTGTAGGAAGAAATTTATGTAAGTATGAGAGTAGTATGATTTGTTTATTT 463
QY 302 CACTTTCAATCAGTTAAATAAATGATAAATTTTGGAGCTGTGAAGATAAATACCA 361
DB 464 ATTTAAATTTAATAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 523
QY 362 AATAAAATAATAAAGTGAATTTATGTAAGTTAAATAAATAAATAAATCAGTATGA 415
DB 524 TTTATTTAAATAAATTTGTAATTAATAAGTATTTAGGTTGATTTGTTTTCGA 577

RESULT 10
ADE37774
ID ADE37774 standard; DNA; 3000 BP.
XX
AC ADE37774;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human chemically treated H-cadherin nucleotide sequence SEQ ID NO:20.
XX
KW chemically pretreated genomic DNA; human; versican; TPBF; H-cadherin;
KW calcitonin; EYA4; cytosstatic; gene therapy;
KW colon cell proliferative disorder; cytosine methylation state;
KW single nucleotide polymorphism; SNP; disease analysis; CpG dinucleotide;
KW gene; ds.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
XX WO2003072820-A2.
XX
XX 04-SEP-2003.
XX
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PF 27-FEB-2003; 2003WO-EP002034.  
XX  
PR 27-FEB-2002; 2002EP-00004551.  
XX  
XX (EPIC-) EPIGENOMICS AG.  
XX  
PI Adorjan P, Burger M, Maier S, Lesche R, Cottrell S, Mooney S;  
XX  
XX WPI; 2003-731619/69.  
DR  
XX  
XX New nucleic acid comprising a sequence of at least 18 bases in length of  
PT a segment of the chemically pretreated genomic DNA, useful for treating  
PT colon cell proliferative disorders.  
XX  
XX Claim 1; SEQ ID NO 20; 147pp; English.  
PS  
XX  
XX The present invention describes a nucleic acid (I) comprising a sequence  
CC of at least 18 bases in length of a segment of the chemically pretreated  
CC genomic DNA of any of the 5 sequences of 965, 16579, 3000, 1984, or 7833  
CC bp, which represent human versican, TPEF, H-cadherin, calcitonin and EYA4  
CC respectively (see ADB37755 to ADE37759), or its complement. Also  
CC described: (1) an oligomer, in particular an oligonucleotide or peptide  
CC nucleic acid (PNA)-oligomer comprising in each case of at least one base  
CC sequence having a length of at least 9 nucleotides which is complementary  
CC to, or hybridises under moderately stringent or stringent conditions to a  
CC pretreated genomic DNA; (2) a set of oligomers comprising at least two of  
CC the oligomer of (1); (3) manufacturing an arrangement of different  
CC oligomers (array) fixed to a carrier material; (4) an array of different  
CC oligonucleotide- and/or PNA-oligomer sequences, which are arranged on a  
CC plane solid phase in the form of a rectangular or hexagonal lattice; (5)  
CC a composition of matter comprising the nucleic acid and a buffer  
CC comprising 1-5 mM magnesium chloride, 100-500 micromole dNTP, 0.5-5 units  
CC of taq polymerase, and the oligomer; (6) detecting, differentiating or  
CC distinguishing between colon cell proliferative disorders; and (7)  
CC detecting a colon cell proliferative disorder. (I) has cytostatic  
CC activity, and can be used in gene therapy. The versican, TPEF, H-  
CC cadherin, calcitonin and EYA4 genes, and the polypeptides expressed by  
CC them, can be used for detecting, differentiating or distinguishing  
CC between colon cell proliferative disorders. The oligomers are useful for  
CC detecting the cytosine methylation state and/or single nucleotide  
CC polymorphisms (SNPs) within nucleic acid sequences. The array is useful  
CC for analysing diseases associated with the methylation state of the CpG  
CC dinucleotides. The present sequence is used in the exemplification of the  
XX present invention.  
XX  
XX Sequence 3000 BP; 679 A; 0 C; 788 G; 1533 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 14.5%; Score 73.2; DB 9; Length 3000;  
XX Best Local Similarity 48.6%; Pred. No. 0.0031;  
XX Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;  
XX  
QY 2 AAAACTGCAATGCAACGCTGCTTATTTTATCTTTATGTCATCAAGTTCTGAAAGAGT 61  
DB 164 AAATTTTGAGTTTGTAGTTTATTTTATATGTAATGGAAGAAATTAATTTGTAATAA 223  
QY 62 TAAAAATGTTACTTCATGATTCATTATTTATATTTTATTTTTCGCTCAATGATTTT 121  
DB 224 TTAATTTGTTTATTTATATTTTATTTTATGCTATATTAATTTGTTTGTAGG 283  
QY 122 TTATTAACATGATTCCTTCTGATATATGAAATGAGTCTMAAGCTTCATAAATTT 181  
DB 284 TTAGAATGTTTATTAATATGTTTAAATTTTGTGTTAAATTTTATTTTGTAGATTT 343  
QY 182 ATAACTTTAGAATGATTCATAACACAGTATGTAATTTGAACTTCAGTAAATGGTGC 241  
DB 344 TTTTATTTTGTAGAAATTAGAAAGGAATATATTTGTTGTAATTTATTTTAA 403  
QY 242 TAGCAAGCATTTCTCTGATTTTATGTAATTTTATGACAGCAAAATTCCTCTGGCT 301  
DB 404 AATAAATTTGTAGGAAGAAATATTTAGTAAGTGTAGTATGATGATGATGATTTTATTT 463  
QY 302 CACTTTTCATCAGTTAAATTAATATGATTAATTTTGGAGCTGTGAGATGAAATACCA 361



CC and polypeptide from the present invention are useful for treating colon  
CC cell proliferative disorders. The EYA4 gene, the polypeptide expressed  
CC from the EYA4 gene and kit are useful for detecting, differentiating or  
CC distinguishing between colon cell proliferative disorders. The oligomers  
CC are useful for detecting the cytosine methylation state and/or single  
CC nucleotide polymorphisms (SNPs) within nucleic acid sequences. The array  
CC is useful for analysing diseases associated with the methylation state of  
CC the CpG dinucleotides. The present sequence represents a chemically  
CC pretreated human EYA4 gene, which is given in the exemplification of the  
CC present invention. Human EYA4 is mapped to chromosome 6, more  
CC specifically to 6q22.3.

XX  
SQ Sequence 29993 BP; 8706 A; 0 C; 5856 G; 15431 T; 0 U; 0 Other;  
Query Match 14.5%; Score 73.2; DB 9; Length 29993;  
Best Local Similarity 48.6%; Pred. No. 0.0026;  
Matches 201; Conservative 0; Mismatches 213; Indels 0; Gaps 0;  
QY 2 AAAAAGTGAATGCAACTGCTTATTTTAACTTATGTAAGTCTTGAAGAGT 61  
DB 1830 AAATTTGAGTTTGTAGTTTATATGTAAGTGAAGTGAAGTGAAGTGAAGT 1889  
QY 62 TAAAAATGTTACTGATTCATTTATTTATTTATTTATTTATTTATTTATTTATTT 121  
DB 1890 TAAAAATGTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1949  
QY 122 TTATTAACATGATTTCTTTCTGATATTTGATATTTGATATTTGATATTTGATATTT 181  
DB 1950 TTAGATGTTGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAA 2009  
QY 182 ATAACTTTAGAAATGATTTCTTAATACCAACGATGATTAATTTGATTTGATTTGATTT 241  
DB 2010 TTTTATTTTGAAGTATGAAAGGAAATATATTTGTTGTTGTTGTTGTTGTTGTTTAA 2069  
QY 242 TACGAAGCCATTTCTTTGATTTTATGTAAGTCTTGAAGTCTTGAAGTCTTGAAGTCT 301  
DB 2070 AATAAATTTGAGGAAGATTTATTTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2129  
QY 302 CACTTTCAATCAGTTAAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 361  
DB 2130 ATTTAAATTTAATATATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 2189  
QY 362 AATAAATTAATAAAGTGTATTTATGATGAATGAATGAATGAATGAATGAATGAATGAATGA 415  
DB 2190 TTTATTAATAAATAAATTTGTAATTAAGTATTTAGGGTTGATATTTGTTTGA 2243

RESULT 12  
ADB54123  
ID ADB54123 standard; DNA; 3000 BP.  
XX  
AC ADB54123;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE Pretreated genomic DNA region 47.  
XX

KW colon cell proliferative disorder; non methylated CpG dinucleotide;  
KW cytosine; cancer; adenoma; carcinoma; cytosine methylation state; ds.  
OS Unidentified.  
XX  
PN WO2003072821-A2.  
XX  
PD 04-SEP-2003.  
XX  
PF 27-FEB-2003; 2003WO-EP002035.  
XX  
PR 27-FEB-2002; 2002EP-00004551.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX

PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;

PI Rujan T, Schmitt A;  
XX  
DR WPI; 2003-731620/69.

XX  
PT Detecting and differentiating between colon cell proliferative disorders  
PT associated with a gene or its regulatory regions comprises contacting a  
PT target nucleic acid in a biological sample obtained from the subject with  
PT a reagent.

XX  
PS Claim 32; SEQ ID NO 179; 74pp; English.

XX  
CC The invention relates to a novel method for detecting and differentiating  
CC between colon cell proliferative disorders associated with at least one  
CC gene or its regulatory regions. The method comprises contacting a target  
CC nucleic acid in a biological sample obtained from the subject with at  
CC least one reagent or a series of reagents, where the reagent or series of  
CC reagents, distinguishes between methylated and non methylated CpG  
CC dinucleotides within the target nucleic acid. The molecules of the  
CC invention demonstrate cytostatic activity whilst the method may be useful  
CC for detecting and differentiating between colon cell proliferative  
CC disorders, including cancers such as colon adenoma and colon carcinoma.  
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for  
CC determining cytosine methylation state or single nucleotide  
CC polymorphisms. The current sequence is that of the pretreated genomic DNA  
CC region of the invention. This sequence is not shown within the  
CC specification but is taken from Wipoweb.

XX  
SQ Sequence 3000 BP; 679 A; 174 C; 788 G; 1359 T; 0 U; 0 Other;

Query Match 14.2%; Score 71.6; DB 9; Length 3000;  
Best Local Similarity 48.3%; Pred. No. 0.0056;  
Matches 200; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

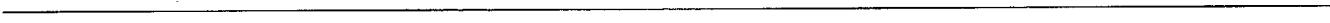
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DB 164 AAATTTGAGTTTGTAGTTTATATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 223  
QY 62 TAAAAATGTTACTGATTCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 121  
DB 224 TTAATTTGTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 283  
QY 122 TTATTAACATGATTTCTTTCTGATATTTGATATTTGATATTTGATATTTGATATTT 181  
DB 284 TTAGATGTTGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAAAT 343  
QY 182 ATAACTTTAGAAATGATTTCTTAATACCAACGATGATTAATTTGATTTGATTTGATTTG 241  
DB 344 TTTTATTTTGAAGTATGAAAGGAAATATTTGTTGTTGTTGTTGTTGTTGTTGTTTAA 403  
QY 242 TACGAAGCCATTTCTTTGATTTTATGTAAGTCTTGAAGTCTTGAAGTCTTGAAGTCT 301  
DB 404 AATAAATTTGAGGAAGATTTATTTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 463  
QY 302 CACTTTCAATCAGTTAAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 361  
DB 464 ATTTTAAATTTAATATATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 523  
QY 362 AATAAATTAATAAAGTGTATTTATGATGAATGAATGAATGAATGAATGAATGAATGAATGA 415  
DB 524 TTTATTAATAAATAAATTTGTAATTAAGTATTTAGGGTTGATATTTGTTTGA 577

RESULT 13  
ADE37764  
ID ADE37764 standard; DNA; 3000 BP.  
XX  
AC ADE37764;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human chemically treated H-cadherin nucleotide sequence SEQ ID NO:10.  
XX  
KW chemically pretreated genomic DNA; human; versican; TPEF; H-cadherin;





Job time : 291.715 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 13:06:29 ; Search time 55.9993 Seconds  
(without alignments)  
5004.527 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_10700\_11204

Perfect score: 505

Sequence: 1 gaacaactgaatgcacaact.....ggaccattcaatggagaaaa 505

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/FCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	59.6	11.8	20674	4	US-09-641-638-651
C 2	59	11.7	176373	3	US-09-128-155-17
C 3	55.8	11.0	19124	2	US-08-487-826B-13
C 4	55.6	11.0	2614	4	US-09-004-056-1
C 5	55	10.9	6866	4	US-10-204-708-19
C 6	54.4	10.8	615	3	US-08-998-416-186
C 7	52.6	10.4	640681	4	US-09-790-988-1
C 8	52.4	10.4	786431	4	US-09-751-389-3
C 9	52	10.3	11049	4	US-10-204-708-22
C 10	51.8	10.3	20674	4	US-09-641-638-651
C 11	51.6	10.2	832	4	US-09-621-976-2813
C 12	51.6	10.2	22067	4	US-09-820-001-3
C 13	51.4	10.2	1218	2	US-08-731-722-4
C 14	51.4	10.2	11049	4	US-10-204-708-22
C 15	50.8	10.1	10640	4	US-09-417-485D-5
C 16	50.6	10.0	1200	3	US-09-018-584A-37
C 17	50.2	9.9	658	3	US-08-998-416-595
C 18	50	9.9	636	3	US-08-998-416-1137
C 19	50	9.9	32042	4	US-09-245-281-44
C 20	50	9.9	32042	4	US-09-340-620A-63
C 21	49.8	9.9	116592	4	US-09-818-512-3
C 22	49.8	9.9	392000	4	US-10-027-983-11
C 23	49.6	9.8	98844	4	US-09-791-211-10
C 24	49.2	9.7	51952	3	US-08-947-823-1
C 25	49	9.7	10409	3	US-08-772-440-33
C 26	48.8	9.7	3926	2	US-08-731-722-1
C 27	48.8	9.7	3926	2	US-08-731-722-1

Sequence 2, Appli  
Sequence 2, Appli  
Sequence 32, Appl  
Sequence 29, Appl  
Sequence 1, Appli  
Sequence 20, Appl  
Sequence 2813, Ap  
Sequence 3, Appli  
Sequence 20, Appl  
Sequence 21, Appl  
Sequence 22, Appl  
Sequence 1, Appli  
Sequence 2344, Ap  
Sequence 207, App  
Sequence 207, App  
Sequence 11, Appli

28 48.8 9.7 3926 2 US-08-731-722-2  
29 48.8 9.7 3926 2 US-08-731-722-2  
30 48.8 9.7 8093 4 US-10-204-708-32  
31 48.4 9.6 5666 4 US-10-204-708-29  
32 48.4 9.6 8920 2 US-08-446-855A-1  
33 48.4 9.6 8920 3 US-09-150-741-1  
34 48.2 9.5 6866 4 US-10-204-708-20  
35 48 9.5 832 4 US-09-621-976-2813  
36 48 9.5 53332 4 US-09-801-861-3  
37 48 9.5 246240 2 US-08-724-394A-20  
38 48 9.5 246240 2 US-08-724-394A-21  
39 48 9.5 246240 2 US-08-724-394A-22  
40 47.8 9.4 6866 4 US-09-056-075-1  
41 47.6 9.4 6866 4 US-10-204-708-20  
42 47.4 9.4 516 4 US-09-621-976-2344  
43 47.4 9.4 29604 3 US-08-781-891-207  
44 47.4 9.4 29604 4 US-09-618-166-207  
45 47.2 9.3 2251 3 US-08-991-677-11

#### ALIGNMENTS

#### RESULT 1

US-09-641-638-651/C  
Sequence 651, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
FILE REFERENCE: GENSET 051CPI  
CURRENT APPLICATION NUMBER: US/09/641,638  
CURRENT FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 651  
LENGTH: 20674  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1123..3123  
OTHER INFORMATION: 5'regulatory region  
NAME/KEY: exon  
LOCATION: 3124..3297  
OTHER INFORMATION: exon 1  
NAME/KEY: exon  
LOCATION: 3871..4072  
OTHER INFORMATION: exon 2  
NAME/KEY: exon  
LOCATION: 5552..5633  
OTHER INFORMATION: exon 3  
NAME/KEY: exon  
LOCATION: 5758..5880  
OTHER INFORMATION: exon 4  
NAME/KEY: exon  
LOCATION: 5996..6099  
OTHER INFORMATION: exon 5  
NAME/KEY: exon  
LOCATION: 6349..6509  
OTHER INFORMATION: exon 6

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, NAME/KEY: exon
, LOCATION: 7379..7522
, OTHER INFORMATION: exon 7
, NAME/KEY: exon
, LOCATION: 8645..8854
, OTHER INFORMATION: exon 8
, NAME/KEY: exon
, LOCATION: 12254..12340
, OTHER INFORMATION: exon 9
, NAME/KEY: exon
, LOCATION: 12854..13023
, OTHER INFORMATION: exon 10
, NAME/KEY: exon
, LOCATION: 13308..13429
, OTHER INFORMATION: exon 11
, NAME/KEY: exon
, LOCATION: 16567..16667
, OTHER INFORMATION: exon 12
, NAME/KEY: exon
, LOCATION: 16775..16945
, OTHER INFORMATION: exon 13
, NAME/KEY: exon
, LOCATION: 17063..17554
, OTHER INFORMATION: exon 14
, NAME/KEY: misc.feature
, LOCATION: 17555..20674
, OTHER INFORMATION: 3'regulatory region
, NAME/KEY: allele
, LOCATION: 1128
, OTHER INFORMATION: 10-508-191 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 1182
, OTHER INFORMATION: 10-508-245 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 1559
, OTHER INFORMATION: 10-509-284 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 1570
, OTHER INFORMATION: 10-509-295 : deletion of C
, NAME/KEY: allele
, LOCATION: 1827
, OTHER INFORMATION: 10-510-173 : variable motif ATTGA or TTTT
, NAME/KEY: allele
, LOCATION: 2048
, OTHER INFORMATION: 10-511-62 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 2323
, OTHER INFORMATION: 10-511-337 : insertion of T
, NAME/KEY: allele
, LOCATION: 2341
, OTHER INFORMATION: 10-512-36 : polymorphic base G or C
, NAME/KEY: allele
, LOCATION: 2623
, OTHER INFORMATION: 10-512-318 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 2832
, OTHER INFORMATION: 10-513-250 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 2844
, OTHER INFORMATION: 10-513-262 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 2934
, OTHER INFORMATION: 10-513-352 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 2947
, OTHER INFORMATION: 10-513-365 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 3802
, OTHER INFORMATION: 12-206-81 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 4062
, OTHER INFORMATION: 10-343-231 : deletion of C
, NAME/KEY: allele
, LOCATION: 4088
, OTHER INFORMATION: 12-206-366 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 4109
, OTHER INFORMATION: 10-343-278 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 4170
, OTHER INFORMATION: 10-343-339 : polymorphic base G or T
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, OTHER INFORMATION: 10-346-141 : polymorphic base A or G
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, LOCATION: 6141
, OTHER INFORMATION: 10-346-263 : polymorphic base G or C
, NAME/KEY: allele
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, NAME/KEY: allele
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, NAME/KEY: allele
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, OTHER INFORMATION: 10-347-348 : polymorphic base A or G
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, LOCATION: 7668
, OTHER INFORMATION: 10-348-391 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 8608
, OTHER INFORMATION: 10-349-47 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 8658
, OTHER INFORMATION: 10-349-97 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 8703
, OTHER INFORMATION: 10-349-142 : polymorphic base G or C
, NAME/KEY: allele
, LOCATION: 8777
, OTHER INFORMATION: 10-349-216 : deletion of CTG
, NAME/KEY: allele
, LOCATION: 8785
, OTHER INFORMATION: 10-349-224 : polymorphic base G or T
, NAME/KEY: allele
, LOCATION: 8926
, OTHER INFORMATION: 10-349-368 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 12171
, OTHER INFORMATION: 10-350-72 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 12429
, OTHER INFORMATION: 10-350-332 : polymorphic base C or T
, NAME/KEY: allele
, LOCATION: 13341
, OTHER INFORMATION: 10-507-170 : polymorphic base A or G
, NAME/KEY: allele
, LOCATION: 13492
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OTHER INFORMATION: 10-507-321 : polymorphic base A or C  
NAME/KEY: allele  
LOCATION: 13524  
OTHER INFORMATION: 10-507-353 : polymorphic base C or T  
NAME/KEY: allele  
LOCATION: 13535

Query Match 11.8%; Score 59.6; DB 4; Length 20674;  
Best Local Similarity 49.1%; Pred. No. 0.0011;  
Matches 158; Conservative 0; Mismatches 164; Indels 0; Gaps 0;  
QY 101 TATTTTGGCTCAATGATTTTATTAACATGATTTCTTCTCGATATATGAATGGA 160  
DB 11560 TTTTAAATTAATAATTTTCTTAGCTATTAAATTTAAATTTAAATTTAAATTA 11501  
QY 161 GTCTCAAGCTTCATAATTTATTAACCTTTAGAAATGATTTCTTAATAACAAGTATGTAAT 220  
DB 11500 TTTAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAAAT 11441  
QY 221 GTACATTCGAGTAATGCTAGACGACATTTCTCTGATTTTGTAGTAACTTTTATG 280  
DB 11440 TAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAAAT 11381  
QY 281 ACAGCAAAATTTCTTCTGGCTCACTTTCAATCAGTTAAATTAATGATAATTTTGGGA 340  
DB 11380 AAATTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTA 11321  
QY 341 AGCTGTGAAGTAAATTAACCAATTAATAATATAATAAGTGAATTTATGAGTAAAT 400  
DB 11320 ATTAATTTAAGTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 11261  
QY 401 AAAAATCAGTATGATGAATA 422  
DB 11260 AATTTAATTTAAATTTAAATA 11239

RESULT 2  
US-09-128-155-17  
Sequence 17, Application US/09128155  
Patent No. 6117654  
GENERAL INFORMATION:  
APPLICANT: Fan, Yang  
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
FILE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: 09404/052001  
CURRENT APPLICATION NUMBER: US/09/128,155  
EARLIER FILING DATE: 1998-08-03  
EARLIER FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: US 60/091,650  
EARLIER FILING DATE: 1997-08-04  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 176373  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)...(176373)  
OTHER INFORMATION: n = A,T,C or G

Query Match 11.7%; Score 59; DB 3; Length 176373;  
Best Local Similarity 78.0%; Pred. No. 0.0018;  
Matches 71; Conservative 0; Mismatches 20; Indels 0; Gaps 0;  
QY 415 ATGGAATAAATTTGAGATTCAGAGTATCCATACATCTGTAATCAACTAATTTCTCA 474  
DB 167654 ATGGAATAAATTTGAGATTCAGAGTATCCATACATCTGTAATCAACTAATTTCTCA 167713  
QY 475 CAAGGCTGTAGGACCAATTCATGAGAAA 505

DB 167714 CAAGGTGCCAAGACCATTCAATGAGGAAA 167744  
RESULT 3  
US-08-487-826B-13/C  
Sequence 13, Application US/08487826B  
Patent No. 593827  
GENERAL INFORMATION:  
APPLICANT: Sim, Kim L.  
APPLICANT: Chitnis, Chetan  
APPLICANT: Miller, Louis H.  
APPLICANT: Peterson, David S.  
APPLICANT: Su, Xin-zhaun  
APPLICANT: Wellens, Thomas E.  
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe Martens Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: California  
COUNTRY: US  
ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/487,826B  
FILING DATE: 10-SEP-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH121.001CPI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-487-826B-13

Query Match 11.0%; Score 55.8; DB 2; Length 19124;  
Best Local Similarity 48.6%; Pred. No. 0.0061;  
Matches 153; Conservative 0; Mismatches 162; Indels 0; Gaps 0;  
QY 17 AACTGCTTATTTTAACTTATTTGTAAGTATTTGTAAGTATTTGTAAGTATTTGTAAGTATTT 76  
DB 15885 AATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 15826  
QY 77 CATGATTCATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 136  
DB 15825 TTTTATTTTAAATAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 15766  
QY 137 CTTTCTGATATTTGAAATGAGTCTCAAGCTTCAATAATTTTATTTTATTTTATTTTATTTTATTT 196  
DB 15765 AATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 15706  
QY 197 ATTCTAATAACAGGTATGTAATTTGTAAGTATTTGTAAGTATTTGTAAGTATTTGTAAGTATTT 256  
DB 15705 GTTTTATGATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 15646  
QY 257 CTGATTTTATGTAAGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 316

Db	15645	TTTTTTTAAACATTTTTTTTTTATATATAAAAAATTTTTTTTAAATTTTTTTTTTGGATATACT	15586
Qy	317	AAATAAATGATAAAT	331
Db	15585	TTTTCATTTTTTATT	15571

## RESULT 4

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US-09-004-056-1/c
; Sequence 1, Application US/09004056A
; Patent No. 6566586
; GENERAL INFORMATION:
; APPLICANT: Calgene LLC
; TITLE OF INVENTION: Plant Expansin Promoter Sequences
; FILE REFERENCE: 125
; CURRENT APPLICATION NUMBER: US/09/004,056A
; CURRENT FILING DATE: 1998-01-07
; EARLIER APPLICATION NUMBER: 60034914
; EARLIER FILING DATE: 1997-07-01
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2614
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (930)
; OTHER INFORMATION: unknown nucleotide
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (947)
; OTHER INFORMATION: unknown nucleotide
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (956)
; OTHER INFORMATION: unknown nucleotide
US-09-004-056-1

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RECEIVED

RESULT 5  
 US-10-204-708-19  
 ; Sequence 19, Application US/10204708  
 ; Patent NO. 6677731  
 ; GENERAL INFORMATION.

```

/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
/ TITLE OF INVENTION: by Assessing DNA Methylation
/ FILE REFERENCE: 5013.1012
/ CURRENT APPLICATION NUMBER: US/10/204,708
/ CURRENT FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: PC7/EP01/03971
/ PRIOR FILING DATE: 2001-04-06
/ PRIOR APPLICATION NUMBER: DE 10019058.8
/ PRIOR FILING DATE: 2000-04-06
/ PRIOR APPLICATION NUMBER: DE 10019173.8
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 98
/ SEQ ID NO 19
/ LENGTH: 6866
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-19

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9 T. LISA

```

: RESULT: 6
: US-08-998-416-186
: ; Sequence 186, Application US/08938416
: ; Patent No. 6239264
: ; GENERAL INFORMATION:
: ; APPLICANT: Philippaen, Peter
: ; APPLICANT: Pohlmann, Rainer
: ; APPLICANT: Steiner, Sabine
: ; APPLICANT: Mohr, Christine
: ; APPLICANT: Wendland, Jergen
: ; APPLICANT: Knechtle, Philipp
: ; APPLICANT: Rebeschung, Corinne
: ; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
:

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;; TITLE OF INVENTION: AND USES THEREOF  
;; NUMBER OF SEQUENCES: 1152  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: No. 6239264artis Corporation  
;; STREET: 3054 Cornwallis Road  
;; CITY: Research Triangle Park  
;; STATE: No. 6239264th Carolina  
;; COUNTRY: USA  
;; ZIP: 27709  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/998,416  
;; FILING DATE: 24-DEC-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: CH 0016/97  
;; FILING DATE: 31-DEC-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Meigs, J. Timothy  
;; REGISTRATION NUMBER: 38,241  
;; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 919-541-8587  
;; TELEFAX: 919-541-8689  
;; INFORMATION FOR SEQ ID NO: 186:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 615 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; ORIGINAL SOURCE:  
;; ORGANISM: PAG1074RP  
;; US-08-998-416-186

Query Match 10.8%; Score 54.4; DB 3; Length 615;  
Best Local Similarity 48.2%; Pred. No. 0.0079;  
Matches 184; Conservative 0; Mismatches 196; Indels 2; Gaps 1;  
  
QY 28 TTATATCTTATTTGTCATAGTTTGTAAAGAGTTTAAAGTTTCTGATTCAT 87  
DB 220 TAGTTCAAATTTTAAATAGTTTAAATATTTAGATATATTTCTTTAATA 279  
  
QY 88 TTATATTTTATATTTTTCGCTCTAATGATTTTATTAACATGATTCCTCTGAT 147  
DB 280 AATTATTAATAGATTATCAATAATTAATATATTTATTTATTTATTTAAAT 339  
  
QY 148 ATATTGAATGGAGTCTCAAGCTTCATTAATTTATTAACCTTTAGAAATGATTCATAAC 207  
DB 340 ATATTTTATTTATTAAGATTTAATTTATTTAAATATTTGTAATATTTATTTAT 399  
  
QY 208 AACGTATGTAATGTAACATTCAGT--AATGGTCTAGCAAGCCATTTCTCTGATTTT 265  
DB 400 AATATCTATTTTATTAATATTTATTTGATTTATTTATTTAACTTTTATAAGAAATAT 459  
  
QY 266 TAGTAACCTTTATGACACAAATTTGCTTCGCTCCTCAATCAGTTAAATAATG 325  
DB 460 TATTAATTAATTTTAACTTTAACTTTCTTATTTATTTATTTATTTAAAT 519  
  
QY 326 ATAAATAATTTTGAAGCTGTGAAGATAAAATACCAATAAATAATATAAAGTGATTT 385  
DB 520 ATATTCATTTTATTTATTTATTTATTTATTTATTTAAATTAATTTATTTATTTATCA 579  
  
QY 386 ATATGAAGTTAAATAAATAAT 407  
DB 580 TTATTTTAAATTAATAAATAAT 601

RESULT 7

US-09-790-988-1/c  
; Sequence 1, Application US/09790988  
; Patent No. 6632935  
; GENERAL INFORMATION:  
; APPLICANT: SHIGENOBU, SHUJI  
; APPLICANT: WATANABE, HIDEKI  
; APPLICANT: HATTORI, MASAHIRA  
; APPLICANT: SAKAKI, YOSHIYUKI  
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS  
; FILE REFERENCE: 081356/0159  
; CURRENT APPLICATION NUMBER: US/09/790,988  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: JP2000-107160  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 640681  
; TYPE: DNA  
; ORGANISM: Buchnera sp.  
US-09-790-988-1  
  
Query Match 10.4%; Score 52.6; DB 4; Length 640681;  
Best Local Similarity 47.7%; Pred. No. 0.041;  
Matches 195; Conservative 0; Mismatches 204; Indels 10; Gaps 1;  
  
QY 26 ATTTTAACTTATTTGTCATATAAGTTTGTAAAGAGTTAAATAATTTGTTACTTCATGTTATTC 85  
DB 527077 ATGTTATTAATTTTAGAGTTAAATAATTTTAAAGTCTATTTTGTAGTATTTTAAATGAAATA 527018  
  
QY 86 ATTTATATTTTATTTTTCGCTCTAATGATTTTATTAACATGATTTCTTTCTG 145  
DB 527017 TTGTTATTTAGATCTACTTTTATTTATTTTATTTTAAATATTTTCTTTT 526958  
  
QY 146 ATATATTTGAATGGAGTCTCAAGCTTCATAATTTTATAACTTTTAAAGTGA 197  
DB 526957 TAATATTTTATTTTAAATTTTCAAGTTTATATATATGATCATGAAATAATAGATCTACT 526898  
  
QY 198 --TTCTAATAACAACTGATGTAATTTGTAACATGTCAGTAAATGGTGTACGAGCCATTTTC 255  
DB 526897 TTTTGTAGTATGAAATAAATGATTTTCTTTATTTTAAATATAGAAATAAATTTT 526838  
  
QY 256 TCTTGATTTTGTAAACTTTTATGACAGCAAAATTTGCTTCTGGCTCAGTTTCAATCAGT 315  
DB 526837 TTAATAATAGTAAACAATGTTATTTAAATAGATATTAATAAGAAATAATTTTAAATAT 526778  
  
QY 316 TAAATAAATGATAAATAATTTTGGAGCTGTGAAGATAAATAACCAATAAATAATAATA 375  
DB 526777 TAAACTTACTTTAAATAATTTAGAAATATGGGTTTATCAGACTAATAGATATATAT 526718  
  
QY 376 AAGTGTATTTATGATGAAGTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 424  
DB 526717 AATAATAATTTTAAATCAGTATTTTATTTTAAATAGTTTGAATAAATAAATAAATAAATA 526669

RESULT 8  
US-09-751-389-3/c  
; Sequence 3, Application US/09751389  
; Patent No. 6630334  
; GENERAL INFORMATION:  
; APPLICANT: GUGLER, Karl et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; FILE REFERENCE: CL001067  
; CURRENT APPLICATION NUMBER: US/09/751,389  
; CURRENT FILING DATE: 2001-01-02  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 786431  
; TYPE: DNA  
; ORGANISM: Human

337	ATTATCCTCCAAAAATTATACCTAATAAATTCCTTTAAACAATCACCTATTATTTT	278
3262	TTTTTAGTAAACTTTTATGACAGCAAAATTTGGCTCTGGCTCAGCTTTCAATCAGTTAAATA	321
3277	TTTTAAAAAGCAATCTTTTCATATAAACTCTTTAAAAAATATATCTCTATTATATAA	218
3232	AATGATAAATAATTTTGGAGCTGTGAAGATAAAATACCAATATAAATAATATATAAAAGTG	381
3217	TTTTTAAAAATACAATATATAAATAAAAAATTCACATAAAAAATTAACCTACTT	158
3382	ATTATATGAGCTTAAAAATAAAAAT	407
3157	AAATAAATCCCATAAAACTAAATAT	132

## RESULT 10

US-09-641-638-651  
Sequence 651, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GENSET.051CPI  
CURRENT APPLICATION NUMBER: US/09/641,638  
CURRENT FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent .pm

```

;
; NAME/KEY: misc_feature
; LOCATION: (1)...(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Query Match          10.4%; Score 52.4; DB 4; Length 786431;
Best Local Similarity 60.6%; Pred No. 0.046;
Matches 86; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy      364  TAAATAATATAAAGTGATTTATATGAAGTTAAATAAATAATCAGTATGATGAATAA 423
Db      367580  TATAGTAAACCAAAACAGCATGTGTCTGCATGAAATCGAAACATAGACCAATGGAATAAT 367521

Qy      424  ACTTGAGAGTCCAGAGAAGTTATCCCATACATCTGTAAATCACTAAATTTCTCACAAAGGTGT 483
Db      367520  AATAGAGAACCCAGAAACAATCCACACACTCAGTAACTCATTTTTGACAAAGATGC 367461

Qy      484  AAGGACCAATCAATCGAGAAA 505
Db      367460  TAAGACATACACTGGGAAAA 367439

```

## RESULT 9

```

RESULTS
US-10-204-708-2/c
; Sequence 22, Application US/10204708
; Patent No. 667731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: FIEBENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/033971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 22
; LENGTH: 11049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-22

```

	Query Match	10.3%;	Score 52;	DB 4;	Length 11049;
	Best Local Similarity	47.7%;	Pred. No. 0.033;		
	Matches 184;	Conservative	0;	Mismatches 200;	Indels 2; Gaps 1
Qy	24	TTATTTTAACTCTATTGTGACATAAGATTGTTAAAAAGACTTTAAAAATTTGTTACTTTCATGTAT	83		
Db	517	TTTTTTAAAAAAACCTACTAAAAAACTTTTAAATTAATTTTATATTTTCAATTAATTATAA	458		
Qy	84	TCATTTTATATTTTATATATTATTTT - GCGCTCAAAGATTTTTTTATTAACATGATTTCCCTTT	141		
Db	457	ACAAACATTCCTAATAATTAACCTCATATATATATCCATAATAATTTCTTAAAAATCAATAT	398		
Qy	142	CTGTATATATTTGAATGGAGTCTCAAAGCTTCATAAATTTTATAACTTTTAGAAGATGATTC	201		
Db	397	CTAAAAATTAATAAATAAACTACAAAAATTTTAAAAAAATTTTTTCTACTATAAATTTATCAA	338		
Qy	202	AATAACAACGATGATTAATTTGTAACTATTCAGATTAATGGTGCTACGAAGCCATTTTCTCTTCA	261		

```
OTHER INFORMATION: exon 9
NAME/KEY: exon
LOCATION: 12854..13023
OTHER INFORMATION: exon 10
NAME/KEY: exon
LOCATION: 13308..13429
OTHER INFORMATION: exon 11
NAME/KEY: exon
LOCATION: 16567..16667
OTHER INFORMATION: exon 12
NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon 14
NAME/KEY: misc feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1128
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1182
OTHER INFORMATION: 10-508-245 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295 : deletion of C
NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173 : variable motif ATTTA or TTTTTT
NAME/KEY: allele
LOCATION: 2048
OTHER INFORMATION: 10-511-62 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION: 10-511-337 : insertion of T
NAME/KEY: allele
LOCATION: 2341
OTHER INFORMATION: 10-512-36 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 2623
OTHER INFORMATION: 10-512-318 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2832
OTHER INFORMATION: 10-513-250 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2844
OTHER INFORMATION: 10-513-262 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 2934
OTHER INFORMATION: 10-513-352 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 4062
OTHER INFORMATION: 10-343-231 : deletion of C
NAME/KEY: allele
LOCATION: 4088
OTHER INFORMATION: 12-206-366 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 4170
OTHER INFORMATION: 10-343-339 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6019
OTHER INFORMATION: 10-346-141 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6141
OTHER INFORMATION: 10-346-263 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6183
OTHER INFORMATION: 10-346-305 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6338
OTHER INFORMATION: 10-347-74 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 10-347-165 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 10-347-203 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 10-347-220 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 6534
OTHER INFORMATION: 10-347-271 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 6611
OTHER INFORMATION: 10-347-348 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION: 10-348-391 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 10-349-97 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 8703
OTHER INFORMATION: 10-349-142 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 8777
OTHER INFORMATION: 10-349-216 : deletion of CTG
NAME/KEY: allele
LOCATION: 8785
OTHER INFORMATION: 10-349-224 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 8926
OTHER INFORMATION: 10-349-368 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12171
OTHER INFORMATION: 10-350-72 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12429
OTHER INFORMATION: 10-350-332 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13341
OTHER INFORMATION: 10-507-170 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 13492
OTHER INFORMATION: 10-507-321 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 13524
OTHER INFORMATION: 10-507-353 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 13535
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Query Match

10.3%; Score 51.8; DB 4; Length 20674;



```

; LENGTH: 1218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 17-1
US-08-731-722-4

Query Match      10.2%; Score 51.4; DB 2; Length 1218;
Best Local Similarity 45.4%; Pred. No. 0.034;
Matches 184; Conservative 0; Mismatches 221; Indels 0; Gaps 0;

QY      17  AACTGTCCTTATTTTAAATCTTATTGTGCATACAAAGTTTGTAAGAAGAGTGTAAAAAATGGTACTT 76
        |||
Db       807  AAATAATTATATCTTTTAAAGATATATAACITTTAAAABAAAAATTAABAATGAABAATC 748

QY      77  CATGTAATCATTTATATTTTTATATATTTTGGCGTCAATGATTTTTTTTAAACATGATTT 136
        |||
Db       747  TTCTAATAAGAAATATATTTTTATTATAAATATTAATTTATTTCTTTATTAAAGTAAAT 688

QY      137  CCTTTTCGTGATATATGAAATGGAGTCTCAAAGCTTCATAAAATTATAAATTTAGAAATG 196
        |||
Db       687  AAGAATTAACAATTTTCTATTAAAAAATAAAACCCTTTCTCTATTGAAAAATTTCTTTATAG 628

QY      197  ATTCTAATAACAAGTATGTAATTGTBAACATTTGCAGTAATGGCGCTACGAGCCATTTCT 256
        |||
Db       627  CTATTATTAAAGGTTTCATAGGGTCTACTGTTTAAATTCAGATTATTATTATTAGAAATATA 568

QY      257  CTTGANTTTTAGTAAACCTTTTATGACACGACAAATTTGGTCTTGGCTCACTTTCAATCAGTT 316
        |||
Db       567  GTAAAGCTCTTCCAATTTTATATAATGTTAAATTTCTGTGGATTTACACAATTTAAAT 508

QY      317  AAAATAATGATAAATAATTTTGGNAGCTGTGAAGATAAAATACCAATAAATAATATAA 376
        |||
Db       507  AATTAAATATTATAATAAAATATATTTCTATTAGAAGTATTTTCATTTTATTTTTTTT 448

```

```

1 GENERAL INFORMATION:
2
3 APPLICANT: Long, David M.
4
5 APPLICANT: Metz, Anneke M.
6
7 APPLICANT: Lowe, Ruschelle A.
8
9 TITLE OF INVENTION: telomerase Reverse Transcriptase (TERT) Genes
10
11 FILE REFERENCE: 47714-5009-US
12
13 CURRENT APPLICATION NUMBER: US/09/417.485D
14
15 CURRENT FILING DATE: 2002-06-14
16
17 NUMBER OF SEQ ID NOS: 49
18
19 SOFTWARE: PatentIn Ver. 2.1
20
21 SEQ ID NO 5
22
23 LENGTH: 10640
24
25 TYPE: DNA
26
27 ORGANISM: Plasmodium falciparum
28
29 FEATURE:
30
31 NAME/KEY: CDS
32
33 LOCATION: (834)..(7395)
34
35 OTHER INFORMATION: TERT gene

```

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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1821)..(1837)
; OTHER INFORMATION: m at position 1821 = a or c; w at position 1837 =
; OTHER INFORMATION: a or t. Xaa (amino acid) at position 330 = Leu or
; OTHER INFORMATION: Ile; Xaa at position 335 = Asp or Gly.
US-09-417-485D-5

Query Match      10.1%; Score 50.8; DB 4; Length 10640;
Best Local Similarity 47.0%; Pred. NO. 0.058;
Matches 191; Conservative 0; Mismatches 212; Indels 3; Gaps 1;

QY 7 TTGAATGCACAACTGCTTATTTTAACTTATTTGACATAAGTTTGTAAAGAGCTTAAAA 66
Db 9286 TTGTAACCTCGAAATATGGTTAAAAAATAAATAAATAAATAAATAAATAAATAA 9345
QY 67 ATGTGTACTTCATGTAATCAATTTATTTATTTATTTTGGCTAATGATTTTTTATT 126
Db 9346 TAGTATATTTTAAATAGTTTATGATTTATTTTTTTTTTTTTTTTTTTTTTATT 9405
QY 127 AACATGATTCCTTTTCATATATTGAATGGAGCTCAAGCTTCATTAATTTATAAC 186
Db 9406 TATTCATTTTTCTTTTIGATATTTTCCAAAGAAATATACTATATATATATGTAGTGC 9465
QY 187 TTTAGAAATGATTTAAATAACAACGATATGTAATTTGTAACATTCGAGTAATGGTCTACGA 246
Db 9466 TTAATTTTATTATGTGATGATATATACAAAGATGGTATCAATTTAGATATTTTATCCAA 9525
QY 247 AGCCATTTCTCTTGTATTTTGTAACTTTTATGACAGCAAAATTTGCTTGGCTCACTT 306
Db 9526 A---ATGTATATGTAATATAATAATTTATATATATATAATAATTTTATATATGTCCTA 9582
QY 307 TCATTCAGTTAAATAAATGATAAATAATTTTGGAGCTGTGAAGATAAATAAATACCAATAA 366
Db 9583 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 9642
QY 367 AATAATATAAAGTATTTTATATGAGTTTAAATAAATAAATAAATAAATAAATAA 412
Db 9643 ACTACTAAAAATGTAATACATATTTATGAAAAATAAATAAATAAATAAATAAATAA 9688
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Search completed: March 4, 2004, 16:42:05  
Job time : 59.9993 secs



QY 121 TTATTAACATGATTTCTTTCTGATATATTGAAATGGAGCTTCAAGCTTCATAAAT 180  
DB 5605 TTATTAACATGATTTCTTTCTGATATATTGAAATGGAGCTTCAAGCTTCATAAAT 5664  
QY 181 TATAACTTTAGAAATGATTCFAATAACACGTATGTAATGTAATTAACATGCAAGTAAATGGTG 240  
DB 5665 TATAACTTTAGAAATGATTCFAATAACACGTATGTAATGTAATTAACATGCAAGTAAATGGTG 5724  
QY 241 CTACGAAGCCATTTCTCTTGATTTTATGTAACCTTTTATGACAGCAAAATTTGCTTCTGGC 300  
DB 5725 CTACGAAGCCATTTCTCTTGATTTTATGTAACCTTTTATGACAGCAAAATTTGCTTCTGGC 5784  
QY 301 TCACCTTTCAATCAGTTAAATGATAAATGATAAATTTTGAAGCTGTGAAGATAAAATACC 360  
DB 5785 TCACCTTTCAATCAGTTAAATGATAAATGATAAATTTTGAAGCTGTGAAGATAAAATACC 5844  
QY 361 AAATAAAATAATATAAAGTATGATTTATGTAAGTTTAAATGATAAATGATAAATGATAAATACC 420  
DB 5845 AAATAAAATAATATAAAGTATGATTTATGTAAGTTTAAATGATAAATGATAAATGATAAATACC 5904  
QY 421 TAAACTTGAGAGTCCAGAGTTTATCCCATACATCTGTAATCAACTAATTTCTCAAGGG 480  
DB 5905 TAAACTTGAGAGTCCAGAGTTTATCCCATACATCTGTAATCAACTAATTTCTCAAGGG 5964  
QY 481 TGTAAAGGACCATTCATCGAGAAA 505  
DB 5965 TGTAAAGGACCATTCATCGAGAAA 5989

## RESULT 2

US-09-966-880A-35  
; Sequence 35, Application US/09966880A  
; Patent No. US20020164743A1  
; GENERAL INFORMATION:  
; APPLICANT: Muramatsu, Masamichi  
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE  
; FILE REFERENCE: 06501-088001  
; CURRENT APPLICATION NUMBER: US/09/966,880A  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: PCT/JP00/01918  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: JP 11-371382  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: JP 11-178999  
; PRIOR FILING DATE: 1999-06-24  
; PRIOR APPLICATION NUMBER: JP 11-87192  
; PRIOR FILING DATE: 1999-03-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 11204  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-966-880A-35

Query Match 100.0%; Score 505; DB 9; Length 11204;  
Best Local Similarity 100.0%; Pred. No. 8.3e-82;  
Matches 505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAACTTGAATGCAACTGCTTATTTTATCTTATGTAATGTAAGTTTGTAAAGAG 60  
DB 10700 GAAACTTGAATGCAACTGCTTATTTTATCTTATGTAATGTAAGTTTGTAAAGAG 10759  
QY 61 TAAAAATTTGTTACTTCAATGATTTTATTTATTTATTTTGGCTCAATGATTT 120  
DB 10760 TAAAAATTTGTTACTTCAATGATTTTATTTATTTATTTTGGCTCAATGATTT 10819  
QY 121 TTATTAACATGATTTCTTTCTGATATATTGAAATGGAGCTTCAAGCTTCATAAAT 180  
DB 10820 TTATTAACATGATTTCTTTCTGATATATTGAAATGGAGCTTCAAGCTTCATAAAT 10879

QY 181 TATAACTTTAGAAATGATTTCTTAATAACACGTATGTAATTTGTAACATTTGCAAGTAAATGGTG 240  
DB 10880 TATAACTTTAGAAATGATTTCTTAATAACACGTATGTAATTTGTAACATTTGCAAGTAAATGGTG 10939  
QY 241 CTACGAAGCCATTTCTCTTGATTTTATGTAACCTTTTATGACAGCAAAATTTGCTTCTGGC 300  
DB 10940 CTACGAAGCCATTTCTCTTGATTTTATGTAACCTTTTATGACAGCAAAATTTGCTTCTGGC 10999  
QY 301 TCACCTTTCAATCAGTTAAATGATAAATGATAAATTTTGAAGCTGTGAAGATAAAATACC 360  
DB 11000 TCACCTTTCAATCAGTTAAATGATAAATGATAAATTTTGAAGCTGTGAAGATAAAATACC 11059  
QY 361 AAATAAAATAATATAAAGTATGATTTATGTAAGTTTAAATGATAAATGATAAATGATAAATACC 420  
DB 11060 AAATAAAATAATATAAAGTATGATTTATGTAAGTTTAAATGATAAATGATAAATGATAAATACC 11119  
QY 421 TAAACTTGAGAGTCCAGAGTTTATCCCATACATCTGTAATCAACTAATTTCTCAAGGG 480  
DB 11120 TAAACTTGAGAGTCCAGAGTTTATCCCATACATCTGTAATCAACTAATTTCTCAAGGG 11179  
QY 481 TGTAAAGGACCATTCATCGAGAAA 505  
DB 11180 TGTAAAGGACCATTCATCGAGAAA 11204

## RESULT 3

US-09-966-880A-7  
; Sequence 7, Application US/09966880A  
; Patent No. US20020164743A1  
; GENERAL INFORMATION:  
; APPLICANT: Honjo, Tasuku  
; TITLE OF INVENTION: NOVEL CYTIDINE DEAMINASE  
; FILE REFERENCE: 06501-088001  
; CURRENT APPLICATION NUMBER: US/09/966,880A  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: PCT/JP00/01918  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: JP 11-371382  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: JP 11-178999  
; PRIOR FILING DATE: 1999-06-24  
; PRIOR APPLICATION NUMBER: JP 11-87192  
; PRIOR FILING DATE: 1999-03-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 2818  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (80)...(673)  
; FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)...(79)  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: (677)...(2818)  
US-09-966-880A-7

Query Match 85.0%; Score 429.4; DB 9; Length 2818;  
Best Local Similarity 99.8%; Pred. No. 2.5e-68;  
Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAACTTGAATGCAACTGCTTATTTTATCTTATGTAATGTAAGTTTGTAAAGAG 60  
DB 2367 GAAACTTGAATGCAACTGCTTATTTTATCTTATGTAATGTAAGTTTGTAAAGAG 2426  
QY 61 TAAAAATTTGTTACTTCAATGATTTTATTTATTTTATTTTGGCTCAATGATTT 120  
DB 2427 TAAAAATTTGTTACTTCAATGATTTTATTTATTTTATTTTGGCTCAATGATTT 2486



1985	CTACGAGCCATTCCTTGAATTTTGTAAACTTTTATGACGCAAAATTTGCTTCTGGC	2044
Db		
301	TCACCTTCAATCAGTTAAATAAATGATAAATAATTTTGAAGCTGTGAAGATAAAATACC	360
QY		
2045	TCACCTTCAATCAGTTAAATAAATGATAAATAATTTTGAAGCTGTGAAGATAAAATACC	2104
Db		
361	AAATAAATAAATAAAGTGATTTATATGAAGTTAAAAATAAAAAATCAGTATGATGGAA	420
QY		
2105	AAATAAATAAATAAAGTGATTTATATGAAGTTAAAAATAAAAAATCAGTATGATGGAA	2164
Db		
421	TAAACTTG 428	
QY		
2165	TAAACTTG 2172	
Db		

```

RESULT 5
US-10-311-455-1997
/ Sequence 1997, Application US/10311455
/ Publication No. US20030143606A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System
/ TITLE OF INVENTION: cytosine methylation
/ FILE REFERENCE: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311,455
/ CURRENT FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 1997
/ LENGTH: 6375
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1997

```

Query Match	14.2%;	Score	71.6;	DB	14;	Length	6375;
Best Local Similarity	48.3%;	Pred.	No.	0.019;			
Matches	200;	Conservative	0;	Mismatches	214;	Indels	0;
Gaps	0;						
QY	2	AAAACTTGTAATGCACAACTGCTCTATTATTTAAATCTTATTTGACATAAGTTTGTGTAAAGAGT	61				
Db	3164	AAATTTTGAGTTTTAGTTTTTATATGCGAAATGGAGAAAAATAATTTGTAAAAATTAA	3223				
QY	62	TAAAAATTTGTTACTTTCATGTAATTCATTATATTTTATATATTTTTCGGTCTAATGATTTT	121				
Db	3224	TTAAATTTGTTTATTTATATATTTTTTTTTTTAGTGTATATTAATTTGGTATTTTTTCGTTTGG	3283				
QY	122	TTATTTAAACATGATTTTCCTTTTTCGATATATTGAAATGGAGTCTCAAAGCTTCATAAAATTT	181				
Db	3284	TTAGAAATGTTTTTTTAAATTAATGTTTTTAAATTCGTTTGGTTAAATTTATTTGTTAGAAAT	3343				
QY	182	ATAACTTTAGAAATGATTTCTAAATACAAACGATGTAAATGTGTAAATTCGACAGTAATGGTGC	241				
Db	3344	TTTTTTTATTTTGAGAAATTAGAAAAGGAAATATTATGTTTGGTAATGTTTATATTTTTTAA	3403				
QY	242	TACGAAGCCATTTCTCTTGATTTTTTTAGTAAAACTTTTTATGACAGCAAAATTTGCTTCGGCT	301				
Db	3404	AATAAAAATTTGTAGGAAAGAAATATTTTAGTAAGTGATGAGAGTAGTAACGATTTGTTTTTAT	3463				
QY	302	CACCTTTCAATCACTTAAATAAAAATGATAATAATTTTTGGAAGCTGTGAAGATAAAAAATACCA	361				
Db	3464	ATTTTTAAATTTAATAATATATTTTTTTTTTACAGTTTTTTTAAATGATTGTAGATAATTTTTTA	3523				
QY	362	AATAAAAATATAATAAAGTGATTTATATGAAAGTTAAAAATAAAAAATCAGTATGCA	415				

Db 3524 TTTATTAAAAAATAATGTAATTAAGAATTAGGGTGTGATATCTGTTTTGA 3577

RESULT 6  
US-10-312-841-1/c  
; Sequence 1, Application US/10312841  
; Publication No. US20030186277A1  
; GENERAL INFORMATION:  
; APPLICANT: Epigenetics AG  
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC  
; FILE REFERENCE: EOI/1208/WO  
; CURRENT APPLICATION NUMBER: US/10/312.841  
; CURRENT FILING DATE: 2002-12-30  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 3673778  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
; NAME/KEY: unsure  
; LOCATION: (3294164)  
US-10-312-841-1

Query Match 13.0%; Score 65.4; DB 14; Length 3673778;  
Best Local Similarity 46.9%; Pred. No. 0.21; Indels 0; Gaps 0;  
Matches 204; Conservative 0; Mismatches 231;

Qy 42 ACATAAGCTTGTTAAAGAGTTAAAAATGTTCCTCATGTATTCATTATATATTTATATT 101  
Db 730168 ATATTATAAAAAAAAATACCTAAACAAAATTTATAAAATATCTTATATTTCCCTCACTTTA 730109

Qy 102 ATTTCGGTCTAATGATTTTTTATTACATGATTTCCCTTTCTGATATATGAAATGGAG 161  
Db 730108 TCATCACTCAAATAAACAACCTTCCTAATTAATATTTATAAATTAATTAATCCAATAAA 730049

Qy 162 TCTCAAGCTTCATAAATTTTATACTTTAGAAATGATCTTAATAACCAACGTATGTAAATTG 221  
Db 730048 AAAATAACATAAACCTTAACAATAACAATTAACCAACTTCATATAACAAAAATCCCCAAC 729989

Qy 222 TAACATTGCAGTAATGTGTGTCAGGCCATTTCTCTGATTTTCTAGTAACTTTTATGA 281  
Db 729988 ATAATATCAATCAATCCTTAAATATCAAAAACCTCTTATTTTCTTTCTTTAAATCAAC 729929

Qy 282 CAGCAAAATTTGCTTCTGGCTCACCTTCAATCAGTTAAATAAATGATAAATAATTTTGGAA 341  
Db 729928 ATTTAAAAATATCTACGTCCCATTTAAAAAAAATAATTAATAATTAACACATAATTTAA 729869

Qy 342 GCTGTGAGATAAATACCAATAAATAATATAAAGTAGATTTATAGAGTTAAATA 401  
Db 729868 CATAAAAAATACAAATATCAATATAATAATAATAAATAAATAAATAAATAAATAAATAAATA 729809

Qy 402 AAAAAATCAGTATGATGGAATAAACTTGAGAGTCAGAGAGTCAGAGAGTTATCCCATACATCTGTAATC 461  
Db 729808 TAAATTAATAAATAAATAAATAAATAATTAATATATCTTAACTTAACAAAAATAAAAAATCAA 729749

Qy 462 AACATAATTTCTCAC 476  
Db 729748 AATAATAATATTAA 729734

RESULT 7  
US-09-796-692-8856/c  
; Sequence 8856, Application US/09796692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8856  
; LENGTH: 469  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (443)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (463)  
; OTHER INFORMATION: n=A,T,C or G  
US-10-040-862-8856

Query Match 12.7%; Score 64; DB 14; Length 469;  
Best Local Similarity 65.3%; Pred. No. 0.019; Indels 0; Gaps 0;  
Matches 94; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 361 AAATAAAATAATATAAAAGTGATTATATGAAGTTAAATAAAAAATCAGTATGATGAA 420  
Db 278 AACTAAATAACCAAAACAGGCTGGTACTGGCATAAAGATAAACAATTAGACCAATAGAA 219  
QY 421 TAACTTCAGAGTCGAGAGTATCCCATACATCTGTAATCAACTAATTTCTCACAAGG 480  
Db 218 TAGAATTGAGAGTCGAGAGTAAACTCATACATATCTTCAATTGAATTTCTACAAGG 159  
QY 481 TGTAGGACCATTCATCGAGAAA 504  
Db 158 TGTCAAGGACCATCACTCAGAAA 135

RESULT 9  
US-10-057-475B-8856/c  
; Sequence 8856, Application US/10057475B  
; Publication No. US2004002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clapper, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Ordenez, Nadia  
; APPLICANT: Carter, Lauren  
; APPLICANT: McNeill, Patricia Dianne

; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Thera  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-014402US  
; CURRENT APPLICATION NUMBER: US/10/057,475B  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10979  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8856  
; LENGTH: 469  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)--(469)  
; OTHER INFORMATION: n = g, a, c or t  
US-10-057-475B-8856

Query Match 12.7%; Score 64; DB 15; Length 469;  
Best Local Similarity 65.3%; Pred. No. 0.019; Indels 0; Gaps 0;  
Matches 94; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 361 AAATAAAATAATATAAAAGTGATTATATGAAGTTAAATAAAAAATCAGTATGATGAA 420  
Db 278 AACTAAATAACCAAAACAGGCTGGTACTGGCATAAAGATAAACAATTAGACCAATAGAA 219  
QY 421 TAACTTCAGAGTCGAGAGTATCCCATACATCTGTAATCAACTAATTTCTCACAAGG 480  
Db 218 TAGAATTGAGAGTCGAGAGTAAACTCATACATATCTTCAATTGAATTTCTACAAGG 159  
QY 481 TGTAGGACCATTCATCGAGAAA 504  
Db 158 TGTCAAGGACCATCACTCAGAAA 135

RESULT 10  
US-10-154-884B-8856/c  
; Sequence 8856, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Mannion, Jane  
; APPLICANT: Better, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Thera  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013521US  
; CURRENT APPLICATION NUMBER: US/10/154,884B  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/190,479  
PRIOR FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: US 60/200,545  
PRIOR FILING DATE: 2000-04-27  
PRIOR APPLICATION NUMBER: US 60/200,303  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,779  
PRIOR FILING DATE: 2000-04-28  
PRIOR APPLICATION NUMBER: US 60/200,999  
PRIOR FILING DATE: 2000-05-01  
PRIOR APPLICATION NUMBER: US 60/202,084  
PRIOR FILING DATE: 2000-05-04  
PRIOR APPLICATION NUMBER: US 60/206,201  
PRIOR FILING DATE: 2000-05-22  
PRIOR APPLICATION NUMBER: US 60/218,950  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 60/222,903  
PRIOR FILING DATE: 2000-08-03  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 11290  
SOFTWARE: Fast-Seq for Windows Version 3.0  
SEQ ID NO 8856  
LENGTH: 469  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(469)  
OTHER INFORMATION: n = g, a, c or t  
US-10-154-884B-8856

Query Match 12.7%; Score 64; DB 15; Length 469;  
Best Local Similarity 65.3%; Pred. No. 0.019;  
Matches 94; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 361 AATATAAATAATATAAAGTGATTATATGAACTTAAATAAATAAATCAGTATGATGAA 420  
DB 278 AACTAAATAACCAAAACAGGCTGGTACTGGCATAAGATAAACATTTAGACCAATAGAA 219  
QY 421 TAAACTTGAGAGTCCAGAGTTATCCATACATCTGTATCAACTAATTTCTCACAAGG 480  
DB 218 TAGAATTGAGACTGCAGAGTAACTCATACATATCTTCAATTGAAATTTCTACAAGG 159  
QY 481 TGTAAAGGACCAATCAATGGAGAA 504  
DB 158 TGTCAAGGACCAATCAATGGAGAA 135

RESULT 11  
US-10-001-843-11  
Sequence 11, Application US/10001843  
Publication No. US20020132255A1  
GENERAL INFORMATION:  
APPLICANT: Salceda, Susana  
APPLICANT: Macina, Roberto  
APPLICANT: Recipon, Hervé  
APPLICANT: Cafferkey, Robert  
APPLICANT: Sun, Yongming  
APPLICANT: Liu, Chenghua  
APPLICANT: Turner, Leah  
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and P  
FILE REFERENCE: DEX-0267  
CURRENT APPLICATION NUMBER: US/10/001,843  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/249,992  
PRIOR FILING DATE: 2000-11-20  
NUMBER OF SEQ ID NOS: 218  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 11  
LENGTH: 1925  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-001-843-11

Query Match 12.7%; Score 64; DB 13; Length 1925;  
Best Local Similarity 65.3%; Pred. No. 0.03;  
Matches 94; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 361 AATATAAATAATATAAAGTGATTATATGAACTTAAATAAATAAATCAGTATGATGAA 420  
DB 972 AACTAAATAACCAAAACAGGCTGGTACTGGCATAAGATAAACATTTAGACCAATAGAA 1031  
QY 421 TAAACTTGAGAGTCCAGAGTTATCCATACATCTGTATCAACTAATTTCTCACAAGG 480  
DB 1032 TAGAATTGAGACTGCAGAGTAACTCATACATATCTTCAATTGAAATTTCTACAAGG 1091  
QY 481 TGTAAAGGACCAATCAATGGAGAA 504  
DB 1092 TGTCAAGGACCAATCAATGGAGAA 1115

RESULT 12  
US-09-835-232-6  
Sequence 6, Application US/09835232  
Patent No. US20020098489A1  
GENERAL INFORMATION:  
APPLICANT: Leder, Philip  
APPLICANT: Leader, Benjamin  
TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES  
TITLE OF INVENTION: AND USES THEREOF  
FILE REFERENCE: 00383/052002  
CURRENT APPLICATION NUMBER: US/09/835,232  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: US 60/196,811  
PRIOR FILING DATE: 2000-04-13  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Fast-Seq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 180216  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(180216)  
OTHER INFORMATION: n = A,T,C or G  
US-09-835-232-6

Query Match 12.7%; Score 64; DB 9; Length 180216;  
Best Local Similarity 56.6%; Pred. No. 0.14;  
Matches 138; Conservative 0; Mismatches 105; Indels 1; Gaps 1;  
QY 262 TTTTGTAGTAACTTTTATGACAGCAAAATTTGCTTCTGCTCACTTTCAATCAGTTAAATA 321  
DB 56089 TTATTTGARACCAACAAAAAACCAATAGCCAAAGTAATCTTGATCAAAAAGACAAAA 56148  
QY 322 AATGATAAATAATTTTGGAGCTGTGAAGATAAAATACCAA-ATAAAATAATATAAAGT 380  
DB 56149 CCAGAGAAATCACACAACCCAGATTGAAAATATATTACAAAGCTATAGTAATCAAAACAG 56208  
QY 381 GATTATATCAAGTTAAATATAAATAATCAGTATGATGGAATAAATTTGAGAGTCCAGAAG 440  
DB 56209 TATGTTGGTGGCATAAATAATAGACATGTCAGTGGGATAGAAATGGAGTTCAGAAA 56268  
QY 441 TTATCCCATACATCTGTAACTCAACTAATTTCTCACAAGGGTGAAGACCAATTCATGGA 500  
DB 56269 TAAACCCAGCTAACTACAGTCAATTTGATTGCAACAAAGGTGTCAAGAAACACAGAATGGG 56328  
QY 501 GAAA 504  
DB 56329 GAAA 56332  
RESULT 13  
US-10-308-485-6  
Sequence 6, Application US/10308485  
Publication No. US20030170683A1

```

; GENERAL INFORMATION:
; APPLICANT: Leder, Phillip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-10-308-485-6

Query Match          12.7%  Score 64; DB 14; Length 180216;
Best Local Similarity 56.8%; Pred. No. 0.14;
Matches 138; Conservative 0; Mismatches 105; Indels 1; Gaps 1;

QY 262 TTTTATGTAACCTTTTATGACGACAAATTTCTCTGGCTCACTTTCAATCAAGTTAAATA 321
DB 56089 TTATTTGAAACCAACAAAAAACCATAATAGCCAAAGTAATCTTGATCAAAAAGGACAAAA 56148

QY 322 AATGATAAATAATTTTGGAGCTGTGAAGATAAATAACCAA-ATAAATAATATAAAGT 380
DB 56149 CCAGAGAAATCACACACACAGATTTGAAATATATTACAAAGCTAGTAATCAAAACAG 56208

QY 381 GATTTATATGAAGTTAAATAAATAATCAGTATGATGGAATAAATCTTGAGAGTCCAGAG 440
DB 56209 TATGGTGGTGCATAAATAATAGACACATCGTCCAGTGGATAGAGTGTCCAGAAA 56268

QY 441 TTATCCATACATCTGTAATCACTAATTTCTCAAGAGGTGTAGGACCATTCATGGA 500
DB 56269 TAAACCCAGCTAACTACAGTCAATGTTTTCGCAACAAAGGTGTGCAAGAACACAGAAATGG 56328

QY 501 GAAA 504
DB 56329 GAAA 56332

RESULT 14
US-10-027-632-311405
; Sequence 311405, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67377
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-67377

Query Match          12.2%  Score 61.8; DB 15; Length 505;
Best Local Similarity 62.7%; Pred. No. 0.048;
Matches 96; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 352 TAAATACCAATAAATAATAATAAAGTGAATTTATATGAAGTTAAATAAATAAATCAGT 411
DB 238 TACAATGCGATAGCAATCAATCAAGACAGTGTGCTACTGCGATAGCAATAAAGATAGAAA 297

QY 412 ATGATGGAATAAATCTGAGAGTCCAGAGTTATCCCATACATCTGTAATCAACTAATTC 471
DB 298 TCAATGGAATGGAATGAGAGTCTGGAAGTATATCCATACATCTGTGCTCACTGAGTTT 357

QY 472 TCACAAGGGTGAAGGACCATTCATCGGAGAAA 504
DB 351 TGAAGGAGGCTCCAGGACCGTTCAATGGGAAA 383

RESULT 15
US-10-027-632-67377
; Sequence 67377, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67377
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-67377

Query Match          12.2%  Score 61.8; DB 15; Length 505;
Best Local Similarity 62.7%; Pred. No. 0.048;
Matches 96; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 352 TAAATACCAATAAATAATAATAAAGTGAATTTATATGAAGTTAAATAAATAAATCAGT 411
DB 238 TACAATGCGATAGCAATCAATCAAGACAGTGTGCTACTGCGATAGCAATAAAGATAGAAA 297

QY 412 ATGATGGAATAAATCTGAGAGTCCAGAGTTATCCCATACATCTGTAATCAACTAATTC 471
DB 298 TCAATGGAATGGAATGAGAGTCTGGAAGTATATCCATACATCTGTGCTCACTGAGTTT 357

QY 472 TCACAAGGGTGAAGGACCATTCATCGGAGAAA 504
DB 351 TGAAGGAGGCTCCAGGACCGTTCAATGGGAAA 383
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Db 358 TGAAGAAGGCTCCAGGACCGTTCAATGGGAAA 390

Search completed: March 4, 2004, 19:00:27  
Job time : 258.462 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 12:54:45 ; Search time 1974.73 Seconds  
(without alignments)  
7636.686 Million cell updates/sec

Title: US-09-966-880A-35\_COPY\_10700\_11204

Perfect score: 505  
Sequence: 1 gaaacttgatgcacact.....ggaccattcaatggagaaaa 505

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

```
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc1:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_pig:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	286	56.6	442	9	AI016902 ou31d03.x
C 2	256	50.7	268	9	AA879422 cj9ic11.s
C 3	78.2	15.5	1201	13	BX439779 BX439779
C 4	76	15.0	1013	29	CNS06RPQ AL412260 T7 end of

C 5	75.6	15.0	1201	9	AL532464
C 6	75.6	15.0	1201	13	BX424465
C 7	75.2	14.9	1200	13	BX437758
C 8	74.8	14.8	1201	9	AL536104
C 9	74.6	14.8	1101	29	CNS0001J
C 10	73.6	14.6	1101	29	CNS000F1G
C 11	73.4	14.5	1056	13	BX415058
C 12	73.4	14.5	1101	29	CNS000RVL
C 13	72.8	14.4	1064	13	BX361825
C 14	72.6	14.4	1056	13	BX415058
C 15	72.6	14.4	1101	29	CNS000RQ7
C 16	72.6	14.4	1201	13	BX424465
C 17	72.2	14.3	1098	13	BX377526
C 18	72	14.3	1200	13	BX437739
C 19	71.6	14.2	1133	13	BX444099
C 20	71.2	14.1	1201	9	AL536104
C 21	71	14.1	843	29	CNS000CS1
C 22	70.4	13.9	887	13	BX441520
C 23	70.4	13.9	1043	29	CNS0145P
C 24	70.4	13.9	1201	13	BX439779
C 25	70.2	13.9	1200	13	BX436510
C 26	70	13.9	793	28	BZ882481
C 27	70	13.9	1200	13	BX415878
C 28	70	13.9	1200	13	BX437739
C 29	70	13.9	1201	13	BX336467
C 30	69.8	13.8	1101	29	CNS0003DQ
C 31	69.6	13.8	483	14	CA389449
C 32	69.6	13.8	899	13	BX453223
C 33	69.6	13.8	1061	13	BX437039
C 34	69.6	13.8	1200	13	BX436510
C 35	69.4	13.7	843	29	CNS0003L
C 36	69.4	13.7	945	29	CNS04D0K
C 37	69.4	13.7	1201	13	BX446296
C 38	69.2	13.7	1098	13	BX377526
C 39	69.2	13.7	1200	13	BX415878
C 40	68.8	13.6	691	13	BX436603
C 41	68.6	13.6	1101	29	CNS000RVL
C 42	68.6	13.6	1563	28	CC206942
C 43	68.4	13.5	734	29	CNS010MP
C 44	68.4	13.5	964	13	BX341256
C 45	68.4	13.5	1101	29	CNS000EQL

#### ALIGNMENTS

RESULT 1  
AI016902/c

LOCUS AI016902 442 bp mRNA linear EST 17-MAR-1999  
DEFINITION ou31d03.x1 Soares\_NFL\_T\_CBC\_S1 Homo sapiens cDNA clone  
IMAGE:1627877 3', mRNA sequence.

ACCESSION AI016902

VERSION AI016902.1

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 442)

AUTHORS NCI-CGAP

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index

COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 426 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 433.

Location/Qualifiers

1. .442

/organism="Homo sapiens"

FEATURES

source

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/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clone="IMAGE:1627877"  
/lab_host="DH10B"  
/clone_lib="Soares_NFL_T_GBC_S1"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCI CGAP GCB1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo. "
```

## ORIGIN

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Query Match 56.6%; Score 286; DB 9; Length 442;  
Best Local Similarity 100.0%; Pred. No. 2.5e-32;  
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GAAAACTTGAATGACCAACTGCTTATTTTAACTTATTTGACATAAGTTTGTAAAGAG 60  
DB 286 GAAACTTGAATGACCAACTGCTTATTTTAACTTATTTGACATAAGTTTGTAAAGAG 227  
QY 61 TAAAAATTTGATTCATGATTCATTTATTTATTTATTTTTCGCTCTAATGATTT 120  
DB 226 TAAAAATTTGATTCATGATTCATTTATTTATTTATTTTTCGCTCTAATGATTT 167  
QY 121 TTTATTAACATGATTTCTTTCTGATATATTGAATGGAGTCTCAAGCTTCATAAAT 180  
DB 166 TTTATTAACATGATTTCTTTCTGATATATTGAATGGAGTCTCAAGCTTCATAAAT 107  
QY 181 TATTAATTTAGAAATGATTTCAATAACACGATGTAATTTGTAACATTCAGTAATGGTG 240  
DB 106 TATAACTTTAGAAATGATTTCAATAACACGATGTAATTTGTAACATTCAGTAATGGTG 47  
QY 241 CTACGAAGCCATTTCTCTGATTTTGTAGTAACCTTTATGACAGCA 286  
DB 46 CTACGAAGCCATTTCTCTGATTTTGTAGTAACCTTTATGACAGCA 1
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```
RESULT 2  
AA879422/c  
LOCUS AA879422 268 bp mRNA linear EST 19-MAY-1998  
DEFINITION oJ91c11.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone  
IMAGE:1505684 3', mRNA sequence.  
ACCESSION AA879422  
VERSION AA879422.1 GI:2988533  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens
```

```
REFERENCE  
1 (bases 1 to 268)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
INSDAT Length: 685 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 252.  
Location/Qualifiers  
1..268  
/organism="Homo sapiens"  
/mol_type="mRNA"  
/db_xref="taxon:9606"
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FEATURES  
source
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/clone="IMAGE:1505684"  
/lab_host="DH10B"  
/clone_lib="Soares_NFL_T_GBC_S1"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site 1: Not I; Site 2: Eco RI;  
Equal amounts of plasmid DNA from three normalized  
libraries (fetal lung NBHL19W, testis NHT, and B-cell  
NCI CGAP GCB1) were mixed, and ss circles were made in  
vitro. Following HAP purification, this DNA was used as  
tracer in a subtractive hybridization reaction. The driver  
was PCR-amplified cDNAs from pools of 5,000 clones made  
from the same 3 libraries. The pools consisted of  
I.M.A.G.E. clones 297480-302087, 682632-687239,  
726408-728711, and 729096-731399. Subtraction by Bento  
Soares and M. Fatima Bonaldo. "
```

## ORIGIN

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Query Match 50.7%; Score 256; DB 9; Length 268;  
Best Local Similarity 99.6%; Pred. No. 7.4e-28;  
Matches 267; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 152 TGAATAGGAGTCTCAAGCTTCATAAAATTTATACTTTAGAAATGATTTCTAATAACAAG 211  
DB 268 TGAATAGGAGTCTCAAGCTTCATAAAATTTATACTTTAGAAATGATTTCTAATAACAAG 209  
QY 212 TATGTAATTTGTAACATTCAGTAATGGTGTACGAAGCCATTTCTTGAATTTTAGTAA 271  
DB 208 TATGTAATTTGTAACATTCAGTAATGGTGTACGAAGCCATTTCTTGAATTTTAGTAA 149  
QY 272 ACTTTTA-TGACAGCAAAATTTGCTTCTGGCTCACATTTCAATCAGTTAAATAAATGATAAA 330  
DB 148 ACTTTTATGACAGCAAAATTTGCTTCTGGCTCACATTTCAATCAGTTAAATAAATGATAAA 89  
QY 331 TAAATTTGGAAGCTGTGAAGATAAATAACCAATAAATAATAATAATAAAGTGAATTTATATG 390  
DB 88 TAAATTTGGAAGCTGTGAAGATAAATAACCAATAAATAATAATAATAAAGTGAATTTATATG 29  
QY 391 AAGTTAAATAAATAAATAAATCAGTATGATGG 418  
DB 28 AAGTTAAATAAATAAATAAATCAGTATGATGG 1
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## RESULT 3

```
EX439779  
LOCUS EX439779 1201 bp mRNA linear EST 15-MAY-2003  
DEFINITION BX439779 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE014YF05  
3-PRIME mRNA sequence.  
ACCESSION EX439779  
VERSION EX439779.1 GI:30771778  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens
```

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REFERENCE  
1 (bases 1 to 1201)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
Bp 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
Library was constructed by life technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 3370.r For  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS0DE014CC03NP1&cluster=3370.r. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DE014CC03NP1.
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FEATURES  
source  
1..1201  
/organism="Homo sapiens"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS06E014F05"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pcMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match      15.5%; Score 78.2; DB 13; Length 1201;
Best Local Similarity 38.3%; Pred. No. 0.012;
Matches 151; Conservative 70; Mismatches 169; Indels 4; Gaps 1;

QY 35 TTATTGTCATAGTTGTTAAAGAGTTAAATTTGTTACTTCATGTTTCAATTTATTT 94
DB 786 TTWTTTAAATATAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 845

QY 95 TTATATTATTTTGGCTCAATGATTTT---TATTAACATGATTTCTCTTCGATATA 150
DB 846 TAAATATTAATAAAWAAAAAATAAAATTTTAAATTTTAAATTTTAAATTTTAAWA 905

QY 151 TTGAATGGAGTCTCAAGCTTCATTAATTTTAACTTTTGAAGATGTTCTTAATCAAC 210
DB 906 WAAATTTTAAWATAATTAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAWA 965

QY 211 GTATGTAATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGAT 270
DB 966 TAAATATTAATAAAWTTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1025

QY 271 AACTTTTATGACAGCAATTTTGCTTCTGCTGCTCACTTTCAATCAGTTTAAATGATA 330
DB 1026 WAAATWATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1085

QY 331 TAATTTTGGAGCTGTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 390
DB 1086 AAAAATAAAWATAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1145

QY 391 AAGTTTAAATTAATAAAATCAGTATGATGGAATAAA 424
DB 1146 AAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 1179

RESULT 4
CNS06RPO/c
LOCUS
DEFINITION
T7 end of clone AW0AA016E05 of library AW0AA from strain CLIB 89 of
Yarrowia lipolytica, genomic survey sequence.
ACCESSION
AL412260
VERSION
AL412260.1 GI:12182622
KEYWORDS
GSS.
SOURCE
Yarrowia lipolytica
Yarrowia lipolytica
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
REFERENCE
1 (bases 1 to 1013)
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bollotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Licorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE
20584711
PUBMED
11152876
REFERENCE
2 (bases 1 to 1013)
Casaregola,S., Neuveglise,C., Lepingle,A., Bon,E., Feyrerol,C.,
Artiguenave,F., Wincker,P. and Gaillardin,C.
Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia

```

```

lipolytica
FEBS Lett. 487 (1), 95-100 (2000)
MEDLINE
20584727
PUBMED
11152892
REFERENCE
3 (bases 1 to 1013)
Genoscope.
Direct Submission
TITLE
Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
FEATURES
Location/Qualifiers
1..1013
/organism="Yarrowia lipolytica"
/mol_type="genomic DNA"
/strain="CLIB 89"
/db_xref="taxon:4952"
/clone="AW0AA016E05"
/clone_lib="AW0AA"
/notes="end : T7"

ORIGIN

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Best Local Similarity 44.4%; Pred. No. 0.027;
Matches 192; Conservative 27; Mismatches 212; Indels 1; Gaps 1;

QY 27 TTTTATCTTATGTCATACATGTTTCTAAAGAGTTTAAATTTGTTACTTCATGATTTCA 86
DB 955 TTWTATATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 896

QY 87 TTTTATATTTTATTTATTTTGGCTCTAATGATTTTATTTAATCATGATTTCTCTTTCTGA 146
DB 895 AWAATAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 836

QY 147 TATATTGAATGGAGTCTCAAGCTTCATAAATTTTATACTTTAGAAATGATTTCTAATA 206
DB 835 TTTTATTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 776

QY 207 CAACGATGTAATTTGTAACATTTGCAGTAATGCTGTACGAGCCATTTCTCTTGATTTT 266
DB 775 AATAATATTTTATTTTAAATAAAWAAAAATAAAATAATTTATTTATTTATTTATTTAT 716

QY 267 AGTAAACTTTTATGACAGCAATTTGCTTCTGCTCAGTTTCAATCAGTTTAAATGA 326
DB 715 AAAATTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 656

QY 327 TAAATATTTTGGAGCTGTGAAGATAAAATACCAATAAAATAATTTATTTATTTATTTAT 386
DB 655 TAAATATTTT---AAAATTTTAAATAAAWAAATTTATTTATTTATTTATTTATTTATTT 597

QY 387 TATGAAGTTTAAATAAAATCAGTATGATGGAATTAATTTAGAGTCCAGAGTTATCC 446
DB 596 TATAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 537

QY 447 CATACATCTGTA 458
DB 536 AATTATATTTA 525

RESULT 5
AL532464/c
LOCUS
DEFINITION
AL532464 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
CS0DM0121N10 3-PRIME, mRNA sequence.

```

AL532464  
AL532464.2 GI:31070296  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
REFERENCE  
1 (bases 1 to 1201)  
AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished (2001)  
COMMENT  
On Feb 13, 2001 this sequence version replaced gi:12795957.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS0DM012G05NFI.  
FEATURES  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="CS0DM012YN10"  
/tissue\_type="FETAL LIVER"  
/dev\_stage="fetal"  
/clone\_lib="Homo sapiens FETAL LIVER"  
/notes="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."  
ORIGIN  
Query Match 15.0%; Score 75.6; DB 9; Length 1201;  
Best Local Similarity 33.5%; Pred. No. 0.028;  
Matches 126; Conservative 89; Mismatches 160; Indels 1; Gaps 1;  
QY 20 TGCTCTTATTTTAACTTATGTCATAGTTGTTAAAGAGTTAAATTTGTTACTTCAT 79  
DB 1189 TAWTAAWTTTAAWAAWTTAAWTTTAAWAAWTTAAWTTTAAWAAWTTAAWTTAAW 1130  
QY 80 GTATTCATTTATATTTTATATTTTGGCTCTAATGATTTTATTAACATGATTTCT 139  
DB 1129 WAAAWTTTAAWAAWTTAAWTTTAAWAAWTTAAWTTTAAWAAWTTAAWTTAAW 1070  
QY 140 TTCTCGATATATGAATGAGGCTCAAGCTTCATAATTTAATTAACCTTAGAATGAT 199  
DB 1069 WTWTATAWTTTAAWTTTAAWTTTAAWAAWAAWTTAAWAAWTTAAWAAWTTAAW 1010  
QY 200 CTATTAACAACGATGTAATGTAACATTCGAGTATGTCGACGAGCCATTTCTCT 259  
DB 1009 TAAWTTTAAWAAWTTAAWAAWTTTAAWAAWTTTAAWAAWTTTAAWAAWTTAAW 951  
QY 260 GATTTTGTAGTAACTTTATGACAGCAAAATTTGCTTCGCTCACTTCATCAGTTAA 319  
DB 950 AWTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAW 891  
QY 320 TAAATGATAATATTTTGAAGCTGTGAAGATAAATACCAATATAATATAAAG 379  
DB 890 TTTTWTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAW 831  
QY 380 TGATTTATATGAATTT 395  
DB 830 TCTTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAWTTTAAW 815  
RESULT 6  
BX424465/c  
LOCUS  
DEFINITION  
BX424465 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE002YF24  
EST 13-MAY-2003

5-PRIME, mRNA sequence.  
BX424465  
BX424465.1 GI:30659708  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
REFERENCE  
1 (bases 1 to 1201)  
AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 4172.r for  
more information about this cluster, see  
http://www.genoscope.cns.fr/  
cgi-bin/cluster.cgi?seq=CS5AA0042D12QPKcluster-4172.r. Contact :  
Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CS5AA0042D12QPK.  
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ORIGIN  
Query Match 15.0%; Score 75.6; DB 13; Length 1201;  
Best Local Similarity 47.5%; Pred. No. 0.028;  
Matches 126; Conservative 26; Mismatches 113; Indels 0; Gaps 0;  
QY 15 ACAACTGCTTTATTTTAACTTATGTCATAGTTTGTAAAGAGTTAAATTTGTTAC 74  
DB 955 ANWTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 896  
QY 75 TTCAATGATTCATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTAT 134  
DB 895 TWTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 836  
QY 135 TTCCTTTTCGATATATGAAATGGAGCTTCAAGCTTCATAATTTTATTAACCTTAGAAA 194  
DB 835 TTTTWTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 776  
QY 195 TGATTTCTAATAACAACGATGTAATGTAACATTCGAGTATGTCGACGAGCCATTT 254  
DB 775 TTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 716  
QY 255 CTCTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 279  
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RESULT 7  
BX437758/c  
LOCUS  
DEFINITION  
BX437758 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YB01  
5-PRIME, mRNA sequence.  
ACCESSION  
BX437758  
KEYWORDS  
SOURCE  
Homo sapiens (human)  
EST. 30773605

AL536104.2 GI:31260974  
EST.  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE 1 (bases 1 to 1201)  
FULL-LENGTH CDNA LIBRARIES AND NORMALIZATION  
Li W.B., Gruber C., Jessee J. and Polayes D.  
UNPUBLISHED (2001)  
COMMENT On Feb 13, 2001 this sequence version replaced gi:12799597.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: segre@genoscope.cns.fr, web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSDF022BB09Q21.  
Location/Qualifiers  
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enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."  
FEATURES  
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was primed with a NotI-oligo (dT) primer. Five prime end  
enriched, double-strand cDNA was digested with Not I and  
cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."  
Query Match 14.8%; Score 74.8; DB 9; Length 1201;  
Best Local Similarity 33.1%; Pred. No. 0.036;  
Matches 127; Conservative 86; Mismatches 171; Indels 0; Gaps 0;  
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DBb 775 TTTATRWATWATWTTTWTWTTTWTWKTAAATWATAATWTTAAWTTTTTWTATTWTAW 834  
QY 84 TCATTATATTTATATATTTCGGCTCAATGATTTTTTATTAAACATGATTCCTCTTC 143  
DBb 835 TAAAAWTTTWTATTTWTTATTTTWTATAAAAATTTATTTTAAATTTTAAWTTTATWT 894  
QY 144 TCATATATGAAATGGAGCTCTCAAGCTTCATAAAATTTATAACTTTAGAAATGATCTTAA 203  
DBb 895 TTTTATTTATAAATTTTAWAAWATTTWAAAATWTTAGTAAWAAWAAATATATAW 954  
QY 204 TAAACAATGATGTAATGTCACATTGCAGTAATGGTGCTACGAGCCATTTCTCTGATT 263  
DBb 955 TAWGRTAAATAWWWWTAAWAAWATATATWTTAAAAAWAAWTTWAAATATWTTTATWTTW 1014  
QY 264 TTTAGTAACTTTTATGACAGCAAAATTTGCTTCCTGGCTCAGTTTCAATCAGTTAAATAAA 323  
DBb 1015 TTTTWTWTTTWWATSTATATAAAAWTATWTTTTTAAATATWATAWTTWTTTAAAWWA 1074  
QY 324 TGATAAAATATTTGGAGCTGTGAGATATAAATACCAATTAATATATATAATAGATGAT 383  
DBb 1075 WRTTWTWTTTAAWAAWAAWATTTTWTWTAWAAAAWAAAAAATATADAWATWTTTGA 1134  
QY 384 TTATATGAAGTTAAAAATAAAAAAT 407  
DBb 1135 TATTATTATWTTTWTADAWDAT 1158  
RESULT 9  
CNS0021J/c  
LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR05N11 of RPc1-98 library from Drosophila melanogaster (fruit

## fly), genomic survey sequence.

REFERENCE	ACCESION	VERSION	KEYWORDS	SOURCE	ORGANISM	ACCESION	VERSION	KEYWORDS	SOURCE	ORGANISM
1	AL061936	AL061936.1	GI:4940214	Drosophila melanogaster (fruit fly)	Drosophila melanogaster	AL061936	AL061936.1	GI:4940214	Drosophila melanogaster	Drosophila melanogaster
					Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.					
					1 (bases 1 to 1101)					
					Genoscope.					

TITLE JOURNAL	COMMENT	REFERENCE AUTHORS TITLE JOURNAL	COMMENT
Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org">http://www.fruitfly.org</a> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and		

Aaron Mammoer in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named KPCL-98 and was constructed by partial *Eco*KI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <http://bacpac.med.buffalo.edu/drosophila.bac.htm>.

FEATURES	source
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Query Match 14.8%; Score 74.6; DB 29; Length 1101;  
 Best Local Similarity 44.6%; Pred. No. 0.041;  
 Matches 181; Conservative 10; Mismatches 215; Indels 0; Gaps 0;

ORIGIN	Query Match	Best Local Match
QY	20	TGTCCTATTAAATCTTATTGTACATAAGTTGTAAAGAGTTTAAAAAATTGTTACTTCAT 79
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Db	346	TT 287
QY	140	TTTCGTATATATGAATGAGAGCTCAAGCTCATATAATTTATACTTTAGAAATGATT 199
Db	286	TT 227
QY	200	CTAATAACAACGTATGAAATTTGTAACATTCAGATTAATGGTGTACGAAGCCATTTCTCT 259
Db	226	TGTT 167
QY	260	GATTTTTAGTAAACTTTTTATGACACAAATTTGCTCTCGCTCACCTTTCAATCAGTTAAA 319
Db	166	TTTTTTTTTTAAACTTTTCATGAAACACTTTTTTTTDTNTTTTATTTAHMTTMTTAAA 107
QY	320	TAAATGATAATAATTTTGGAGCTGTGAAGATATAAATACCAATATAAATAATATAAAG 379
Db	106	TTAAAAAATTATNATTTMTNTTTTNNAAAAAATAAAAAAAMANNNAANAAAAAAG 47
QY	380	TGATTTATATCAAGCTTAAATATAAAATCAGTATGATGGATTAAC 425
Db	46	AGNEBAANVAAAAACAAANNAANAAAAAMAAAAAANNAANAAAAAC 1

[illegible]

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QY 386 ATATGAAGTTAAATATAAATAATCAGTAT 413
Db 707 AAAATAATATTAAATATAATAAAT 680

RESULT 11
BX415058 1056 bp mRNA linear EST 15-MAY-2003
LOCUS BX415058 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP004YG19
DEFINITION 3-PRIME, mRNA sequence.
ACCESSION BX415058
VERSION BX415058.1 GI:30767520
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/InvitrogenCorporation.1600
Faraday Avenue Genoscope sequence ID: CS0CAP004AD10NP1.
Location/Qualifiers
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 14.5%; Score 73.4; DB 13; Length 1056;
Best Local Similarity 34.2%; Pred. No. 0.063;
Matches 163; Conservative 82; Mismatches 232; Indels 0; Gaps 0;

QY 2 AAAACTTGATCGACACAGTCTTATTTTAACTTATGTCATCAAGTTGTAAGAGT 61
Db 531 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 590

QY 62 TAAAAATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 121
Db 591 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 650

QY 122 TTATTAACATGATTTCCCTTTCTGATATATGAAATGAGTCTCAAGCTTCATAAATTT 181
Db 651 KTTTTTATADWDATWAATATWTWTGKAGWAAAAAAATKATKATKTKTAWAAAA 710

QY 182 ATAACTTTAGATGATCTTATACACAGTATGAATGTGAACATTCGACATGATGTC 241
Db 711 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 770

QY 242 TACGAAGCATTCTCTGATTTTATGAAACTTTTATGACAGCAAAATTCGCTCTGCT 301
Db 771 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 830

QY 302 CACTTTCATCAGTAAATAAATGAATAATATTTTGAAGCTGTGAAGATAAATACCA 361
Db 831 WAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 890

QY 362 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 421

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Db 891 RWAARAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 950
QY 422 AAACCTTGAGAGTCCAGAGTTATCCATCATCTGTATCACTTAATTTCTCACAAG 478
Db 951 AAAAATTTTATAGGAGCGTTTAAATAAATAAATAAATAAATAAATAAATAAATAA 1007

CNS00EVL 1101 bp DNA linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069706
VERSION AL069706.1 GI:4949849
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
FEATURES
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Matches 160; Conservative 69; Mismatches 175; Indels 3; Gaps 2;

QY 3 AAACCTTGAATGACAACTGCTCTTATTTTAACTTATGTCATCAAGTTGTAAGAGT 62
Db 988 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 929

QY 63 AAAAAATGTTACTTCATGATTCATTTATATTTATATTTTGGCTCTAATGATTTT 122
Db 928 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 869

QY 123 TATTAACATGATTTCTCTTCTGATATATGAAATGAGTCTCAAGCTTCATAAATTTA 182
Db 868 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 810

QY 183 TAACTTTAGAAATGATCTTAATAACAACTATGTAATTTGTAACATTCGAGTAATGGT 242
Db 809 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 750

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195	QY	TGATCTCTAATACCAACGTCATGTAATTGCTGCACTAATGGTCTACGAAGCCATT	254
821	DB	AAAAWATWTAATATTATTAATATATATWTAATAWAAATTTTAAATATAWAAATAAT	880
255	QY	CTCTTGATTTTAGTAAACTTTTATGACAGCAAAATTCCTCTGCTGCCTCACTTTCATCAG	314
881	DB	WTTTAAWTTTTTTTTTATTTTTTTTATTTTTTTTTTTTTTTTTTTTAAATAAAAAAWAW	940
315	QY	TAAATAAATGATAAATAATTTTGGAACTGTGAAGATAAAATACCAATAAATAAATAAT	374
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**DEFINITION** linear EST 15-MAY-2003  
CSOCAP004YG19.  
**ACCESSION** BX415058  
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**KEYWORDS** 3'-PRIME, mRNA sequence.  
**SOURCE** BX415058.1 GI:30767520  
**ORGANISM** Homo sapiens (human)  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**AUTHORS** Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
**TITLE** Full-length cdna libraries and normalization  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Genoscope  
Genoscope - Centre National de Sequencage  
Bp 191 91006 EVRY cedex - France  
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr  
Library was constructed by Life Technologies, a division of  
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paradise Avenue Genoscope sequence ID : CSOCAP004AD10NP1.

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1. .1056
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN

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QY	123	TATTAACATGATTCCTTTTCGATATATGAAATGGAGCTCAAAAGCTTCATAAATTA	182		
DB	898	TTTTTWTYAAAACAATTTTTTWWTTATATAAAATTTAATAAAATTTTTTTTTTWWTTTTWW	839		
QY	183	TAACTTTAGAAATGATCTTAATAACACAGCTATGTAATTTGAACATTCAGTATGGTCT	242		
DB	838	WWWTT	779		

Db	778	WWWWWTTWTANNNNNNNA	TTTTTTTTTTWAAAAA	AAAAATWTTTTTTTTTTTTTTTTTTTT	719
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Db	718	TTTTTTTTTTTTTTWAMAM	MMTATMAAMTTTTTTT	TWCTMCAYAWAWATAWTTWATHHTA	659
Qy	363	ATAAAATAATAAAAGTGAT	TATATATGAAGTTAAAAA	ATAAAATCAGTATGATGGAATA	422
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RESULT 15  
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LOCUS  
DEFINITION  
1101 bp DNA linear GSS 04-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC:  
BACR23P01 of RCI-98 library from *Drosophila melanogaster* (fruit  
fly), genomic survey sequence.  
AL069440  
AL069440.1 GI:4949583  
GSS.  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 1101)  
REFERENCE

Direct Submission  
 Title: Direct Submission  
 Journal: BP 191 91006 ERY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 Comment: Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mammosser in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial,  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
 pi and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at <http://bacpac.med.buffalo.edu/drosophila/bac.htm>.

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906	AAWCATTWTWTAAWWTAAATTTTAACTTTTAACTTTTAAWTTAAAAATTTTAAATTAANA	847		
62	TAAAAATTTCTTACTTCATGCTATTCATTTATATTTTATATTTTTCGCTCTAATGATTTT	121		
846	AAARWATTAAGAAATTTATATWATATATWAAAWATATATATTTATWAAATTTTATAAWATTT	767		

[illegible]

Search completed: March 4, 2004, 16:38:51  
Job time : 1987.73 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 22:01:47 ; Search time 78 Seconds  
(without alignments)  
4247.509 Million cell updates/sec

Title: US-09-966-880A-7\_COPY\_80\_676

Perfect score: 597

Sequence: 1 atggacagcctcttgatgaa.....ttcgtactttgggactttga 597

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 353258

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*

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- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	13	2.2	19	4	US-09-018-125-9
C 6	13	2.2	19	4	US-09-495-052-4
7	13	2.2	20	1	US-08-171-718-3
C 8	13	2.2	20	3	US-08-882-501-5
9	13	2.2	20	3	US-08-478-087-3
C 10	13	2.2	20	3	US-09-418-641-46
C 11	13	2.2	20	3	US-09-280-803-41
C 12	13	2.2	20	4	US-09-861-159-78
13	13	2.2	20	4	US-09-679-299A-100
C 14	12	2.0	14	1	US-08-375-116A-122
15	12	2.0	15	1	US-07-962-569A-1
C 16	12	2.0	15	1	US-08-242-664-27
C 17	12	2.0	15	1	US-08-484-138-27
18	12	2.0	15	1	US-08-464-148-10
19	12	2.0	15	1	US-08-385-500-10
20	12	2.0	15	1	US-08-846-784-10
21	12	2.0	15	2	US-08-889-291-35
22	12	2.0	15	3	US-09-098-244-35
23	12	2.0	15	4	US-09-375-314-35
24	12	2.0	15	4	US-09-767-395-35
C 25	12	2.0	15	5	PTUS-955-06379-27
26	12	2.0	16	3	US-08-817-145-8
C 27	12	2.0	16	4	US-09-629-222A-41

28 12 2.0 17 1 US-08-152-313-59 Sequence 59, Appl  
29 12 2.0 17 1 US-08-050-073-138 Sequence 138, App  
30 12 2.0 17 1 US-08-050-073-159 Sequence 159, App  
31 12 2.0 17 1 US-08-579-223-59 Sequence 59, Appl  
32 12 2.0 17 1 US-08-758-306-1283 Sequence 1283, Ap  
33 12 2.0 17 3 US-08-181-664-46 Sequence 46, Appl  
34 12 2.0 17 4 US-09-866-108A-7364 Sequence 7364, Ap  
35 12 2.0 17 4 US-09-866-108A-7365 Sequence 7365, Ap  
36 12 2.0 17 4 US-09-866-108A-7366 Sequence 7366, Ap  
37 12 2.0 17 4 US-09-866-108A-7367 Sequence 7367, Ap  
38 12 2.0 17 4 US-09-866-108A-7368 Sequence 7368, Ap  
39 12 2.0 17 4 US-09-866-108A-7369 Sequence 7369, Ap  
40 12 2.0 17 5 PCT-US94-12947A-59 Sequence 59, Appl  
41 12 2.0 18 1 US-09-178-002-9 Sequence 9, Appl  
42 12 2.0 18 1 US-08-050-073-121 Sequence 121, App  
43 12 2.0 18 1 US-08-050-073-158 Sequence 158, App  
44 12 2.0 18 2 US-09-197-378-17 Sequence 17, Appl  
45 12 2.0 18 2 US-09-205-860-28 Sequence 28, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-422-978-10030/c  
; Sequence 10030, Application US/09422978

; Patent No. 6537751

; GENERAL INFORMATION:

; APPLICANT: Cohen, Daniel

; APPLICANT: Blumenfeld, Marta

; APPLICANT: Chumakov, Ilya

; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

; FILE REFERENCE: GENSET-020CP1

; CURRENT APPLICATION NUMBER: US/09/422,978

; CURRENT FILING DATE: 1999-10-20

; EARLIER APPLICATION NUMBER: US 09/298,850

; EARLIER FILING DATE: 1999-04-21

; EARLIER APPLICATION NUMBER: US 60/109,732

; EARLIER FILING DATE: 1998-11-23

; EARLIER APPLICATION NUMBER: US 60/082,614

; EARLIER FILING DATE: 1998-04-21

; NUMBER OF SEQ ID NOS: 11796

; SEQ ID NO 10030

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: primer\_bind

; LOCATION: 1..20

; OTHER INFORMATION: downstream amplification primer 99-8910 for SEQ 2165, in comple

US-09-422-978-10030

Query Match

Best Local Similarity 2.5%; Score 15; DB 4; Length 20;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 GAGGAGTTCCTTTA 38

Db 15 GAGGAGTTCCTTTA 1

##### RESULT 2

US-08-651-692-1

; Sequence 1, Application US/08651692

; Patent No. 5856099

; GENERAL INFORMATION:

; APPLICANT: Loren Miraglia, Thomas Geiger,

; APPLICANT: Clarence Frank Bennett and Nicholas M. Dean

; TITLE OF INVENTION: Compositions and Methods for

; TITLE OF INVENTION: Modulating Type I Interleukin-1 Receptor Expression

; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Jane Massey Licata



STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/651,692  
FILING DATE: Herewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0144  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-651-692-1

Query Match 2.3%; Score 14; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGCGTCGGCGGCT 386  
DB 7 GGCGTCGGCGGCT 20

RESULT 3  
US-08-651-692-2  
Sequence 2, Application US/08651692  
Patent No. 5856099  
GENERAL INFORMATION:  
APPLICANT: Loren Miraglia, Thomas Geiger,  
APPLICANT: Clarence Frank Bennett and Nicholas M. Dean  
TITLE OF INVENTION: Compositions and Methods for  
Modulating Type I Interleukin-1 Receptor Expression  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 210 Lake Drive East, Suite 201  
CITY: Cherry Hill  
STATE: NJ  
COUNTRY: USA  
ZIP: 08002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/651,692  
FILING DATE: Herewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0144  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 779-2400  
TELEFAX: (609) 779-8488  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
US-08-651-692-2

Query Match 2.3%; Score 14; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGCGTCGGCGGCT 386  
DB 2 GGCGTCGGCGGCT 15

RESULT 4  
US-09-357-072-30/c  
Sequence 30, Application US/09357072  
Patent No. 6015712  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: Brenda F. Baker  
APPLICANT: Hong Zhang  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF PADD EXPRESSION  
FILE REFERENCE: R1S-0027  
CURRENT APPLICATION NUMBER: US/09/357,072  
CURRENT FILING DATE: 1999-07-19  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 30  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-357-072-30

Query Match 2.2%; Score 13; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CTGCACTTTGGTT 142  
DB 14 CTGCACTTTGGTT 2

RESULT 5  
US-09-018-125-9  
Sequence 9, Application US/09018125A  
Patent No. 6468983  
GENERAL INFORMATION:  
APPLICANT: Silverman, Robert H.  
APPLICANT: Kondo, Seiji  
APPLICANT: Cowell, John K.  
APPLICANT: Li, Guiying  
APPLICANT: Torrence, Paul F.  
TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES  
TITLE OF INVENTION: EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES  
FILE REFERENCE: 8656-022  
CURRENT APPLICATION NUMBER: US/09/018,125A  
CURRENT FILING DATE: 1999-02-03  
EARLIER APPLICATION NUMBER: 60/044,507  
FILING DATE: 1997-04-21

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; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-018-125-9

Query Match          2.2%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGGTGCAAT 407
Db 3 CCGGGGTGCAAT 15

RESULT 6
US-09-495-052-4/c
; Sequence 4, Application US/09495052
; Patent No. 6479258
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES
; FILE REFERENCE: DIVER1460-11
; CURRENT APPLICATION NUMBER: US/09/495,052
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide probe
US-09-495-052-4

Query Match          2.2%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GTTCGTCCTCCCA 520
Db 15 GTTCGTCCTCCCA 3

RESULT 7
US-08-171-718-3
; Sequence 3, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gussella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
```

```
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-171-718-3

Query Match          2.2%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ACATCCTTTTCAC 130
Db 8 ACATCCTTTTCAC 20

RESULT 8
US-08-882-501-5/c
; Sequence 5, Application US/08882501
; Patent No. 6054269
; GENERAL INFORMATION:
; APPLICANT: GARNIER, Fabien
; APPLICANT: GERBAUD, Guy
; APPLICANT: GALIMAND, Marc
; APPLICANT: COURVALIN, Patrice
; APPLICANT: DUKTA-MALEN, Sylvie
; APPLICANT: CHARLES, Murielle
; APPLICANT: EVERS, Stefan
; APPLICANT: CASADEWALL, Barbara
; TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR
; TITLE OF INVENTION: DETECTING ENTEROCOCCI AND STREPTOCOCCI BACTERIAL STRAINS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,501  
FILING DATE: 25-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: McDowell, Leslie A.  
REGISTRATION NUMBER: 34,872  
REFERENCE/DOCKET NUMBER: 03495.0155-00000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
US-08-882-501-5

Query Match 2.2%; Score 13; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GCCTCTACTTCTG 347  
Db 15 GCCTCTACTTCTG 3

RESULT 9  
US-08-478-087-3  
Sequence 3, Application US/08478087  
Patent No. 6077685  
GENERAL INFORMATION:  
APPLICANT: Trofater, James A.  
APPLICANT: MacCollin, Mia M.  
APPLICANT: Gusella, James F.  
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,087  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/171,718  
FILING DATE: 22-DEC-1993  
APPLICATION NUMBER: US 08/108,808  
FILING DATE: 19-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/022,034  
FILING DATE: 25-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/026,063  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Anne  
REGISTRATION NUMBER: 36,463

REFERENCE/DOCKET NUMBER: 0609.3850003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-478-087-3

Query Match 2.2%; Score 13; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 ACATCCTTTTTCAC 130  
Db 8 ACATCCTTTTTCAC 20

RESULT 10  
US-09-418-641-46/c  
Sequence 46, Application US/09418641A  
Patent No. 6124133  
GENERAL INFORMATION:  
APPLICANT: Jennifer K. Taylor  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION  
FILE REFERENCE: RTS-0105  
CURRENT APPLICATION NUMBER: US/09/418,641A  
CURRENT FILING DATE: 1999-10-15  
NUMBER OF SEQ ID NOS: 89  
SEQ ID NO 46  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-418-641-46

Query Match 2.2%; Score 13; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GAACCGAGGAAG 30  
Db 13 GAACCGAGGAAG 1

RESULT 11  
US-09-280-805-41/c  
Sequence 41, Application US/09280805  
Patent No. 6184212  
GENERAL INFORMATION:  
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.  
APPLICANT: Graham, Brett P. Monia  
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 271  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: U.S.A.  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PC  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.0  
CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/280,805
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 09/048,810
; APPLICATION NUMBER: March 26, 1998
; FILING DATE: March 26, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Licata, Jane Massey
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-810-1515
; TELEFAX: 609-810-1454
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-09-280-805-41

Query Match 2.2%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GAGCCCGAGGGC 376
DB 19 GAGCCCGAGGGC 7

RESULT 12
US-09-861-159-78/c
; Sequence 78, Application US/09861159
; Patent No. 6485974
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPN2 EXPRESSION
; FILE REFERENCE: RTS-0243
; CURRENT APPLICATION NUMBER: US/09/861,159
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-861-159-78

Query Match 2.2%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 TGACAGTGTCTACA 120
DB 13 TGACAGTGTCTACA 1

RESULT 13
US-09-679-299A-100
; Sequence 100, Application US/09679299A
; Patent No. 6566135
; GENERAL INFORMATION:
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 6 EXPRESSION
; FILE REFERENCE: RTS-0187
; CURRENT APPLICATION NUMBER: US/09/679,299A
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 164

; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-679-299A-100

Query Match 2.2%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 447 TACTTTGTAGAA 459
DB 4 TACTTTGTAGAA 16

RESULT 14
US-08-375-116A-122/c
; Sequence 122, Application US/08375116A
; Patent No. 5631146
; GENERAL INFORMATION:
; APPLICANT: Szoostak, Jack W.
; APPLICANT: Huizenga, David B.
; TITLE OF INVENTION: DNA APTAMERS AND CATALYSTS THAT BIND
; TITLE OF INVENTION: ADENOSINE AND/OR ADENOSINE 5'-PHOSPHATES AND METHODS FOR
; TITLE OF INVENTION: ISOLATION THEREOF
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/375,116A
; APPLICATION NUMBER: US/08/375,116A
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/266001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 9617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-375-116A-122

Query Match 2.0%; Score 12; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTTCTCCGCTA 191
DB 13 CTTCTCCGCTA 2

RESULT 15
US-07-962-569A-1
; Sequence 1, Application US/07962569A
; Patent No. 5391497

GENERAL INFORMATION:  
APPLICANT: MENON, RAVI S.  
APPLICANT: JEFFERS, KATHLEEN F.  
APPLICANT: CHANG, YING-FON  
APPLICANT: HAM, RICHARD G.  
TITLE OF INVENTION: HUMAN K-CASEIN  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FREDERICK W. PEPPER, PH. D.  
STREET: 11545 W. BERNARDO COURT, STE. 302  
CITY: SAN DIEGO  
STATE: CA  
COUNTRY: USA  
ZIP: 92127  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/962,569A  
FILING DATE: 19921013  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PEPPER PH.D., FREDERICK W.  
REGISTRATION NUMBER: 31,286  
REFERENCE/DOCKET NUMBER: 920224.01  
TELEPHONE: (619) 451-1120  
TELEFAX: (619) 451-9628  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..15  
US-07-962-569A-1

Query Match 2.0%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTGCTCTTCTC 186  
Db 13 TTGCTCTTCTC 2

RESULT 17  
US-08-484-138-27/c  
Sequence 27, Application US/08484138  
Patent No. 5652350  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,138  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-977-9550  
TELEFAX: 212-664-0525  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-484-138-27

Query Match 2.0%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:  
APPLICANT: MENON, RAVI S.  
APPLICANT: JEFFERS, KATHLEEN F.  
APPLICANT: CHANG, YING-FON  
APPLICANT: HAM, RICHARD G.  
TITLE OF INVENTION: HUMAN K-CASEIN  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FREDERICK W. PEPPER, PH. D.  
STREET: 11545 W. BERNARDO COURT, STE. 302  
CITY: SAN DIEGO  
STATE: CA  
COUNTRY: USA  
ZIP: 92127  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/962,569A  
FILING DATE: 19921013  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PEPPER PH.D., FREDERICK W.  
REGISTRATION NUMBER: 31,286  
REFERENCE/DOCKET NUMBER: 920224.01  
TELEPHONE: (619) 451-1120  
TELEFAX: (619) 451-9628  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..15  
US-07-962-569A-1

Query Match 2.0%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CTCCTGGAGCC 257  
Db 3 CTCCTGGAGCC 14

RESULT 16  
US-08-242-664-27/c  
Sequence 27, Application US/08242664  
Patent No. 5571937  
GENERAL INFORMATION:  
APPLICANT: Watanabe, Kyoichi A.  
APPLICANT: Ren, Wu-Yun  
APPLICANT: Weil, Roger  
TITLE OF INVENTION: Complementary DNA and Toxins  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:

Query Match 2.0%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCTC 186  
Db 13 TTGCTCTTCTC 2

RESULT 18  
US-08-464-148-10  
; Sequence 10, Application US/08464148  
; Patent No. 5710026  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND  
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,148  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/385,500  
; FILING DATE: 08-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 13952-21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-5043  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (primer)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..15  
; OTHER INFORMATION: /standard\_name="ZC2683"  
US-08-464-148-10

Query Match 2.0%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred.No.1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
Db 3 CTCCTGGAGCCC 14

RESULT 19  
US-08-385-500-10  
; Sequence 10, Application US/08385500  
; Patent No. 5712117  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND  
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/846,784  
; FILING DATE: 30-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/385,500  
; FILING DATE: 08-FEB-1995  
; ATTORNEY/AGENT INFORMATION:

; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/385,500  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 13952-21  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 467-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (primer)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..15  
; OTHER INFORMATION: /standard\_name="ZC2683"  
US-08-385-500-10

Query Match 2.0%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred.No.1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
Db 3 CTCCTGGAGCCC 14

RESULT 20  
US-08-846-784-10  
; Sequence 10, Application US/08846784  
; Patent No. 5747645  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND  
; TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/846,784  
; FILING DATE: 30-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/385,500  
; FILING DATE: 08-FEB-1995  
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (primer)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..15
; OTHER INFORMATION: /standard_name="ZC2683"
;
; US-08-846-784-10
;
; Query Match 2.0%; Score 12; DB 1; Length 15;
; Best Local Similarity 100.0%; Pred. No. 1.2e+04;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 246 CTCCTGGAGCCC 257
; Db 3 CTCCTGGAGCCC 14
;
; RESULT 21
; US-08-889-291-35
; Sequence 35, Application US/08889291
; Patent No. 594519
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; APPLICANT: Derbyshire, Elaine J
; APPLICANT: McCafferty, John G
; APPLICANT: Vaughan, Tristan J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,291
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/GB97/01835
; FILING DATE: 08-JUL-1997
; APPLICATION NUMBER: GB 9614292.2
; FILING DATE: 08-JUL-1996
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; APPLICATION NUMBER: GB 9712818.5
; FILING DATE: 18-JUN-1997
; APPLICATION NUMBER: GB 9712818.5
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/34063
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-098-244-35
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-889-291-35
;
; Query Match 2.0%; Score 12; DB 2; Length 15;
; Best Local Similarity 100.0%; Pred. No. 1.2e+04;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 246 CTCCTGGAGCCC 257
; Db 3 CTCCTGGAGCCC 14
;
; RESULT 22
; US-09-098-244-35
; Sequence 35, Application US/09098244
; Patent No. 6180336
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane K
; APPLICANT: Derbyshire, Elaine J
; APPLICANT: McCafferty, John G
; APPLICANT: Vaughan, Tristan J
; APPLICANT: Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,244
; FILING DATE: 17-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/889,291
; FILING DATE: 08-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01835
; FILING DATE: 08-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9614292.2
; FILING DATE: 08-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9624880.2
; FILING DATE: 29-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9712818.5
; FILING DATE: 18-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/34800
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-098-244-35
;
; Query Match 2.0%; Score 12; DB 3; Length 15;
; Best Local Similarity 100.0%; Pred. No. 1.2e+04;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
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Db 3 CTCCTGGAGCCC 14

RESULT 23

US-09-375-314-35  
; Sequence 35, Application US/09375314  
; Patent No. 6342588  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, Jane K  
; APPLICANT: Derbyshire, Elaine J  
; APPLICANT: McCafferty, John G  
; APPLICANT: Vaughan, Tristan J  
; APPLICANT: Johnson, Kevin S  
; TITLE OF INVENTION: Labelling and selection of molecules  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/375,314  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/889,291  
; FILING DATE: 08-JUL-1997  
; APPLICATION NUMBER: PCT/GB97/01835  
; FILING DATE: 08-JUL-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9614292.2  
; FILING DATE: 08-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9624880.2  
; FILING DATE: 29-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9712818.5  
; FILING DATE: 18-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/34063  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-09-375-314-35

Query Match 2.0%; Score 12; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
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Db 3 CTCCTGGAGCCC 14

RESULT 24

US-09-767-395-35  
; Sequence 35, Application US/09767395

; Patent No. 6489123

; GENERAL INFORMATION:  
; APPLICANT: Osbourn, Jane K  
; APPLICANT: Derbyshire, Elaine J  
; APPLICANT: McCafferty, John G  
; APPLICANT: Vaughan, Tristan J  
; APPLICANT: Johnson, Kevin S  
; TITLE OF INVENTION: Labelling and selection of molecules  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/767,395  
; FILING DATE: 23-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/098,244  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: PCT/GB97/01835  
; FILING DATE: 08-JUL-1997  
; APPLICATION NUMBER: GB 9614292.2  
; FILING DATE: 08-JUL-1996  
; APPLICATION NUMBER: GB 9624880.2  
; FILING DATE: 29-NOV-1996  
; APPLICATION NUMBER: GB 9712818.5  
; FILING DATE: 18-JUN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David W. Clough  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/34800  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-09-767-395-35

Query Match 2.0%; Score 12; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
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Db 3 CTCCTGGAGCCC 14

RESULT 25

PCT-US95-06379-27/c  
; Sequence 27, Application PCT/TUS9506379  
; GENERAL INFORMATION:  
; APPLICANT: Watanabe, Kyoichi A.  
; APPLICANT: Ren, Wu-Yun  
; APPLICANT: Wei, Roger  
; TITLE OF INVENTION: Complementary DNA and Toxins  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.



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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06379
; FILING DATE: May 13, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44683-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-27

Query Match          2.0%; Score 12; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      175 TTGCTCTCTCTC 186
Db      13 TTGCTCTCTCTC 2

RESULT 26
US-08-817-145-8
; Sequence 8, Application US/08817145
; Patent No. 6025329
; GENERAL INFORMATION:
; APPLICANT: UTSUMI, Jun
; APPLICANT: SUDO, Tetsuo
; APPLICANT: TANAKA, Yasuhiko
; APPLICANT: MATSUI, Mizuo
; TITLE OF INVENTION: THERAPEUTIC AGENT FOR OPHTHALMIC
; TITLE OF INVENTION: DISEASES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP.
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,145
; FILING DATE: 02-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 760-230P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic Primer"
US-08-817-145-8

Query Match          2.0%; Score 12; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      246 CTCCTGGAGGCC 257
Db      2 CTCCTGGAGGCC 13

RESULT 27
US-09-629-222A-41/c
; Sequence 41, Application US/09629222A
; Patent No. 6599700
; GENERAL INFORMATION:
; APPLICANT: Bellacosa, Alfonso
; TITLE OF INVENTION: Methods for Detection of Transition
; TITLE OF INVENTION: Single-Nucleotide Polymorphisms
; FILE REFERENCE: FCCC 96-21
; CURRENT APPLICATION NUMBER: US/09/629,222A
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/463,891
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: PCT/US98/15828
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/053,936
; PRIOR FILING DATE: 1997-07-28
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-629-222A-41

Query Match          2.0%; Score 12; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      116 CTACATCTCTTT 127
Db      15 CTACATCTCTTT 4

RESULT 28
US-08-152-313-59
; Sequence 59, Application US/08152313
; Patent No. 5561041
; GENERAL INFORMATION:
; APPLICANT: Sidransky, David
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY
; TITLE OF INVENTION: ANALYSIS OF SPUTUM
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,313
```

```

; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
; US-08-152-313-59

Query Match 2.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No.1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCATGAA 501
Db 5 GGGCTGCATGAA 16
|||||
|||||

RESULT 29
US-08-050-073-138
; Sequence 138, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

```

/ MOLECULE TYPE: genomic DNA
US-08-050-073-138

Query Match      2.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      244 ACCTCTGGAGC 255
      |||||
Db      1 ACCTCTGGAGC 12

RESULT 30
US-08-050-073-159
/ Sequence 159, Application US/08050073
/ Patent No. 5567809
/ GENERAL INFORMATION:
/ APPLICANT: Apple, Raymond J.
/ APPLICANT: Begovich, Ann B.
/ APPLICANT: Bugawan, Teodorica L.
/ APPLICANT: Erlich, Henry A.
/ APPLICANT: Griffith, Robert L.
/ APPLICANT: Scharf, Stephen J.
/ TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
/ TITLE OF INVENTION: Typing
/ NUMBER OF SEQUENCES: 315
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hoffmann-La Roche Inc.
/ STREET: 340 Kingsland Street
/ CITY: Nutley
/ STATE: New Jersey
/ COUNTRY: U.S.A.
/ ZIP: 07110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/050,073
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Petty, Douglas A.
/ REGISTRATION NUMBER: 35,321
/ REFERENCE/DOCKET NUMBER: 8769
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (510) 814-2974
/ TELEFAX: (510) 814-2977
/ INFORMATION FOR SEQ ID NO: 159:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
US-08-050-073-159

Query Match      2.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      244 ACCTCTGGAGC 255
      |||||
Db      1 ACCTCTGGAGC 12

RESULT 31
US-08-579-223-59
/ Sequence 59, Application US/08579223
/ Patent No. 5726019
/ GENERAL INFORMATION:
/ APPLICANT: Sidransky, David

```

;; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION BY  
;; TITLE OF INVENTION: ANALYSIS OF SPUTUM  
;; NUMBER OF SEQUENCES: 128  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Spensley Horn Jubas & Lubitz  
;; STREET: 1880 Century Park East, Suite 500  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 90067

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/579,223  
;; FILING DATE: 28-DEC-1995  
;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/152,313  
;; FILING DATE: 12-NOV-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Wetherell, Jr., Ph.D., John R.,  
;; REGISTRATION NUMBER: 31,678  
;; REFERENCE/DOCKET NUMBER: PD-2912  
;; TELEPHONE: (619) 455-5100  
;; TELEFAX: (619) 455-5110  
;; INFORMATION FOR SEQ ID NO: 59:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..17

US-08-579-223-59  
Query Match 2.0%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 490 GGGCTGCATGAA 501  
Db 5 GGGCTGCATGAA 16  
|||||

RESULT 32  
US-08-758-306-1283/c  
; Sequence 1283, Application US/08758306  
; Patent No. 5807743  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Dan T.  
; ADDRESSEE: McSwiggen, James A.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TREATMENT OF DISEASES  
; TITLE OF INVENTION: ASSOCIATED WITH  
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
; NUMBER OF SEQUENCES: 1379  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

;; MEDIUM TYPE: storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: FastSeq Version 1.5  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/758,306  
;; FILING DATE: December 3, 1996  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 212/132  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 1283:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-758-306-1283

Query Match 2.0%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

Qy 248 CCTGGAGCCCT 259  
Db 13 CCTGGAGCCCT 2  
|||||

RESULT 33  
US-08-181-664-46  
; Sequence 46, Application US/08181664  
; Patent No. 6025127  
; GENERAL INFORMATION:  
; APPLICANT: Sidransky, David  
; TITLE OF INVENTION: NUCLEIC ACID MUTATION DETECTION IN  
; HISTOLOGIC TISSUE  
; NUMBER OF SEQUENCES: 82  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jubas & Lubitz  
; STREET: 1880 Century Park East, Suite 500  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90067

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/181,664  
;; FILING DATE: JANUARY 14, 1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Wetherell, Jr., Ph.D., John R.  
;; REGISTRATION NUMBER: 31,678  
;; REFERENCE/DOCKET NUMBER: PD-3055  
;; TELEPHONE: (619) 455-5100  
;; TELEFAX: (619) 455-5110  
;; INFORMATION FOR SEQ ID NO: 46:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 17 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single

```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
US-08-181-664-46

Query Match          2.0%; Score 12; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 GGCGTCGATGAA 501
Db 5 GGCGTCGATGAA 16

RESULT 34
US-09-866-108A-7364
; Sequence 7364, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7365
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7365

Query Match          2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGTT 510
Db 5 GAAATTCAGTT 16

RESULT 36
US-09-866-108A-7366
; Sequence 7366, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
```

```
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7366
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7366

Query Match      2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
Db 4 GAAATTCAGTT 15

RESULT 37
US-09-866-108A-7367, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7366
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7366

Query Match      2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
Db 4 GAAATTCAGTT 15

RESULT 37
US-09-866-108A-7367, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
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; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7367
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7367

Query Match      2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
Db 3 GAAATTCAGTT 14

RESULT 38
US-09-866-108A-7368, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7368
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-7368

Query Match      2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
Db 2 GAAATTCAGTT 13

RESULT 39
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```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12947A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD-2912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..17
; PCT-US94-12947A-59

Query Match 2.0%; Score 12; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCATGAA 501
|||
Db 5 GGGCTGCATGAA 16

RESULT 41
US-09-178-002-9
; Sequence 9, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide sense primer
US-09-178-002-9

Query Match 2.0%; Score 12; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 GTAGTGAAGAGG 105
|||||
Db 6 GTAGTGAAGAGG 17

RESULT 42
US-08-050-073-121
; Sequence 121, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.

```

APPLICANT: Scharf, Stephen J.  
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA  
NUMBER OF SEQUENCES: 315  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,073  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 8769  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
US-08-050-073-121  
Query Match 2.0%; Score 12; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 244 ACCTCCTGGAGC 255  
Db 2 ACCTCCTGGAGC 13  
RESULT 43  
US-08-050-073-158/c  
Sequence 158, Application US/08050073  
Patent No. 5567809  
GENERAL INFORMATION:  
APPLICANT: Apple, Raymond J.  
APPLICANT: Begovich, Ann B.  
APPLICANT: Bugawan, Teodorica L.  
APPLICANT: Erlich, Henry A.  
APPLICANT: Griffith, Robert L.  
APPLICANT: Scharf, Stephen J.  
TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA  
NUMBER OF SEQUENCES: 315  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,073

FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A.  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 8769  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 814-2974  
TELEFAX: (510) 814-2977  
INFORMATION FOR SEQ ID NO: 158:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
US-08-050-073-158  
Query Match 2.0%; Score 12; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 244 ACCTCCTGGAGC 255  
Db 17 ACCTCCTGGAGC 6  
RESULT 44  
US-09-197-378-17  
Sequence 17, Application US/09197378  
Patent No. 5959097  
GENERAL INFORMATION:  
APPLICANT: Brett P. Monia  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF MEK2 EXPRESSION  
FILE REFERENCE: RTS-0017  
CURRENT APPLICATION NUMBER: US/09/197,378  
CURRENT FILING DATE: 1998-11-20  
NUMBER OF SEQ ID NOS: 47  
SEQ ID NO 17  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-197-378-17  
Query Match 2.0%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 130 CTGGACTTTGGT 141  
Db 6 CTGGACTTTGGT 17  
RESULT 45  
US-09-205-860-28  
Sequence 28, Application US/09205860  
Patent No. 5981732  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION  
FILE REFERENCE: RTS-0031  
CURRENT APPLICATION NUMBER: US/09/205,860  
CURRENT FILING DATE: 1998-12-04  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 28  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide

US-09-205-860-28

Query Match 2.0%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330  
|||||  
Db 7 AGGATCTTCACC 18

RESULT 46

US-09-256-496-13

Sequence 13, Application US/09256496  
Patent No. 5998206  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION  
FILE REFERENCE: RTS-0056  
CURRENT APPLICATION NUMBER: US/09/256,496  
CURRENT FILING DATE: 1999-02-23  
NUMBER OF SEQ ID NOS: 86  
SEQ ID NO 13  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide

US-09-256-496-13

Query Match 2.0%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330  
|||||  
Db 3 AGGATCTTCACC 14

RESULT 47

US-08-696-497B-15

Sequence 15, Application US/08696497B  
Patent No. 6007231  
GENERAL INFORMATION:  
APPLICANT: Viig, Jan and Bishop, Robert  
TITLE OF INVENTION: Method of Computer Aided  
TITLE OF INVENTION: Diagnostic DNA Test Design, and Apparatus Therefor  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Rines & Rines  
STREET: 81 No. 6007231th State Street  
CITY: Concord  
STATE: NH  
COUNTRY: USA  
ZIP: 03301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft No. 6007231lepad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/696,497B  
FILING DATE: 14-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 6007231e  
ATTORNEY/AGENT INFORMATION:  
NAME: Rines, Robert H.  
REGISTRATION NUMBER: 15,932  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (603) 228-0121  
TELEFAX: (603) 228-0210  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:

US-09-205-860-28

LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: human  
IMMEDIATE SOURCE:  
LIBRARY: genomic  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17/p

US-08-696-497B-15

Query Match 2.0%; Score 12; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
|||||  
Db 3 TCGTCTCTCCAG 14

RESULT 48

US-08-180-470-45

Sequence 45, Application US/08180470  
Patent No. 6045394  
GENERAL INFORMATION:  
APPLICANT: ZABEAU, Marc  
APPLICANT: VOS, Pieter  
TITLE OF INVENTION: SELECTIVE RESTRICTION FRAGMENT  
TITLE OF INVENTION: AMPLIFICATION: A GENERAL METHOD FOR DNA  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: The George Mason Bldg., Washington & Prince  
STREET: Sts.  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/180,470  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/950,011  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Crane-Feuty, Sharon E  
REGISTRATION NUMBER: 36,113  
REFERENCE/DOCKET NUMBER: 010830-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-180-470-45

Query Match 2.0%; Score 12; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-205-860-28

Query Match 2.0%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330  
|||||  
Db 7 AGGATCTTCACC 18

RESULT 46

US-09-256-496-13

Sequence 13, Application US/09256496  
Patent No. 5998206  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION  
FILE REFERENCE: RTS-0056  
CURRENT APPLICATION NUMBER: US/09/256,496  
CURRENT FILING DATE: 1999-02-23  
NUMBER OF SEQ ID NOS: 86  
SEQ ID NO 13  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide

US-09-256-496-13

Query Match 2.0%; Score 12; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330  
|||||  
Db 3 AGGATCTTCACC 14

RESULT 47

US-08-696-497B-15

Sequence 15, Application US/08696497B  
Patent No. 6007231  
GENERAL INFORMATION:  
APPLICANT: Viig, Jan and Bishop, Robert  
TITLE OF INVENTION: Method of Computer Aided  
TITLE OF INVENTION: Diagnostic DNA Test Design, and Apparatus Therefor  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Rines & Rines  
STREET: 81 No. 6007231th State Street  
CITY: Concord  
STATE: NH  
COUNTRY: USA  
ZIP: 03301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft No. 6007231lepad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/696,497B  
FILING DATE: 14-AUG-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: No. 6007231e  
ATTORNEY/AGENT INFORMATION:  
NAME: Rines, Robert H.  
REGISTRATION NUMBER: 15,932  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (603) 228-0121  
TELEFAX: (603) 228-0210  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:

US-09-205-860-28

LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: human  
IMMEDIATE SOURCE:  
LIBRARY: genomic  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17/p

US-08-696-497B-15

Query Match 2.0%; Score 12; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
|||||  
Db 3 TCGTCTCTCCAG 14

RESULT 48

US-08-180-470-45

Sequence 45, Application US/08180470  
Patent No. 6045394  
GENERAL INFORMATION:  
APPLICANT: ZABEAU, Marc  
APPLICANT: VOS, Pieter  
TITLE OF INVENTION: SELECTIVE RESTRICTION FRAGMENT  
TITLE OF INVENTION: AMPLIFICATION: A GENERAL METHOD FOR DNA  
NUMBER OF SEQUENCES: 90  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: The George Mason Bldg., Washington & Prince  
STREET: Sts.  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/180,470  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/950,011  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Crane-Feuty, Sharon E  
REGISTRATION NUMBER: 36,113  
REFERENCE/DOCKET NUMBER: 010830-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

US-08-180-470-45

Query Match 2.0%; Score 12; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: ORES-5003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "probe"  
US-08-649-991-33

Query Match 2.0%; Score 12; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCCTC 186  
DB 4 TTGCTCTTCCTC 15

RESULT 51  
US-08-649-991-34  
Sequence 34, Application US/08649991  
Patent No. 5919462  
GENERAL INFORMATION:  
APPLICANT: Narwa, Remy  
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE  
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR  
TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF  
TITLE OF INVENTION: MATERNOFETAL TRANSMISSION OF HIV-1  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,991  
FILING DATE: 17-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9505914  
FILING DATE: 18-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: ORES-5003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "probe"  
US-08-649-991-34

QY 36 TTACCAATTCAA 47  
DB 6 TTACCAATTCAA 17

RESULT 49  
US-09-972-115A-17  
Sequence 17, Application US/09972115A  
Patent No. 6599728  
GENERAL INFORMATION:  
APPLICANT: Geron Corporation  
APPLICANT: Gregg, Morin B.  
APPLICANT: Mieczyslaw, Piatyszek A.  
TITLE OF INVENTION: A Second Mammalian Telomerase  
FILE REFERENCE: 080/003C  
CURRENT APPLICATION NUMBER: US/09/972,115A  
CURRENT FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: US 60/128,577  
PRIOR FILING DATE: 2000-04-10  
PRIOR APPLICATION NUMBER: US 60/129,123  
PRIOR FILING DATE: 1999-04-13  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: Patent In version 3.1  
SEQ ID NO 17  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-972-115A-17

Query Match 2.0%; Score 12; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
DB 3 CTCCTGGAGCCC 14

RESULT 50  
US-08-649-991-33  
Sequence 33, Application US/08649991  
Patent No. 5919462  
GENERAL INFORMATION:  
APPLICANT: Narwa, Remy  
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE  
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR  
TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF  
TITLE OF INVENTION: MATERNOFETAL TRANSMISSION OF HIV-1  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,991  
FILING DATE: 17-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9505914  
FILING DATE: 18-MAY-1995

Query Match 2.0%; Score 12; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 175 TTGCTCTTCCTC 186  
Db 4 TTGCTCTTCCTC 15  
RESULT 52  
US-08-649-991-35  
Sequence 35 Application US/08649991  
Patent No. 5919462  
GENERAL INFORMATION:  
APPLICANT: Narwa, Remy  
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS DERIVED FROM THE  
TITLE OF INVENTION: HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR  
TITLE OF INVENTION: APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF  
TITLE OF INVENTION: MATERNOFETAL TRANSMISSION OF HIV-1  
NUMBER OF SEQUENCES: 130  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP  
STREET: 1800 M Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20036-5869  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/649,991  
APPLICATION NUMBER: US/08/649,991  
FILING DATE: 17-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9505914  
FILING DATE: 18-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Adler, Reid G.  
REGISTRATION NUMBER: 30,988  
REFERENCE/DOCKET NUMBER: ORES-5003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-467-7000  
TELEFAX: 202-467-7176  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "probe"  
US-08-649-991-35  
Query Match 2.0%; Score 12; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 175 TTGCTCTTCCTC 186  
Db 3 TTGCTCTTCCTC 14  
RESULT 53  
US-09-422-978-11302/c  
Sequence 11302 Application US/09422978  
Patent No. 6537751  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta  
APPLICANT: Chumakov, Ilya  
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
FILE REFERENCE: GENSET 020CPI  
CURRENT APPLICATION NUMBER: US/09/422,978  
CURRENT FILING DATE: 1993-10-20  
EARLIER APPLICATION NUMBER: US 09/298,850  
EARLIER FILING DATE: 1999-04-21  
EARLIER APPLICATION NUMBER: US 60/109,732  
EARLIER FILING DATE: 1998-11-23  
EARLIER APPLICATION NUMBER: US 60/082,614  
EARLIER FILING DATE: 1998-04-21  
NUMBER OF SEQ ID NOS: 11796  
SEQ ID NO 11302  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..19  
OTHER INFORMATION: downstream amplification primer 99-4077 for SEQ 3437, in comple  
US-09-422-978-11302  
Query Match 2.0%; Score 12; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 TGCTCTTCCTCC 187  
Db 15 TGCTCTTCCTCC 4  
RESULT 54  
US-08-388-381-8  
Sequence 8, Application US/08388381  
Patent No. 5552283  
GENERAL INFORMATION:  
APPLICANT: Diamandis, Eleftherios  
APPLICANT: Dunn, James M.  
APPLICANT: Stevens, John K.  
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis  
TITLE OF INVENTION: and targeted Screening for p53 Mutations  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oppedahl & Larson  
STREET: 1992 Commerce Street, Suite 309  
CITY: Yorktown Heights  
STATE: NY  
COUNTRY: USA  
ZIP: 10598-4412  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,381  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/271,946  
FILING DATE: 08-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Marina T. Larson  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN.P-003-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 245-3252  
TELEFAX: (914) 962-4330  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20

NAME/KEY: primer for exon 5 of human p53 gene  
US-08-388-381-9  
Query Match 2.0%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 510 TCGTCTCTCCAG 521  
Db 9 TCGTCTCTCCAG 20  
RESULT 55  
US-08-388-381-9/c  
Sequence 9, Application US/08388381  
Patent No. 5552283  
GENERAL INFORMATION:  
APPLICANT: Diamandis, Eleftherios  
APPLICANT: Dunn, James M.  
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis  
TITLE OF INVENTION: and Targeted Screening for p53 Mutations  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oppedahl & Larson  
STREET: 1992 Commerce Street, Suite 309  
CITY: Yorktown Heights  
STATE: NY  
COUNTRY: USA  
ZIP: 10598-4412  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,381  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/271,946  
FILING DATE: 08-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Marina T. Larson  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN.P-003-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 245-3252  
TELEFAX: (914) 962-4330  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: no  
ANTI-SENSE: yes  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE: human  
FEATURE:

NAME/KEY: primer for exon 6 of human p53 gene  
US-08-388-381-9  
Query Match 2.0%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 510 TCGTCTCTCCAG 521  
Db 18 TCGTCTCTCCAG 7  
RESULT 56  
US-08-375-116A-123/c  
Sequence 123, Application US/08375116A  
Patent No. 5631146  
GENERAL INFORMATION:  
APPLICANT: Szostak, Jack W.  
APPLICANT: Huizenga, David E.  
TITLE OF INVENTION: DNA AP-TAMERS AND CATALYSTS THAT BIND  
TITLE OF INVENTION: ADENOSINE AND/OR ADENOSINE-5'-PHOSPHATES AND METHODS FOR  
TITLE OF INVENTION: ISOLATION THEREOF  
NUMBER OF SEQUENCES: 136  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/375,116A  
FILING DATE: 19-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/266001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-375-116A-123  
Query Match 2.0%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 180 CTTCTCTCCGCTA 191  
Db 16 CTTCTCTCCGCTA 5  
RESULT 57  
US-09-205-860-3  
Sequence 3, Application US/09205860  
Patent No. 5981732  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowart  
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION  
FILE REFERENCE: RTS-0031  
CURRENT APPLICATION NUMBER: US/09/205,860

```

; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-09-205-860-3

Query Match          2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 9 AGGATCTTCACC 20

RESULT 58
US-08-630-019A-37
; Sequence 37, Application US/08630019A
; Patent No. 6015710
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David
; APPLICANT: No. 6015710ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,019A
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,019A
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "peptide nucleic acid (PNA),
; DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by
; DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
; DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
US-08-630-019A-37

Query Match          2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

RESULT 60
US-08-838-545-42
; Sequence 42, Application US/08838545
; Patent No. 6046307
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6046307ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,019A
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "phosphorothioate (PS) nucleic acid"
US-08-630-019A-42

Query Match          2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

RESULT 59
US-08-630-019A-42
; Sequence 42, Application US/08630019A
; Patent No. 6015710
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David
; APPLICANT: No. 6015710ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,019A
; FILING DATE: 09-JUN-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "phosphorothioate (PS) nucleic acid"
US-08-630-019A-42

Query Match          2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12
```

ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,545  
FILING DATE: 09-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,019  
FILING DATE: 09-APR-1996  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "peptide nucleic acid (PNA),  
DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by  
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via  
DESCRIPTION: glycine amino N through a methylenecarbonyl linker"  
US-08-838-545-42

Query Match 2.0%; Score 12; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330  
|||||  
DB 1 AGGATCTTCACC 12

RESULT 61  
US-08-838-545-47  
Sequence 47, Application US/08838545  
Patent No. 6046307  
GENERAL INFORMATION:  
APPLICANT: Shay, Jerry W.  
APPLICANT: Wright, Woodring E.  
APPLICANT: Piatyszek, Mieczyslaw A.  
APPLICANT: Corey, David R.  
APPLICANT: No. 6046307ton, James C.  
TITLE OF INVENTION: Modulation of Mammalian Telomerase by  
TITLE OF INVENTION: Peptide Nucleic Acids  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,545  
FILING DATE: 09-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/630,019  
FILING DATE: 09-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-001610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "phosphorothioate (PS)  
DESCRIPTION: nucleic acid"  
US-08-838-545-47

Query Match 2.0%; Score 12; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330  
|||||  
DB 1 AGGATCTTCACC 12

RESULT 62  
US-08-765-626-8  
Sequence 8, Application US/08765626  
Patent No. 6071726  
GENERAL INFORMATION:  
APPLICANT: Visible Genetics Inc.  
APPLICANT: Diamandis, Eleftherios  
APPLICANT: Dunn, James M.  
APPLICANT: Stevens, John K.  
TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis  
TITLE OF INVENTION: and Targeted Screening for p53 Mutations  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oppedahl & Larson  
STREET: 1992 Commerce Street, Suite 309  
CITY: Yorktown Heights  
STATE: NY  
COUNTRY: USA  
ZIP: 10598-4412  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,626  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08605  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/388,381  
FILING DATE: 14-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Marina T. Larson  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN.P-003-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 245-3252

```
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORGANISM: human
; NAME/KEY: primer for exon 5 of human p53 gene
US-08-765-626-8

Query Match      2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      510 TCGTCTCTCCAG 521
Db       9 TCGTCTCTCCAG 20

RESULT 63
US-08-765-626-9/c
; Sequence 9, Application US/08765626
; Patent No. 6071726
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Diamandis, Eleftherios
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,626
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08605
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 20
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 6 of human p53 gene
US-08-765-626-9

Query Match      2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      510 TCGTCTCTCCAG 521
Db       18 TCGTCTCTCCAG 7

RESULT 64
US-08-777-266A-14
; Sequence 14, Application US/08777266A
; Patent No. 6077833
; GENERAL INFORMATION:
; APPLICANT: Clarence Frank Bennett
; APPLICANT: Timothy A. Vickers
; TITLE OF INVENTION: Oligonucleotide Compositions and
; TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 Proteins
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/777,266A
; FILING DATE: December 31, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
US-08-777-266A-14

Query Match      2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      247 TCCTGGAGCCCC 258
Db       6 TCCTGGAGCCCC 17
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## RESULT 65

US-09-101-886B-15  
; Sequence 15, Application US/09101886B  
; Patent No. 6197507  
; GENERAL INFORMATION:  
; APPLICANT: BERG, THOMAS  
; APPLICANT: TOLLERSUD, OLE K  
; APPLICANT: NILSEN, OIVIND  
; TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BARBARA G. ERNST  
; STREET: 555 13TH STREET, NW SUITE 701E  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/101.886B  
; FILING DATE: 29-JANUARY-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB97/00109  
; FILING DATE: 12-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1181-240  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "oligonucleotide"  
; HYPOTHETICAL: NO  
; ANTI-SENSE: YES

US-09-101-886B-15  
Query Match 2.0%; Score 12; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

378 GCGGCGGCTGCA 389  
|||||  
Db 7 GCGGCGGCTGCA 18

## RESULT 66

US-09-290-640-21/c  
; Sequence 21, Application US/09290640  
; Patent No. 6204055  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcuson, Eric G.  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-0351  
; CURRENT APPLICATION NUMBER: US/09/290,640  
; CURRENT FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-290-640-21  
Query Match 2.0%; Score 12; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 171 GGAATGCTCTT 182  
|||||  
Db 20 GGAATGCTCTT 9  
RESULT 67  
US-08-943-731-546  
; Sequence 546, Application US/08943731  
; Patent No. 6265157  
; GENERAL INFORMATION:  
; APPLICANT: PROCKOP, DARWIN J.  
; APPLICANT: SPOTILA, LORETTA D.  
; APPLICANT: DELTAS, CONSTANTINOS D.  
; APPLICANT: SEREDA, LARISA  
; APPLICANT: LARSON, ANDREA W.  
; APPLICANT: PACK, MICHAEL  
; APPLICANT: COLIGE, ALAIN  
; APPLICANT: EARLY, JAMES  
; APPLICANT: KORKKO, JARMO  
; APPLICANT: ALA-KOKKO, LEENA, et al.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING  
; TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES  
; NUMBER OF SEQUENCES: 666  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.  
; STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND  
; STREET: FLR  
; CITY: PHILADELPHIA  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103-7086  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,731  
; FILING DATE: 03-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,322  
; FILING DATE: 14-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/803,628  
; FILING DATE: 03-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOYLE LEARY Ph.D., KATHRYN  
; REGISTRATION NUMBER: 36,317  
; REFERENCE/DOCKET NUMBER: 9598-27  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-965-1284  
; TELEFAX: 215-567-2991  
; TELEX: 831-494  
; INFORMATION FOR SEQ ID NO: 546:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-943-731-546

```
Query Match      2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 201 CTGGGACCTAGA 212
Db 3 CTGGGACCTAGA 14

RESULT 68
US-09-349-532-42
; Sequence 42, Application US/09349532
; Patent No. 6294650
; GENERAL INFORMATION:
; APPLICANT: Shay, Jerry W.
; APPLICANT: Wright, Woodring E.
; APPLICANT: Piatyszek, Mieczyslaw A.
; APPLICANT: Corey, David R.
; APPLICANT: No. 6294650ton, James C.
; TITLE OF INVENTION: Modulation of Mammalian Telomerase by
; TITLE OF INVENTION: Peptide Nucleic Acids
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/349,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,545
; FILING DATE: 09-APR-1997
; APPLICATION NUMBER: US 08/630,019
; FILING DATE: 09-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "peptide nucleic acid (PNA)",
; DESCRIPTION: where (deoxy(ribose-phosphate linkages are replaced by
; DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
; DESCRIPTION: glycine amino N through a methylenecarbonyl linker"
; US-09-349-532-42

Query Match      2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
Db 1 AGGATCTTCACC 12

RESULT 70
US-09-326-186B-14
; Sequence 14, Application US/09326186B
; Patent No. 6319906
; GENERAL INFORMATION:
; APPLICANT: Bennett, Clarence Frank
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the
; TITLE OF INVENTION: Modulation of the Expression of B7 Protein
; FILE REFERENCE: ISPH-0376
; CURRENT APPLICATION NUMBER: US/09/326,186B
; CURRENT FILING DATE: 1999-06-04
```



; PRIOR APPLICATION NUMBER: 08/777,266  
; PRIOR FILING DATE: 1996-12-31  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-326-186B-14

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258  
|||  
DB 6 TCCTGGAGCCCC 17

RESULT 71  
US-09-326-186B-198  
; Sequence 198, Application US/09326186B  
; Patent No. 6319906  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, Clarence Frank  
; APPLICANT: Vickers, Timothy A.  
; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the  
; FILE REFERENCE: ISPH-0376  
; CURRENT APPLICATION NUMBER: US/09/326,186B  
; CURRENT FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: 08/777,266  
; PRIOR FILING DATE: 1996-12-31  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 198  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-326-186B-198

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258  
|||  
DB 5 TCCTGGAGCCCC 16

RESULT 72  
US-09-662-235-1  
; Sequence 1, Application US/09662235  
; Patent No. 6372436  
; GENERAL INFORMATION:  
; APPLICANT: Pouzyrev, Anatoli Timofeyevich  
; APPLICANT: Riddle, Donald Lee  
; TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF CDNA LIBRARIES ENRICHED IN CLONES  
; FILE REFERENCE: 2733/61965  
; CURRENT APPLICATION NUMBER: US/09/662,235  
; CURRENT FILING DATE: 2000-09-14  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Sequence

; OTHER INFORMATION: Oligonucleotide Primer  
US-09-662-235-1

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
|||  
DB 1 CTCCTGGAGCCC 12

RESULT 73  
US-09-659-845A-172  
; Sequence 172, Application US/09659845A  
; Patent No. 6492170  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION  
; FILE REFERENCE: RTS-0183  
; CURRENT APPLICATION NUMBER: US/09/659,845A  
; CURRENT FILING DATE: 2001-07-23  
; NUMBER OF SEQ ID NOS: 174  
; SEQ ID NO 172  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-659-845A-172

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCGGAGGAGCTT 32  
|||  
DB 5 CCGGAGGAGCTT 16

RESULT 74  
US-09-622-277-6  
; Sequence 6, Application US/09622277  
; Patent No. 6521407  
; GENERAL INFORMATION:  
; APPLICANT: Warenlius, Hilmar Meek  
; APPLICANT: Seabra, Laurence Anthony  
; TITLE OF INVENTION: METHODS FOR DETERMINING CHEMOSENSITIVITY OF CANCER CELLS BASED  
; FILE REFERENCE: 1417-188  
; CURRENT APPLICATION NUMBER: US/09/622,277  
; CURRENT FILING DATE: 2000-10-25  
; PRIOR APPLICATION NUMBER: PCT/GB99/00500  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: GB 9903035.5  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: GB 9814545.1  
; PRIOR FILING DATE: 1998-07-03  
; PRIOR APPLICATION NUMBER: GB 9812151.0  
; PRIOR FILING DATE: 1998-06-05  
; PRIOR APPLICATION NUMBER: GB 9803447.3  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: GB 9803446.5  
; PRIOR FILING DATE: 1998-02-18  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR and DNA sequencing primer for exon 5 antisense

US-09-622-277-6

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
|||||  
DB 9 TCGTCTCTCCAG 20

RESULT 75

US-09-422-978-11732/c  
; Sequence 11732, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/09/422,978  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 11732  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..20  
; OTHER INFORMATION: downstream amplification primer 99-4029 for SEQ 3867, in compleme  
US-09-422-978-11732

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 CGTCTCTCCAGA 522  
|||||  
DB 14 CGTCTCTCCAGA 3

RESULT 76

US-09-198-452A-1338  
; Sequence 1338, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Grifais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 1338  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-1338

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 CTGAGGATCTTC 327

Db

|||||  
9 CTGAGGATCTTC 20

RESULT 77

US-09-601-144-14  
; Sequence 14, Application US/09601144  
; Patent No. 6566514  
; GENERAL INFORMATION:  
; APPLICANT: Wright, Jim A.  
; APPLICANT: Young, Aiping H.  
; APPLICANT: Lee, Yoon S.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDOXIN  
; TITLE OF INVENTION: AND THIOREDOXIN REDUCTASE GENES AND METHODS OF USING  
; FILE REFERENCE: 683-112US-A  
; CURRENT APPLICATION NUMBER: US/09/601,144  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: US 60/073,196  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Human  
US-09-601-144-14

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 TGGATATCTTTT 453  
|||||  
DB 7 TGGATATCTTTT 18

RESULT 78

US-09-665-615B-21/c  
; Sequence 21, Application US/09665615B  
; Patent No. 6653133  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-0502  
; CURRENT APPLICATION NUMBER: US/09/665,615B  
; CURRENT FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US 09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-665-615B-21

Query Match 2.0%; Score 12; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAATTGCTCTT 182  
|||||  
DB 20 GGAATTGCTCTT 9

RESULT 79

US-09-860-473-93/c  
; Sequence 93, Application US/09860473

```

; Patent No. 6656732
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRC-C EXPRESSION
; FILE REFERENCE: RTS-0222
; CURRENT APPLICATION NUMBER: US/09/860,473
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 169
; SEQ ID NO 93
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-860-473-93

Query Match      2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 GTGGCCGACTTT 291
DB 15 GTGGCCGACTTT 4

RESULT 80
US-09-890-010A-1/c
; Sequence 1, Application US/09890010A
; Patent No. 6664042
; GENERAL INFORMATION:
; APPLICANT: Posnett, David N
; TITLE OF INVENTION: DETERMINING VIRAL LOAD IN DOUBLE NEGATIVE T CELLS
; FILE REFERENCE: 19603/2732
; CURRENT APPLICATION NUMBER: US/09/890,010A
; CURRENT FILING DATE: 2001-11-23
; PRIOR APPLICATION NUMBER: PCT/US00/01959
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-890-010A-1

Query Match      2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTCA 328
DB 17 TGAGGATCTTCA 6

RESULT 81
US-09-980-052-61
; Sequence 61, Application US/09980052
; Patent No. 6670130
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/09/980,052
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29

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; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium vaccae
US-09-980-052-61

Query Match      2.0%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AGGTCGCGGTG 76
DB 5 AGGTCGCGGTG 16

RESULT 82
PCT-US95-08605-8
; Sequence 8, Application PC/TUS9508605
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Diamandis, Eleftherios
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for p53 Mutations
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08605
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,946
; FILING DATE: 08-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,381
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina T. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 5 of human p53 gene
; PCT-US95-08605-8

Query Match      2.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US95-08605-8
QY      510 TCGTCTCTCCAG 521
Db      9 TCGTCTCTCCAG 20

RESULT 83
PCT-US95-08605-9/c
; Sequence 9, Application PC/TUS9508605
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Diamandis, Eleftherios
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for p53 Mutations
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08605
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,946
; FILING DATE: 08-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,381
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina I. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; ORGANISM: human
;
; FEATURE:
; NAME/KEY: primer for exon 6 of human p53 gene
; PCT-US95-08605-9

Query Match      2.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US95-08605-9
QY      510 TCGTCTCTCCAG 521
Db      18 TCGTCTCTCCAG 7

RESULT 84
US-08-441-887A-269
; Sequence 269, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 269:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
; US-08-441-887A-269

Query Match      1.8%; Score 11; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; ORGANISM: human
; FEATURE:
; NAME/KEY: primer for exon 5 of human p53 gene
; PCT-US95-08605-8

Query Match      2.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US95-08605-8
QY      510 TCGTCTCTCCAG 521
Db      9 TCGTCTCTCCAG 20

RESULT 83
PCT-US95-08605-9/c
; Sequence 9, Application PC/TUS9508605
; GENERAL INFORMATION:
; APPLICANT: Visible Genetics Inc.
; APPLICANT: Diamandis, Eleftherios
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for p53 Mutations
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08605
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,946
; FILING DATE: 08-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,381
; FILING DATE: 14-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marina I. Larson
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHETICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE: human
; ORGANISM: human
;
; FEATURE:
; NAME/KEY: primer for exon 6 of human p53 gene
; PCT-US95-08605-9

Query Match      2.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US95-08605-9
QY      510 TCGTCTCTCCAG 521
Db      18 TCGTCTCTCCAG 7

RESULT 84
US-08-441-887A-269
; Sequence 269, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 269:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
; US-08-441-887A-269

Query Match      1.8%; Score 11; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

[illegible]

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; OPERATING SYSTEM: System 7.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,797
; FILING DATE: October 21, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: NYBC 265-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-140-797-4
;
Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAAGCCCTGGG 487
DB 15 CAAGCCCTGGG 5

RESULT 89
US-08-182-968A-32/c
; Sequence 32, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-182-968A-32
;
Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
DB 13 AGGCTGAGCCC 3

RESULT 90
US-08-319-492B-440/c
; Sequence 440, Application US/08319492B
; Patent No. 5616488
; GENERAL INFORMATION:
; APPLICANT: Sullivan, Sean M.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
; NUMBER OF SEQUENCES: 751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,492B
; FILING DATE: October 7, 1994
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/276
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 440:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-319-492B-440
;
Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGATACTT 451
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; OPERATING SYSTEM: System 7.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.670A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/140.797
; FILING DATE: October 21, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: NYBC 265-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-486-670A-4

Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAAGCCTGGG 487
DB 15 CAAGCCTGGG 5

RESULT 94
US-08-363-240A-651
; Sequence 651, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 652:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-363-240A-652

Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. NO. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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; OPERATING SYSTEM: System 7.0
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.670A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/140.797
; FILING DATE: October 21, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: NYBC 265-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-486-670A-4

Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. NO. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAAGCCTGGG 487
DB 15 CAAGCCTGGG 5

RESULT 94
US-08-363-240A-651
; Sequence 651, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEFAX: 67-3510
; INFORMATION FOR SEQ ID NO: 652:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-363-240A-652

Query Match 1.8%; Score 11; DB 1; Length 15;
Best Local Similarity 54.5%; Pred. NO. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```



Qy 337 CTCTACTCTG 347  
|:|:|:|:|:  
Db 1 CUCUACUUCG 11

RESULT 96

US-08-292-620A-499  
Sequence 499, Application US/08292620A

Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: INTRACELLULAR ADHESION

TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A

FILING DATE: August 17, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/149

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 499:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-292-620A-499

Query Match 1.8%; Score 11; DB 2; Length 15;

Best Local Similarity 81.8%; Pred. No. 4e+04;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 244 ACCTCCTGGAG 254

|||:|:|:|:|

Db 4 ACCUCCUGGAG 14

RESULT 97

US-08-292-620A-688

Sequence 688, Application US/08292620A

Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

APPLICANT: Sean Sullivan

APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: INTRACELLULAR ADHESION

TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/292,620A

FILING DATE: August 17, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/008,895

FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/149

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 688:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-292-620A-688

Query Match 1.8%; Score 11; DB 2; Length 15;

Best Local Similarity 81.8%; Pred. No. 4e+04;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 244 ACCTCCTGGAG 254

|||:|:|:|:|

Db 4 ACCUCCUGGAG 14

RESULT 98

US-08-292-620A-736

Sequence 736, Application US/08292620A

Patent No. 5837542

GENERAL INFORMATION:

APPLICANT: Susan Grimm

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

APPLICANT: Sean Sullivan

two

two

```

; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 736:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-736

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTCGAG 254
DB 4 ACCUCCUGAG 14

RESULT 99
US-08-774-306A-32/c
; Sequence 32, Application US/08774306A
; Patent No. 5869253
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California

```

two

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; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,306A
; FILING DATE: December 26, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-774-306A-32

Query Match 1.8%; Score 11; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
DB 13 AGGCTGAGCCC 3

RESULT 100
US-08-585-684B-622
; Sequence 622, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995

```

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 622:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-622

Query Match 1.8%; Score 11; DB 2; Length 15;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428  
DB 4 ACCUCAAAGA 14

RESULT 101  
US-08-585-684B-623  
; Sequence 623, Application US/08585684B  
; Patent No. 5877021  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Daniel T.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 2751  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 623:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-623

Query Match 1.8%; Score 11; DB 2; Length 15;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428  
DB 4 ACCUCAAAGA 14

RESULT 102  
US-08-585-684B-624  
; Sequence 624, Application US/08585684B  
; Patent No. 5877021  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Daniel T.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 2751  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 624:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-624

Query Match 1.8%; Score 11; DB 2; Length 15;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428  
DB 4 ACCUCAAAGA 14

RESULT 103  
US-08-585-684B-625  
; Sequence 625, Application US/08585684B  
; Patent No. 5877021  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Daniel T.  
; APPLICANT: Jarvis, Thale

APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 625:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-625

Query Match 1.8%; Score 11; DB 2; Length 15;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTCAAAGA 428  
|||:|||||  
Db 3 ACCUCAAAGA 13

RESULT 104  
US-08-585-684B-1821  
Sequence 1821, Application US/08585684B  
Patent No. 5877021

GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1821:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-1821

Query Match 1.8%; Score 11; DB 2; Length 15;  
Best Local Similarity 72.7%; Pred. No. 4e+04;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAT 51  
|||:|||||  
Db 5 AAUCAAAGAU 15

RESULT 105  
US-08-585-684B-1822  
Sequence 1822, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1822:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-1822

Query Match 1.8%; Score 11; DB 2; Length 15;  
Best Local Similarity 72.7%; Pred. No. 4e+04;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAAT 51  
||:|||||:  
DB 5 AAUUCAAAAU 15

RESULT 106  
US-08-585-684B-1823  
Sequence 1823, Application US/08585684B  
Patent No. 5877021  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Fast-SEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/585,684B  
FILING DATE: January 16, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/000,951  
FILING DATE: July 7, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1823:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-585-684B-1823

Query Match 1.8%; Score 11; DB 2; Length 15;  
Best Local Similarity 72.7%; Pred. No. 4e+04;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAAT 51  
||:|||||:  
DB 5 AAUUCAAAAU 15

RESULT 107  
US-08-422-560A-31  
Sequence 31, Application US/08422560A  
Patent No. 5910626  
GENERAL INFORMATION:  
APPLICANT: Haselkorn, Robert  
APPLICANT: Gornicki, Piotr  
TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE COMPOSITIONS AND  
METHODS FOR USE  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,560A  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/956,700  
FILING DATE: 02-OCT-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARCD:152/WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512-418-3000  
TELEFAX: 512-474-7577  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-422-560A-31

Query Match 1.8%; Score 11; DB 2; Length 15;  
Best Local Similarity 72.7%; Pred. No. 4e+04;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 555 GGTGTGATGACT 565  
||:|||||:  
DB 4 GGUGAUGACT 14

RESULT 108  
US-09-064-156A-32/c  
Sequence 32, Application US/09064156A  
Patent No. 6132966  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
TITLE OF INVENTION: METHOD AND REAGENT FOR  
INHIBITING HEPATITIS C  
TITLE OF INVENTION: VIRUS REPLICATION  
NUMBER OF SEQUENCES: 498  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/064,156A  
FILING DATE: April 21, 1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/774,306  
FILING DATE: December 26, 1996  
APPLICATION NUMBER: 08/182,968  
FILING DATE: January 13, 1994  
APPLICATION NUMBER: 07/882,888  
FILING DATE: May 14, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 234/083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-064-156A-32

Query Match 1.8%; Score 11; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369  
DB 13 AGGCTGAGCCC 3

## RESULT 109

US-09-071-845-499  
Sequence 499, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 499:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-499

Query Match 1.8%; Score 11; DB 3; Length 15;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAG 254  
DB 4 ACCUCUGGAG 14

## RESULT 110

US-09-071-845-688  
Sequence 688, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993

APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 688:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-688

Query Match 1.8%; Score 11; DB 3; Length 15;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254  
DB 4 ACCUCCUGGAG 14

RESULT 111  
US-09-071-845-736  
Sequence 736, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 736:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-736

Query Match 1.8%; Score 11; DB 3; Length 15;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254  
DB 4 ACCUCCUGGAG 14

RESULT 112  
US-09-038-073-622  
Sequence 622, Application US/09038073  
Patent No. 6194150  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
SUITE: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,073  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,684  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 622:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-038-073-622

Query Match 1.8%; Score 11; DB 3; Length 15;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428

Db                   ||||:|||||  
                    4 ACCUCAAAGA 14

RESULT 113  
US-09-038-073-623  
; Sequence 623, Application US/09038073  
; Patent No. 6194150  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Daniel T.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 2751  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,073  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/585,684  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 218/078  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 623:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-09-038-073-623

Query Match                   1.8%; Score 11; DB 3; Length 15;  
Best Local Similarity       81.8%; Pred. No. 4e+04;  
Matches   9; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

QY                   418 ACCTTCAAAGA 428  
                    ||||:|||||  
Db                   4 ACCUCAAAGA 14

RESULT 114  
US-09-038-073-624  
; Sequence 624, Application US/09038073  
; Patent No. 6194150  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Daniel T.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 2751

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,073  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/585,684  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 218/078  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 624:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-09-038-073-624

Query Match                   1.8%; Score 11; DB 3; Length 15;  
Best Local Similarity       81.8%; Pred. No. 4e+04;  
Matches   9; Conservative   2; Mismatches   0; Indels   0; Gaps   0;

QY                   418 ACCTTCAAAGA 428  
                    ||||:|||||  
Db                   4 ACCUCAAAGA 14

RESULT 115  
US-09-038-073-625  
; Sequence 625, Application US/09038073  
; Patent No. 6194150  
; GENERAL INFORMATION:  
; APPLICANT: Stinchcomb, Daniel T.  
; APPLICANT: Jarvis, Thale  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
; NUMBER OF SEQUENCES: 2751  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,073



```
;
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 625:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-625

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 81.8%; Pred. No. 4e+04; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTTCAAGA 428
Db 3 ACCUCAAAGA 13

RESULT 116
US-09-038-073-1821
; Sequence 1821, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1821:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
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```
;
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-1821

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 72.7%; Pred. No. 4e+04; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAAT 51
Db 5 AAUUCAAAAAU 15

RESULT 117
US-09-038-073-1822
; Sequence 1822, Application US/09038073
; Patent No. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/038,073
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1822:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-038-073-1822

Query Match 1.8%; Score 11; DB 3; Length 15;
Best Local Similarity 72.7%; Pred. No. 4e+04; Indels 0; Gaps 0;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAAT 51
Db 5 AAUUCAAAAAU 15

RESULT 118
US-09-038-073-1823
; Sequence 1823, Application US/09038073
```

Patent No. 6194150  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Daniel T.  
APPLICANT: Jarvis, Thale  
APPLICANT: McSwiggen, James  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE  
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES  
NUMBER OF SEQUENCES: 2751  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,073  
FILING DATE:  
Prior Application Data:  
APPLICATION NUMBER: 08/585,684  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/078  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
SEQUENCE CHARACTERISTICS:  
INFORMATION FOR SEQ ID NO: 1823:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-038-073-1823

Query Match 1.8%; Score 11; DB 3; Length 15;  
Best Local Similarity 72.7%; Pred. No. 4e+04;  
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAT 51  
||:|||||:  
Db 5 AAUUCAAAAU 15

RESULT 119  
US-07-879-647A-31  
Sequence 31, Application US/07879647A  
Patent No. 5266689  
GENERAL INFORMATION:  
APPLICANT: Chakraborty, P.R.  
APPLICANT: Dashkevich, M.  
APPLICANT: Elbrecht, A.  
APPLICANT: Feigner, S.D.  
APPLICANT: Liberator, P.A.  
APPLICANT: Profous-Juchelka, H.  
TITLE OF INVENTION: Eimeria Maxima DNA  
TITLE OF INVENTION: Probes  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey

COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb  
MEDIUM TYPE: storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.4  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/879,647A  
FILING DATE: 19920512  
CLASSIFICATION: 435  
Prior Application Data:  
APPLICATION NUMBER: 07/706,628  
FILING DATE: 29-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Tribble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: 184201A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 bases  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-879-647A-31

Query Match 1.8%; Score 11; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365  
|||||||:  
Db 3 CGCAAGGCTGA 13

RESULT 120  
US-07-879-584A-31  
Sequence 31, Application US/07879584A  
Patent No. 5278298  
GENERAL INFORMATION:  
APPLICANT: Chakraborty, P.R.  
APPLICANT: Dashkevich, M.  
APPLICANT: Elbrecht, A.  
APPLICANT: Feigner, S.D.  
APPLICANT: Liberator, P.A.  
APPLICANT: Profous-Juchelka, H.  
TITLE OF INVENTION: Eimeria Brunetti DNA  
TITLE OF INVENTION: Probes  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: 126 Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb  
MEDIUM TYPE: storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 6.0.4  
SOFTWARE: Microsoft Word 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/879,584A  
FILING DATE: 19920512  
CLASSIFICATION: 536  
Prior Application Data:  
APPLICATION NUMBER: 07/706,717

```

; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184191A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-584A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 121
US-07-879-470A-31
; Sequence 31, Application US/07879470A
; Patent No. 528845
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Eibrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Necatrix DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,470A
; FILING DATE: 19920512
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,351
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184221A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-584A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 122
US-07-879-644A-31
; Sequence 31, Application US/07879644A
; Patent No. 529813
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Eibrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Acervulina DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,644A
; FILING DATE: 19920512
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,817
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184181A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-644A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 123
US-07-879-640A-31
; Sequence 31, Application US/07879470A
; Patent No. 528845
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Eibrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Necatrix DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,470A
; FILING DATE: 19920512
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,351
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184221A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-640A-31
```

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; TOPOLOGY: linear
; US-07-879-470A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 122
US-07-879-644A-31
; Sequence 31, Application US/07879644A
; Patent No. 529813
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Eibrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Acervulina DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,644A
; FILING DATE: 19920512
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,817
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184181A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-644A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGGCTGA 365
Db 3 CGCAAGGCTGA 13

RESULT 123
US-07-879-640A-31
; Sequence 31, Application US/07879470A
; Patent No. 528845
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Eibrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Necatrix DNA
; TITLE OF INVENTION: Probes
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,470A
; FILING DATE: 19920512
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,351
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184221A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-640A-31
```

```
; Sequence 31, Application US/07879640A
; Patent No. 5359050
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Elbrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Mitis DNA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,640A
; FILING DATE: 19920512
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,355
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184211A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-640A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365
DB 3 CGCAGGCTGA 13

RESULT 124
US-07-879-594A-31
; Sequence 31, Application US/07879594A
; Patent No. 5449768
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Elbrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Fraeox DNA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
```

```
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,594A
; FILING DATE: 19920512
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/706,360
; FILING DATE: 29-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tribble, Jack L.
; REGISTRATION NUMBER: 32,633
; REFERENCE/DOCKET NUMBER: .184231A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-5321
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-879-594A-31

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365
DB 3 CGCAGGCTGA 13

RESULT 125
US-07-879-469A-31
; Sequence 31, Application US/07879469A
; Patent No. 5563256
; GENERAL INFORMATION:
; APPLICANT: Chakraborty, P.R.
; APPLICANT: Dashkevich, M.
; APPLICANT: Elbrecht, A.
; APPLICANT: Feighner, S.D.
; APPLICANT: Liberator, P.A.
; APPLICANT: Profous-Juchelka, H.
; TITLE OF INVENTION: Eimeria Tenella DNA
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb
; MEDIUM TYPE: storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.4
; SOFTWARE: Microsoft Word 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,469A
; FILING DATE: 19920512
```

US-08-050-073-145

Query Match 1.8%; Score 11; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255  
|||  
Db 1 CCTCCTGGAGC 11

RESULT 127

US-08-050-073-152/C  
; Sequence 152, Application US/08050073  
; Patent No. 5567809  
; GENERAL INFORMATION:  
; APPLICANT: Apple, Raymond J.  
; APPLICANT: Begovich, Ann B.  
; APPLICANT: Bugawan, Teodorica L.  
; APPLICANT: Erlich, Henry A.  
; APPLICANT: Griffith, Robert L.  
; APPLICANT: Scharf, Stephen J.  
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA  
; TITLE OF INVENTION: Typing  
; NUMBER OF SEQUENCES: 315  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/050,073  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petty, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 8769  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 152:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
US-08-050-073-152

Query Match 1.8%; Score 11; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255  
|||  
Db 16 CCTCCTGGAGC 6

RESULT 128

US-08-050-073-154  
; Sequence 154, Application US/08050073  
; Patent No. 5567809  
; GENERAL INFORMATION:  
; APPLICANT: Apple, Raymond J.  
; APPLICANT: Begovich, Ann B.

US-09-966-880a-7\_copy\_80\_676.Oligo.rni

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/706,362  
; FILING DATE: 29-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tridble, Jack L.  
; REGISTRATION NUMBER: 32,633  
; REFERENCE/DOCKET NUMBER: 184241A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-5321  
; TELEFAX: (908) 594-4720  
; TELEX: 138825  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 bases  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-879-469A-31

Query Match 1.8%; Score 11; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365  
|||  
Db 3 CGCAGGCTGA 13

RESULT 126

US-08-050-073-145  
; Sequence 145, Application US/08050073  
; Patent No. 5567809  
; GENERAL INFORMATION:  
; APPLICANT: Apple, Raymond J.  
; APPLICANT: Begovich, Ann B.  
; APPLICANT: Bugawan, Teodorica L.  
; APPLICANT: Erlich, Henry A.  
; APPLICANT: Griffith, Robert L.  
; APPLICANT: Scharf, Stephen J.  
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA  
; TITLE OF INVENTION: Typing  
; NUMBER OF SEQUENCES: 315  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/050,073  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petty, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 8769  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 145:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA

```

; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-050-073-154

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
Db 1 CCTCCTGGAGC 11

RESULT 129
US-07-695-201B-4/c
; Sequence 4, Application US/07695201B
; Patent No. 5994056
; GENERAL INFORMATION:
; APPLICANT: Higuchi, Russell H.
; TITLE OF INVENTION: Homogeneous Methods for Nucleic Acid
; TITLE OF INVENTION: Amplification and Detection
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-third Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/695,201B
; FILING DATE:
; CLASSIFICATION: 435

; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; US-08-050-073-154

Query Match 1.8%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
Db 1 CCTCCTGGAGC 11

RESULT 129
US-07-695-201B-4/c
; Sequence 4, Application US/07695201B
; Patent No. 5994056
; GENERAL INFORMATION:
; APPLICANT: Higuchi, Russell H.
; TITLE OF INVENTION: Homogeneous Methods for Nucleic Acid
; TITLE OF INVENTION: Amplification and Detection
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cetus Corporation
; STREET: 1400 Fifty-third Street
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/695,201B
; FILING DATE:
; CLASSIFICATION: 435

; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; TITLE OF INVENTION: Typing
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 9012A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-470-532-4

Query Match 1.8%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 CCGCTGCTACC 229
Db 11 CCGCTGCTACC 1

RESULT 130
US-08-470-532-4/c
; Sequence 4, Application US/08470532
; Patent No. 6171785
; GENERAL INFORMATION:
; APPLICANT: Higuchi, Russell H.
; TITLE OF INVENTION: Homogeneous Methods for Nucleic Acid
; TITLE OF INVENTION: Amplification and Detection
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,532
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 9012A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-470-532-4

Query Match 1.8%; Score 11; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 CCGCTGCTACC 229
Db 11 CCGCTGCTACC 1
```

```
Db      11  CCGCTGCTACC 1

RESULT 131
US-08-968-208-4/c
; Sequence 4, Application US/08968208
; Patent No. 659478
; GENERAL INFORMATION:
; APPLICANT: Higuchi, Russell H.
; TITLE OF INVENTION: HOMOGENEOUS METHODS FOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 071109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,208
; FILING DATE: 11/12/97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32630
; REFERENCE/DOCKET NUMBER: 9397
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-814-2869
; TELEFAX: 510-814-2977
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-968-208-4

Query Match      1.8%; Score 11; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      219  CCGCTGCTACC 229
Db      11  CCGCTGCTACC 1

RESULT 132
US-08-050-073-155
; Sequence 155, Application US/08050073
; Patent No. 5567809
; GENERAL INFORMATION:
; APPLICANT: Apple, Raymond J.
; APPLICANT: Begovich, Ann B.
; APPLICANT: Bugawan, Teodorica L.
; APPLICANT: Erlich, Henry A.
; APPLICANT: Griffith, Robert L.
; APPLICANT: Scharf, Stephen J.
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA
; NUMBER OF SEQUENCES: 315
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/050,073
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petty, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 8769
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 155:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-050-073-155

Query Match      1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      245  CCTCCTGGAGC 255
Db      1  CCTCCTGGAGC 11

RESULT 133
US-08-390-850-682
; Sequence 682, Application US/08390850
; Patent No. 5612215
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Gustofson, John
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT
; TITLE OF INVENTION: OF ARTHRITIC CONDITIONS
; NUMBER OF SEQUENCES: 1151
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,850
; FILING DATE: February 17, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/354,920
; FILING DATE: December 13, 1994
; APPLICATION NUMBER: 08/152,487
; FILING DATE: NO. 5612215ember 12, 1993
; APPLICATION NUMBER: 07/989,848
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
```

REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 211/084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1500  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 682:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-390-850-682

Query Match 1.8%; Score 11; DB 1; Length 17;  
Best Local Similarity 63.6%; Pred. No. 4e+04;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 129 ACTGGACTTTG 139  
||:||||:|  
Db 1 ACUGGACUUUG 11

RESULT 134  
US-08-435-634-682  
Sequence 682, Application US/08435634  
Patent No. 5731295  
GENERAL INFORMATION:  
APPLICANT: Draper, Kenneth G.  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwiggen, James  
APPLICANT: Gustofson, John  
APPLICANT: Stinchcomb, Dan T.

TITLE OF INVENTION: METHOD AND REAGENT FOR TREATMENT  
TITLE OF INVENTION: OF ARTHRITIC CONDITIONS  
NUMBER OF SEQUENCES: 1151  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/435,634  
FILING DATE: 05-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/390,850  
FILING DATE: February 17, 1995  
APPLICATION NUMBER: 08/354,920  
FILING DATE: December 13, 1994  
APPLICATION NUMBER: 08/152,487  
FILING DATE: No. 5731295, September 12, 1993  
APPLICATION NUMBER: 07/989,848  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 211/084  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1500  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 682:  
SEQUENCE CHARACTERISTICS:

QY 129 ACTGGACTTTG 139  
||:||||:|  
Db 1 ACUGGACUUUG 11

LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-435-634-682

Query Match 1.8%; Score 11; DB 1; Length 17;  
Best Local Similarity 63.6%; Pred. No. 4e+04;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 129 ACTGGACTTTG 139  
||:||||:|  
Db 1 ACUGGACUUUG 11

RESULT 135  
US-08-758-306-405  
Sequence 405, Application US/08758306  
Patent No. 5807743  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.

APPLICANT: McSwiggen, James A.  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TITLE OF INVENTION: TREATMENT OF DISEASES  
TITLE OF INVENTION: ASSOCIATED WITH  
TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR  
TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION  
NUMBER OF SEQUENCES: 1379  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,306  
FILING DATE: December 3, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 405:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-758-306-405

Query Match 1.8%; Score 11; DB 1; Length 17;  
Best Local Similarity 63.6%; Pred. No. 4e+04;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTTGCCCC 547  
||:||||:|  
Db 6 CCUUUGCCCC 16



```
RESULT 136
US-08-758-306-407
; Sequence 407, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-758-306-407

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGGCCCC 547
DB 5 CCUUUGCCCC 15

RESULT 137
US-08-758-306-409
; Sequence 409, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 407:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-758-306-409

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGGCCCC 547
DB 5 CCUUUGCCCC 15
```

```
RESULT 138
US-08-292-620A-1635
; Sequence 1635, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOSOME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-758-306-409

Query Match 1.8%; Score 11; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGGCCCC 547
DB 4 CCUUUGCCCC 14
```



ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1770:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-1770

Query Match 1.8%; Score 11; DB 2; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186  
Db 3 USCUCUCCUC 13

RESULT 141  
US-08-292-620A-1830  
Sequence 1830, Application US/08292620A  
Patent No. 5837542  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440

two

TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1830:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-1830

Query Match 1.8%; Score 11; DB 2; Length 17;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAG 254  
Db 5 ACCUCCUGGAG 15

RESULT 142  
US-08-292-620A-1836  
Sequence 1836, Application US/08292620A  
Patent No. 5837542  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper

TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992

ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1836:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

two

US-08-292-620A-1836

Query Match 1.8%; Score 11; DB 2; Length 17;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAG 254

Db 5 ACCUCCUGAG 15

RESULT 143

US-08-292-620A-1891  
; Sequence 1891, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1891:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-292-620A-1891

Query Match 1.8%; Score 11; DB 2; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186

Db 2 UGCUCUCCUC 12

RESULT 145

US-08-292-620A-1968

; Sequence 1968, Application US/08292620A

Db 5 UGCUCUCCUC 15

RESULT 144

US-08-292-620A-1894

; Sequence 1894, Application US/08292620A

; Patent No. 5837542

; GENERAL INFORMATION:

; APPLICANT: Susan Grimm

; APPLICANT: Dan T. Stinchcomb

; APPLICANT: James McSwiggen

; APPLICANT: Sean Sullivan

; APPLICANT: Kenneth G. Draper

; TITLE OF INVENTION: RIBOZYME TREATMENT OF

; TITLE OF INVENTION: DISEASES OR CONDITIONS

; TITLE OF INVENTION: RELATED TO LEVELS OF

; TITLE OF INVENTION: INTRACELLULAR ADHESION

; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)

; NUMBER OF SEQUENCES: 2390

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/292,620A

; FILING DATE: August 17, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 08/008,895

; FILING DATE: January 19, 1993

; APPLICATION NUMBER: 07/989,849

; FILING DATE: December 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 208/149

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1894:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-292-620A-1894

Query Match 1.8%; Score 11; DB 2; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186

Db 2 UGCUCUCCUC 12

RESULT 145

US-08-292-620A-1968

; Sequence 1968, Application US/08292620A

two

two

```

; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1968:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-1968

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAG 254
DB 5 ACCUCUGGAG 15

RESULT 146
US-08-292-620A-1981
; Sequence 1981, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:

```

two

```

; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1981:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-292-620A-1981

Query Match 1.8%; Score 11; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
DB 5 UGCUCUCCUC 15

RESULT 147
US-08-292-620A-1984
; Sequence 1984, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:

```

two

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292.620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1984:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-1984

Query Match 1.8%; Score 11; DB 2; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186  
:|:|:|:|:|:  
Db 2 UGCUCUCCUC 12

RESULT 148  
US-08-292-620A-1986  
; Sequence 1986, Application US/08292620A  
; Patent No. 5837542  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

two

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292.620A  
FILING DATE: August 17, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1986:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-292-620A-1986

Query Match 1.8%; Score 11; DB 2; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;  
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186  
:|:|:|:|:|:  
Db 5 UGCUCUCCUC 15

RESULT 149  
US-08-532-896-51  
; Sequence 51, Application US/08532896  
; Patent No. 6124115  
; GENERAL INFORMATION:  
; APPLICANT: LIU-THIE, Van  
; APPLICANT: LARIE, Fernand  
; TITLE OF INVENTION: PRODUCTION AND USE OF ISOLATED TYPE 5  
; TITLE OF INVENTION: 17B-HYDROXYSTEROID DEHYDROGENASE  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen  
; STREET: 1180 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: US  
; ZIP: 10036-8403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,896  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Meilman, Edward  
REGISTRATION NUMBER: 24,735  
REFERENCE/DOCKET NUMBER: P/1259-313  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 382-0700  
TELEFAX: (212) 382-0888  
TELEX: 236925  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-532-896-51

Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 GGGTGCACAAATA 408  
|||||  
DB 6 GGGTGCACAAATA 16

RESULT 150  
US-09-071-845-1635  
; Sequence 1635, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620  
; FILING DATE: August 17, 1994  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1635:

SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1635

Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGTCTTCCTC 186  
|||||  
DB 5 UGCUUUCUC 15

RESULT 151  
US-09-071-845-1691  
; Sequence 1691, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620  
; FILING DATE: August 17, 1994  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1691:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1691

Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TGCTCTTCCTC 186  
Db 5 UGCUUCUCC 15

## RESULT 152

US-09-071-845-1770  
; Sequence 1770, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620  
; FILING DATE: August 17, 1994  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1770:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-071-845-1770

Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TGCTCTTCCTC 186  
Db 3 UGCUUCUCC 13

## RESULT 153

US-09-071-845-1830  
; Sequence 1830, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:  
; APPLICANT: Susan Grimm  
; APPLICANT: Dan T. Stinchcomb  
; APPLICANT: James McSwiggen  
; APPLICANT: Sean Sullivan  
; APPLICANT: Kenneth G. Draper  
; TITLE OF INVENTION: RIBOZYME TREATMENT OF  
; TITLE OF INVENTION: DISEASES OR CONDITIONS  
; TITLE OF INVENTION: RELATED TO LEVELS OF  
; TITLE OF INVENTION: INTRACELLULAR ADHESION  
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
; NUMBER OF SEQUENCES: 2390  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,845  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,620  
; FILING DATE: August 17, 1994  
; APPLICATION NUMBER: 08/008,895  
; FILING DATE: January 19, 1993  
; APPLICATION NUMBER: 07/989,849  
; FILING DATE: December 7, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 208/149  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1830:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-071-845-1830

Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 244 ACCTCTCGAG 254  
Db 5 ACCUCCUGAG 15

## RESULT 154

US-09-071-845-1836  
; Sequence 1836, Application US/09071845  
; Patent No. 6132967  
; GENERAL INFORMATION:



APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1836:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1836  
Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 81.8%; Pred. No. 4e+04;  
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGAG 254  
Db 5 ACCUCCUGGAG 15  
RESULT 155  
US-09-071-845-1891  
Sequence 1891, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street

TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1891:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1891  
Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e+04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186  
Db 5 UGCUCUCCUC 15  
RESULT 156  
US-09-071-845-1894  
Sequence 1894, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street

```

; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1894:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1894

```

```

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 54.5%; Pred. No. 4e+04;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 176 TGCCTTCCTC 186
   :|:|:|:|:|
Db 2 UGCUUCUCCUC 12

```

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RESULT 157
US-09-071-845-1968
; Sequence 1968, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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```

; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1968:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-071-845-1968

```

```

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 81.8%; Pred. No. 4e+04;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 244 ACCTCCTGGAG 254
   |||:|:|:|
Db 5 ACCUCCUGGAG 15

```

```

RESULT 158
US-09-071-845-1981
; Sequence 1981, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:

```

CLASSIFICATION:  
PRIOR APPLICATION DATA: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1981:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1981

Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e-04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186  
:|:|:|:|:|:  
Db 5 UGCUUCCUC 15

RESULT 159  
US-09-071-845-1984  
Sequence 1984, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1984:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-071-845-1984

Query Match 1.8%; Score 11; DB 3; Length 17;  
Best Local Similarity 54.5%; Pred. No. 4e-04;  
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186  
:|:|:|:|:|:  
Db 2 UGCUUCCUC 12

RESULT 160  
US-09-071-845-1986  
Sequence 1986, Application US/09071845  
Patent No. 6132967  
GENERAL INFORMATION:  
APPLICANT: Susan Grimm  
APPLICANT: Dan T. Stinchcomb  
APPLICANT: James McSwiggen  
APPLICANT: Sean Sullivan  
APPLICANT: Kenneth G. Draper  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
TITLE OF INVENTION: DISEASES OR CONDITIONS  
TITLE OF INVENTION: RELATED TO LEVELS OF  
TITLE OF INVENTION: INTRACELLULAR ADHESION  
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)  
NUMBER OF SEQUENCES: 2390  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,845  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,620  
FILING DATE: August 17, 1994  
APPLICATION NUMBER: 08/008,895  
FILING DATE: January 19, 1993  
APPLICATION NUMBER: 07/989,849  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/149  
TELEPHONE: (213) 489-1600

```
; ORGANISM: Eimeria tenella
US-09-411-578-17

Query Match          1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      586 TTGGGACTTTG 596
DB      6   TTAGGACTTGTG 16

RESULT 163
US-09-411-578-19
Sequence 19, Application US/09411578
Patent No. 6203801
GENERAL INFORMATION:
APPLICANT: Schaap, Theodorus C
APPLICANT: Kuiper, Catharina M
APPLICANT: Vermeulen, Arnoldus N
TITLE OF INVENTION: Coccidiosis Vaccines
FILE REFERENCE: schaap
CURRENT APPLICATION NUMBER: US/09/411,578
CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 98203384.7
EARLIER FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 98203457.1
EARLIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
LENGTH: 17
TYPE: DNA
ORGANISM: Eimeria tenella
US-09-411-578-19

Query Match          1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      586 TTGGGACTTTG 596
DB      6   TTAGGACTTGTG 16

RESULT 164
US-09-411-578-21
Sequence 21, Application US/09411578
Patent No. 6203801
GENERAL INFORMATION:
APPLICANT: Schaap, Theodorus C
APPLICANT: Kuiper, Catharina M
APPLICANT: Vermeulen, Arnoldus N
TITLE OF INVENTION: Coccidiosis Vaccines
FILE REFERENCE: schaap
CURRENT APPLICATION NUMBER: US/09/411,578
CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: 98203384.7
EARLIER FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 98203457.1
EARLIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 17
TYPE: DNA
ORGANISM: Eimeria tenella
US-09-411-578-21

Query Match          1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      586 TTGGGACTTTG 596
DB      6   TTAGGACTTGTG 16
```

```
QY 586 TTGGGACTTTG 596
Db 6 TTGGGACTTTG 16

RESULT 165
US-08-962-690-17/c
; Sequence 17, Application US/08962690
; Patent No. 6214805
; GENERAL INFORMATION:
; APPLICANT: Torrence, Paul F. H.
; APPLICANT: Silverman, Robert H.
; APPLICANT: Cirino, Nick M.
; APPLICANT: Li, Guiying
; APPLICANT: Xiao, Wei
; APPLICANT: Player, Mark R.
; TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: 8656-019
; CURRENT APPLICATION NUMBER: US/08/962,690
; CURRENT FILING DATE: 1997-11-03
; EARLIER APPLICATION NUMBER: 08/801,896
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 60/011,725
; EARLIER FILING DATE: 1996-02-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-962-690-17

Query Match 1.8%; Score 11; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 540 TTGGCCCTGT 550
Db 14 TTGGCCCTGT 4

RESULT 166
US-08-584-040-5442
; Sequence 5442, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; OPERATING SYSTEM: IBM P.C. DOS 5.0
```

```
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-5442

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 342 CTTCTGTGAGG 352
Db 7 CUUCUGUGAGG 17

RESULT 167
US-08-584-040-5443
; Sequence 5443, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; OPERATING SYSTEM: IBM P.C. DOS 5.0
```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5443:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-5443

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 63.6%; Pred. No. 4e+04;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 342 CTTCTGTGAGG 352  
Db 6 CUUCUGAGG 16

RESULT 168  
US-09-474-432B-592/c  
Sequence 592, Application US/09474432B  
Patent No. 6528640  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Beigelman, Leo  
APPLICANT: Burgin, Alex  
APPLICANT: Beaudry, Amber  
APPLICANT: Karpeisky, Alex  
APPLICANT: Adamic, Jasenka  
APPLICANT: Sweedler, David  
APPLICANT: Zinnen, Shawn  
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides  
FILE REFERENCE: MBHB00-831-B (247/276)  
CURRENT APPLICATION NUMBER: US/09/474,432B  
PRIOR FILING DATE: 1999-12-19  
PRIOR APPLICATION NUMBER: US 60/064,866  
PRIOR FILING DATE: 1997-11-05  
PRIOR APPLICATION NUMBER: US 60/084,727  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: US 09/186,675  
PRIOR FILING DATE: 1998-11-04  
PRIOR APPLICATION NUMBER: US 09/301,511  
PRIOR FILING DATE: 1999-04-28  
NUMBER OF SEQ ID NOS: 1526  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 592  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-474-432B-592

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 243 CACCTCCTGGA 253  
Db 11 CACCTCCTGGA 1

RESULT 169  
US-09-474-432B-700/c  
Sequence 700, Application US/09474432B  
Patent No. 6528640  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Beigelman, Leo  
APPLICANT: Burgin, Alex  
APPLICANT: Beaudry, Amber  
APPLICANT: Karpeisky, Alex

APPLICANT: Adamic, Jasenka  
APPLICANT: Sweedler, David  
APPLICANT: Zinnen, Shawn  
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides  
FILE REFERENCE: MBHB00-831-B (247/276)  
CURRENT APPLICATION NUMBER: US/09/474,432B  
CURRENT FILING DATE: 1999-12-19  
PRIOR APPLICATION NUMBER: US 60/064,866  
PRIOR FILING DATE: 1997-11-05  
PRIOR APPLICATION NUMBER: US 60/084,727  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: US 09/186,675  
PRIOR FILING DATE: 1998-11-04  
PRIOR APPLICATION NUMBER: US 09/301,511  
PRIOR FILING DATE: 1999-04-28  
NUMBER OF SEQ ID NOS: 1526  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 700  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Homo sapiens  
US-09-474-432B-700

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 GGAGCCCTGC 261  
Db 13 GGAGCCCTGC 3

RESULT 170  
US-09-535-012A-12/c  
Sequence 12, Application US/09535012A  
Patent No. 6531281  
GENERAL INFORMATION:  
APPLICANT: Elf Exploration Production  
TITLE OF INVENTION: Method of Detecting Sulphate-Reducing Bacteria  
FILE REFERENCE: 111628-00114  
CURRENT APPLICATION NUMBER: US/09/535,012A  
CURRENT FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: 9903637  
PRIOR FILING DATE: 1999-03-24  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 12  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Desulfovibrio vulgaris  
FEATURE:  
OTHER INFORMATION: asp02 primer  
US-09-535-012A-12

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GAACCGGAGGA 28  
Db 17 GAACCGGAGGA 7

RESULT 171  
US-09-371-772B-2336  
Sequence 2336, Application US/09371772B  
Patent No. 6566127  
GENERAL INFORMATION:  
APPLICANT: Ribozyme Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam  
APPLICANT: McSwiggen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2336
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2336

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 342 CTTCTGTGAGG 352
|:|:|:|
Db 7 CUUCUGUGAGG 17

RESULT 172
US-09-371-772B-2337
; Sequence 2337, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2337
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-2337

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 63.6%; Pred. No. 4e+04;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 342 CTTCTGTGAGG 352
|:|:|:|
Db 6 CUUCUGUGAGG 16

RESULT 173
US-09-371-772B-4172/c
; Sequence 4172, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4172
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4172

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 CTGGCCGCTGC 225
|:|:|:|
Db 17 CTGGCCGCTGC 7

RESULT 174
US-09-371-772B-4173/c
; Sequence 4173, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
; FILE REFERENCE: MHB00.876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4173
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-4173

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 215 CTGGCCGCTGC 225
|:|:|:|
Db 11 CTGGCCGCTGC 1

RESULT 175
US-09-476-387-591/c
; Sequence 591, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpelsky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo  
; FILE REFERENCE: MH000-831-C (249/073)  
; CURRENT APPLICATION NUMBER: US/09/476,387  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 09/474,432  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 09/186,675  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: 60/083,727  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/064,866  
; PRIOR FILING DATE: 1997-11-05  
; NUMBER OF SEQ ID NOS: 1524  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 591  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-476-387-591

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCTCTGGA 253  
|||||  
DB 11 CACCTCTCTGGA 1

RESULT 176  
US-09-476-387-699/c  
; Sequence 699, Application US/09476387  
; Patent No. 6617438  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Beigelman, Leo  
; APPLICANT: Beaudry, Amber  
; APPLICANT: Karpeisky, Alex  
; APPLICANT: Adamic, Jasenka Matulic  
; APPLICANT: Sweedler, Dave  
; APPLICANT: Zinnen, Shawn  
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleo  
; FILE REFERENCE: MH000-831-C (249/073)  
; CURRENT APPLICATION NUMBER: US/09/476,387  
; CURRENT FILING DATE: 2001-04-04  
; PRIOR APPLICATION NUMBER: 09/474,432  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 09/186,675  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: 60/083,727  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/064,866  
; NUMBER OF SEQ ID NOS: 1524  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 699  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-476-387-699

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 GGAGCCCTCTGC 261  
|||||  
DB 13 GGAGCCCTCTGC 3

RESULT 177  
US-09-827-998-183  
; Sequence 183, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDH0RF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Acomica Sequence Listing Engine  
; Patent No. 6656700  
; SEQ ID NO 183  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-183

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTTT 436  
|||||  
DB 7 AGATTATTTTT 17

RESULT 178  
US-09-827-998-184  
; Sequence 184, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDH0RF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Acomica Sequence Listing Engine  
; Patent No. 6656700  
; SEQ ID NO 184  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-184

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTTT 436  
|||||  
DB 6 AGATTATTTTT 16

RESULT 179  
US-09-827-998-185  
; Sequence 185, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong



```
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 185
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-185

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      426 AGATTATTTT 436
Db      5 AGATTATTTT 15

RESULT 180
US-09-827-998-186
; Sequence 186, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 186
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-186

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      426 AGATTATTTT 436
Db      4 AGATTATTTT 14

RESULT 181
US-09-827-998-187
; Sequence 187, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
```

```
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 187
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-187

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      426 AGATTATTTT 436
Db      3 AGATTATTTT 13

RESULT 182
US-09-827-998-188
; Sequence 188, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 188
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-188

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      426 AGATTATTTT 436
Db      2 AGATTATTTT 12

RESULT 183
US-09-827-998-189
; Sequence 189, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 189
; LENGTH: 17
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-189

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 436
Db 1 AGATTATTTT 11

RESULT 184
US-09-827-998-345
; Sequence 345, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 345
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-345

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
Db 7 AAGATTATTTT 17

RESULT 185
US-09-827-998-346
; Sequence 346, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 346
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-346

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
Db 6 AAGATTATTTT 16

RESULT 186
US-09-827-998-347
; Sequence 347, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 347
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-347

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
Db 5 AAGATTATTTT 15

RESULT 187
US-09-827-998-348
; Sequence 348, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 348
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-348

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 435
Db 4 AAGATTATTTT 14

RESULT 188
```

US-09-827-998-349  
; Sequence 349, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDMORF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Acomica Sequence Listing Engine  
; Patent No. 6656700  
; SEQ ID NO 351  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-351  
Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 425 AAGATTATTTT 435  
DB 1 AAGATTATTTT 11  
RESULT 191  
US-09-827-998-648/c  
; Sequence 648, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDMORF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Acomica Sequence Listing Engine  
; Patent No. 6656700  
; SEQ ID NO 648  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-648  
Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 81 CTACCTGTGCT 91  
DB 17 CTACCTGTGCT 7  
RESULT 192  
US-09-827-998-649/c  
; Sequence 649, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDMORF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27

US-09-827-998-349  
; Sequence 349, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDMORF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Acomica Sequence Listing Engine  
; Patent No. 6656700  
; SEQ ID NO 349  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-349  
Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 425 AAGATTATTTT 435  
DB 3 AAGATTATTTT 13  
RESULT 189  
US-09-827-998-350  
; Sequence 350, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDMORF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Acomica Sequence Listing Engine  
; Patent No. 6656700  
; SEQ ID NO 350  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-350  
Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 425 AAGATTATTTT 435  
DB 2 AAGATTATTTT 12  
RESULT 190  
US-09-827-998-351  
; Sequence 351, Application US/09827998  
; Patent No. 6656700  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

```
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 649
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-649

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
      |||||
DB      16 CTACCTGTGCT 6

RESULT 193
US-09-827-998-650/c
; Sequence 650, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 650
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-650

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
      |||||
DB      15 CTACCTGTGCT 5

RESULT 194
US-09-827-998-651/c
; Sequence 651, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 651
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-651

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
      |||||
DB      13 CTACCTGTGCT 3

RESULT 196
US-09-827-998-653/c
; Sequence 653, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 653
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-653

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
      |||||
DB      14 CTACCTGTGCT 4

RESULT 195
US-09-827-998-652/c
; Sequence 652, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 652
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-652

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
      |||||
DB      13 CTACCTGTGCT 3

RESULT 196
US-09-827-998-653/c
; Sequence 653, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 653
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-653

Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
      |||||
DB      14 CTACCTGTGCT 4
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Db      12 CTACCTGTGCT 2
|||||
RESULT 197
US-09-927-998-654/c
; Sequence 654, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/236,359
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 654
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-927-998-654
Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      81 CTACCTGTGCT 91
|||||
Db      11 CTACCTGTGCT 1
|||||
RESULT 198
US-09-749-233-15
; Sequence 15, Application US/09749233
; Patent No. 6680061
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/749,233
; CURRENT FILING DATE: 2000-12-27
; PRIOR FILING DATE: 09/411,578
; PRIOR APPLICATION NUMBER: 98203457.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Eimeria tenella
US-09-749-233-15
Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      586 TTGGGACTTTG 596
|||||
Db      6 TTGGGACTTTG 16
|||||
RESULT 199
US-09-749-233-17
; Sequence 17, Application US/09749233
; Patent No. 6680061
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/749,233
; CURRENT FILING DATE: 2000-12-27
; PRIOR FILING DATE: 09/411,578
; PRIOR APPLICATION NUMBER: 98203457.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Eimeria tenella
US-09-749-233-17
Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      586 TTGGGACTTTG 596
|||||
Db      6 TTGGGACTTTG 16
|||||
RESULT 200
US-09-749-233-19
; Sequence 19, Application US/09749233
; Patent No. 6680061
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/749,233
; CURRENT FILING DATE: 2000-12-27
; PRIOR FILING DATE: 09/411,578
; PRIOR APPLICATION NUMBER: 98203457.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Eimeria tenella
US-09-749-233-19
Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      586 TTGGGACTTTG 596
|||||
Db      6 TTGGGACTTTG 16
|||||
RESULT 201
US-09-749-233-21
; Sequence 21, Application US/09749233
; Patent No. 6680061
; GENERAL INFORMATION:
; APPLICANT: Schaap, Theodorus C
; APPLICANT: Kuiper, Catharina M
; APPLICANT: Vermeulen, Arnoldus N
; TITLE OF INVENTION: Coccidiosis Vaccines
; FILE REFERENCE: schaap
; CURRENT APPLICATION NUMBER: US/09/749,233
; CURRENT FILING DATE: 2000-12-27
; PRIOR FILING DATE: 09/411,578
; PRIOR APPLICATION NUMBER: 98203457.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Eimeria tenella
US-09-749-233-21
Query Match      1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      586 TTGGGACTTTG 596
|||||
Db      6 TTGGGACTTTG 16
|||||
```

;; CURRENT APPLICATION NUMBER: US/09/749,233  
;; CURRENT FILING DATE: 2000-12-27  
;; PRIOR APPLICATION NUMBER: 09/411,578  
;; PRIOR FILING DATE: 1999-10-04  
;; PRIOR APPLICATION NUMBER: 98203457.1  
;; PRIOR FILING DATE: 1998-10-16  
;; NUMBER OF SEQ ID NOS: 41  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 21  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Eimeria tenella  
US-09-749-233-21

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 586 TTGGGACTTTC 586  
Db 6 TTGGGACTTTC 16

RESULT 202  
US-09-866-108A-932  
;; Sequence 932, Application US/09866108A  
;; Patent No. 6686188  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharron G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng  
;; APPLICANT: SHANNON, Mark  
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
;; FILE REFERENCE: AEOICA-7  
;; CURRENT APPLICATION NUMBER: US/09/866,108A  
;; CURRENT FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aecomica Sequence Listing Engine  
;; Patent No. 6686188  
;; SEQ ID NO 932  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108A-932

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 586 TTGGGACTTTC 586  
Db 6 TTGGGACTTTC 16

Qy 359 AGGCTGAGCCC 369  
Db 7 AGGCTGAGCCC 17

RESULT 203  
US-09-866-108A-933  
;; Sequence 933, Application US/09866108A  
;; Patent No. 6686188  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharron G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng  
;; APPLICANT: SHANNON, Mark  
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
;; FILE REFERENCE: AEOICA-7  
;; CURRENT APPLICATION NUMBER: US/09/866,108A  
;; CURRENT FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aecomica Sequence Listing Engine  
;; Patent No. 6686188  
;; SEQ ID NO 933  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108A-933

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 359 AGGCTGAGCCC 369  
Db 6 AGGCTGAGCCC 16

RESULT 204  
US-09-866-108A-934  
;; Sequence 934, Application US/09866108A  
;; Patent No. 6686188  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharron G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng  
;; APPLICANT: SHANNON, Mark  
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 934  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-934

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369  
Db 5 AGGCTGAGCCC 15

RESULT 205  
US-09-866-108A-935  
; Sequence 935, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 935  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-936

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: PCT/US01/00668  
; CURRENT FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 935  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-935

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369  
Db 4 AGGCTGAGCCC 14

RESULT 206  
US-09-866-108A-936  
; Sequence 936, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 936  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-936

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369  
|||||  
Db 3 AGGCTGAGCCC 13

## RESULT 207

US-09-866-108A-937  
; Sequence 937, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AECOMICA-7

; CURRENT APPLICATION NUMBER: US/09/866,108A

; CURRENT FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aecomica Sequence Listing Engine

; Patent No. 6686188

; SEQ ID NO 937

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-866-108A-937

Query Match 1.8%; Score 11; DB 4; Length 17;

Best Local Similarity 100.0%; Pred.No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369

|||||

Db 2 AGGCTGAGCCC 12

## RESULT 208

US-09-866-108A-938

; Sequence 938, Application US/09866108A

; Patent No. 6686188

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang

; APPLICANT: PENN, Sharron G.

; APPLICANT: HANZEL, David K.

; APPLICANT: RANK, David R.

; APPLICANT: CHEN, Wensheng

; APPLICANT: SHANNON, Mark



;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; PRIOR FILING DATE: 2001-01-30  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aecomica Sequence Listing Engine  
;; Patent No. 6686188  
;; SEQ ID NO 1462  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108A-1462

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; 0; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGGG 492  
Db 7 CCTGGGAAGGG 17

RESULT 210  
US-09-866-108A-1463  
;; Sequence 1463, Application US/09866108A  
;; Patent No. 6686188  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharron G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng  
;; APPLICANT: SHANNON, Mark  
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
;; FILE REFERENCE: ACOMICA-7  
;; CURRENT APPLICATION NUMBER: US/09/866,108A  
;; CURRENT FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00685  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aecomica Sequence Listing Engine  
;; Patent No. 6686188  
;; SEQ ID NO 1463  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108A-1463

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 482 CCTGGGAAGGG 492  
Db 6 CCTGGGAAGGG 16

RESULT 211  
US-09-866-108A-1464  
;; Sequence 1464, Application US/09866108A  
;; Patent No. 6686188  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharron G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng  
;; APPLICANT: SHANNON, Mark  
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
;; FILE REFERENCE: ACOMICA-7  
;; CURRENT APPLICATION NUMBER: US/09/866,108A  
;; CURRENT FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: US 60/207,456  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
;; PRIOR FILING DATE: 2000-09-27  
;; PRIOR APPLICATION NUMBER: PCT/US01/00666  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00667  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00685  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00663  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 15755  
;; SOFTWARE: Aecomica Sequence Listing Engine  
;; Patent No. 6686188  
;; SEQ ID NO 1464  
;; LENGTH: 17  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-866-108A-1464

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 482 CCTGGGAAGGG 492  
Db 5 CCTGGGAAGGG 15

RESULT 212  
US-09-866-108A-1465  
;; Sequence 1465, Application US/09866108A  
;; Patent No. 6686188  
;; GENERAL INFORMATION:  
;; APPLICANT: GU, Yizhong  
;; APPLICANT: JI, Yonggang  
;; APPLICANT: PENN, Sharron G.  
;; APPLICANT: HANZEL, David K.  
;; APPLICANT: RANK, David R.  
;; APPLICANT: CHEN, Wensheng

```
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1465
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1465

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CTTGGGAAGGG 492
Db 4 CTTGGGAAGGG 14

RESULT 213
US-09-866-108A-1466
; Sequence 1466, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1465
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1465

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CTTGGGAAGGG 492
Db 4 CTTGGGAAGGG 14

RESULT 214
US-09-866-108A-1467
; Sequence 1467, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1467
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1466
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1466

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 482 CTTGGGAAGGG 492
Db 3 CTTGGGAAGGG 13

RESULT 214
US-09-866-108A-1467
; Sequence 1467, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1467

Query Match 1.8%; Score 11; DB 4; Length 17;
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Best Local Similarity 100.0%; Pred. No. 4e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGG 492  
Db 2 CCTGGGAAGG 12

RESULT 215

US-09-866-108A-1468  
; Sequence 1468, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15735  
; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 1468  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-1468

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGG 492  
Db 1 CCTGGGAAGG 11

RESULT 216

US-09-866-108A-7363  
; Sequence 7363, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15735  
; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 1468  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-1468

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 482 CCTGGGAAGG 492  
Db 1 CCTGGGAAGG 11

RESULT 217

US-09-866-108A-7370  
; Sequence 7370, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15735  
; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 1468  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-7363

APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 15735  
SOFTWARE: Aemica Sequence Listing Engine  
Patent No. 6686188  
SEQ ID NO 7363  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-866-108A-7363

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGT 509  
Db 7 GAAATTCAGT 17

RESULT 217

US-09-866-108A-7370  
; Sequence 7370, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15735  
; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 7363  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-7363

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04; Mismatches 0; Indels 0; Gaps 0;

Qy 499 GAAATTCAGT 509  
Db 7 GAAATTCAGT 17

RESULT 217

US-09-866-108A-7370  
; Sequence 7370, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15735  
; SOFTWARE: Aemica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 7363  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-7363

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 AAAATTCAGTT 510  
Db 1 AAAATTCAGTT 11

RESULT 218  
US-09-866-108A-9635/c  
; Sequence 9635, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 7370  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-7370

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 AAAATTCAGTT 510  
Db 1 AAAATTCAGTT 11

RESULT 218  
US-09-866-108A-9635/c  
; Sequence 9635, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 9635  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-9635

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188  
Db 17 CTCCTCTCCG 7

RESULT 219  
US-09-866-108A-9636/c  
; Sequence 9636, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 15755  
; SOFTWARE: Aecomica Sequence Listing Engine  
; Patent No. 6686188  
; SEQ ID NO 9636  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-866-108A-9636

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CTCCTCTCCG 188  
Db 16 CTCCTCTCCG 6

RESULT 220  
US-09-866-108A-9637/c  
; Sequence 9637, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.

```

; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9637
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9637

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCTCCG 188
Db 15 CTCCTCTCTCCG 5

RESULT 221
US-09-866-108A-9638/c
; Sequence 9638, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9637
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9637

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCTCCG 188
Db 15 CTCCTCTCTCCG 5

RESULT 221
US-09-866-108A-9638/c
; Sequence 9638, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; Remaining Prior Application data removed - See File Wrapper or PALM.

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9638
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9638

Query Match 1.8%; Score 11; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCTCCG 188
Db 14 CTCCTCTCTCCG 4

RESULT 222
US-09-866-108A-9639/c
; Sequence 9639, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9639
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9639

```

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCCG 188  
Db 13 CTCCTCTCCG 3

## RESULT 223

US-09-866-108A-9640/c  
; Sequence 9640, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.  
; APPLICANT: HANZEL, David K.  
; APPLICANT: RANK, David R.  
; APPLICANT: CHEN, Wensheng  
; APPLICANT: SHANNON, Mark  
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
; FILE REFERENCE: AEOMICA-7  
; CURRENT APPLICATION NUMBER: US/09/866,108A  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 15755

SOFTWARE: Aecomica Sequence Listing Engine

Patent No. 6686188

SEQ ID NO 9640

LENGTH: 17

TYPE: DNA

ORGANISM: Homo sapiens

US-09-866-108A-9640

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCCG 188  
Db 12 CTCCTCTCCG 2

## RESULT 224

US-09-866-108A-9641/c  
; Sequence 9641, Application US/09866108A  
; Patent No. 6686188  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: JI, Yonggang  
; APPLICANT: PENN, Sharron G.

APPLICANT: HANZEL, David K.  
APPLICANT: RANK, David R.  
APPLICANT: CHEN, Wensheng  
APPLICANT: SHANNON, Mark  
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE  
FILE REFERENCE: AEOMICA-7  
CURRENT APPLICATION NUMBER: US/09/866,108A  
CURRENT FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 15755

SOFTWARE: Aecomica Sequence Listing Engine

Patent No. 6686188

SEQ ID NO 9641

LENGTH: 17

TYPE: DNA

ORGANISM: Homo sapiens

US-09-866-108A-9641

Query Match 1.8%; Score 11; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 CTCCTCTCCG 188  
Db 11 CTCCTCTCCG 1

## RESULT 225

US-08-248-848-56/c  
; Sequence 56, Application US/08248848  
; Patent No. 5523217  
; GENERAL INFORMATION:  
; APPLICANT: Lupeki, James R.  
; APPLICANT: Versalovic, James  
; APPLICANT: Koeth, Thearith  
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using  
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification  
; Patent No. 5523217  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/248,848

;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/781,424  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Paul, Thomas D.  
;; REGISTRATION NUMBER: 32,714  
;; REFERENCE/DOCKET NUMBER: D-5394  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 713/651-5325  
;; TELEFAX: 713/651-5246  
;; TELEX: 762829  
;; INFORMATION FOR SEQ ID NO: 56:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 18 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: YES  
US-08-248-848-56

Query Match 1.8%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 CGGACTGGGAC 207  
DB 17 CGGACTGGGAC 7

RESULT 226  
US-08-248-848-57  
; Sequence 57, Application US/08248848  
; Patent No. 5523217  
; GENERAL INFORMATION:  
; APPLICANT: Lupski, James R.  
; APPLICANT: Versalovic, James  
; APPLICANT: Koeuth, Thearith  
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using  
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification  
; Patent No. 5523217  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/248,848  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/781,424  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5394  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713/651-5325  
; TELEFAX: 713/651-5246  
; TELEX: 762829  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: YES  
US-08-248-848-57

Query Match 1.8%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 CGGACTGGGAC 207  
DB 2 CGGACTGGGAC 12

RESULT 227  
US-08-050-073-190/c  
; Sequence 190, Application US/08050073  
; Patent No. 5567809  
; GENERAL INFORMATION:  
; APPLICANT: Apple, Raymond J.  
; APPLICANT: Begovich, Ann B.  
; APPLICANT: Bugawan, Teodorica L.  
; APPLICANT: Erlich, Henry A.  
; APPLICANT: Griffith, Robert L.  
; APPLICANT: Schaff, Stephen J.  
; TITLE OF INVENTION: Methods and Reagents for HLA DRBeta DNA  
; TITLE OF INVENTION: Typing  
; NUMBER OF SEQUENCES: 315  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,073  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Petry, Douglas A.  
; REGISTRATION NUMBER: 35,321  
; REFERENCE/DOCKET NUMBER: 8769  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2974  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 190:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
US-08-050-073-190

Query Match 1.8%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCTGGGAC 254  
DB 17 ACCTCTGGGAC 7

RESULT 228

US-08-480-547A-18/c  
; Sequence 18, Application US/08480547A  
; Patent No. 5652131  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Corbin, Jackie D.  
; APPLICANT: Ferguson, Kenneth M.  
; APPLICANT: Francis, Sharon H.  
; APPLICANT: Kadacek, Ann  
; APPLICANT: Loughney, Kate  
; APPLICANT: McAllister-Lucas, Linda M.  
; APPLICANT: Sonnenburg, William K.  
; APPLICANT: Thomas, Melissa K.  
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific  
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Marchall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,547A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5652131and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32791  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-480-547A-18  
Query Match 1.8%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 317 TCAGGATCTTC 327  
DB 15 TCAGGATCTTC 5  
RESULT 229  
US-08-111-077-56/c  
; Sequence 56, Application US/08111077  
; Patent No. 5691136  
; GENERAL INFORMATION:  
; APPLICANT: Lupski, James R.  
; APPLICANT: Versalovic, James  
; APPLICANT: Koeuth, Thearith  
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using  
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/111,077  
; FILING DATE: 19930824  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5394  
; TELECOMMUNICATION INFORMATION:

CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77010-3095  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/111,077  
FILING DATE: 19930824  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul, Thomas D.  
REGISTRATION NUMBER: 32,714  
REFERENCE/DOCKET NUMBER: D-5394  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713/651-5325  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: YES  
US-08-111-077-56  
Query Match 1.8%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 197 CGGACTGGGAC 207  
DB 17 CGGACTGGGAC 7  
RESULT 230  
US-08-111-077-57  
; Sequence 57, Application US/08111077  
; Patent No. 5691136  
; GENERAL INFORMATION:  
; APPLICANT: Lupski, James R.  
; APPLICANT: Versalovic, James  
; APPLICANT: Koeuth, Thearith  
; TITLE OF INVENTION: Fingerprinting Bacterial Strains Using  
; TITLE OF INVENTION: Repetitive DNA Sequence Amplification  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Fulbright & Jaworski  
; STREET: 1301 McKinney, Suite 5100  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77010-3095  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/111,077  
; FILING DATE: 19930824  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul, Thomas D.  
; REGISTRATION NUMBER: 32,714  
; REFERENCE/DOCKET NUMBER: D-5394  
; TELECOMMUNICATION INFORMATION:



Fri Mar 5 09:50:05 2004

TELEPHONE: 713/651-5325  
TELEFAX: 713/651-5246  
TELEX: 762829  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: YES  
US-08-111-077-57

Query Match 1.8%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 CGGACTGGGAC 207  
Db 2 CGGACTGGGAC 12

RESULT 231  
US-08-250-847B-18/c  
; Sequence 18, Application US/08250847B  
; Patent No. 5702936  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Corbin, Jackie D.  
; APPLICANT: Ferguson, Kenneth M.  
; APPLICANT: Francis, Sharron H.  
; APPLICANT: Kadlecck, Ann  
; APPLICANT: Loughney, Kate  
; APPLICANT: McAllister-Lucas, Linda M.  
; APPLICANT: Sonnenburg, William K.  
; APPLICANT: Thomas, Melissa K.  
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific  
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/250,847B  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/068,051  
FILING DATE: 27-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5702936and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32083  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA

US-08-250-847B-18

Query Match 1.8%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTC 327  
Db 15 TGAGGATCTTC 5

RESULT 232  
US-08-363-240A-1234/c  
; Sequence 1234, Application US/08363240A  
; Patent No. 5705388  
; GENERAL INFORMATION:  
; APPLICANT: Couture, Larry  
; APPLICANT: McSwiggen, James  
; APPLICANT: Bisgaler, Charles  
; APPLICANT: Pape, Michael  
; TITLE OF INVENTION: METHOD AND REAGENT FOR  
; TITLE OF INVENTION: PREVENTION, INHIBITION OF  
; TITLE OF INVENTION: PROGRESSION AND REGRESSION  
; TITLE OF INVENTION: OF VASCULAR DISEASES  
; NUMBER OF SEQUENCES: 1243  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,240A  
FILING DATE: December 23, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 210/096  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 1234:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-240A-1234

Query Match 1.8%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 ACCTCAGTCTG 318  
Db 16 ACCTCAGTCTG 6

RESULT 233  
US-08-465-095-3/c  
; Sequence 9, Application US/08465095

Patent No. 5949534  
GENERAL INFORMATION:  
APPLICANT: Grotendorst, Gary R.  
APPLICANT: Iida, Naoka  
TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,095  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/179,656  
FILING DATE: 07-JAN-1994  
APPLICATION NUMBER: 08/001,177  
FILING DATE: 07-JAN-1993  
APPLICATION NUMBER: 07/472,377  
FILING DATE: 01-FEB-1990

ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth A. Hanley  
REGISTRATION NUMBER: 33,505  
REFERENCE/DOCKET NUMBER: GZI-003C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-465-095-9

Query Match 1.8%; Score 11; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TGAAGAAGACTT 475  
DB 15 TGAAGAAGACTT 5

RESULT 234  
US-09-205-922-30/c  
Sequence 30, Application US/09205922  
Patent No. 5951455  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-11 EXPRESSION  
FILE REFERENCE: RTS-0030  
CURRENT APPLICATION NUMBER: US/09/205,922  
CURRENT FILING DATE: 1998-12-04  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 30

LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide  
US-09-205-922-30

Query Match 1.8%; Score 11; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ATCTTCACGCGC 332  
DB 13 ATCTTCACGCGC 3

RESULT 235  
US-09-205-922-62  
Sequence 62, Application US/09205922  
Patent No. 5951455  
GENERAL INFORMATION:  
APPLICANT: Lex M. Cowsett  
TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-11 EXPRESSION  
FILE REFERENCE: RTS-0030  
CURRENT APPLICATION NUMBER: US/09/205,922  
CURRENT FILING DATE: 1998-12-04  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 62

LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-205-922-62

Query Match 1.8%; Score 11; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTTCTCTCCGCT 190  
DB 7 CTTCTCTCCGCT 17

RESULT 236  
US-08-463-949A-18/c  
Sequence 18, Application US/08463949A  
Patent No. 5955583  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Corbin, Jackie D.  
APPLICANT: Ferguson, Kenneth M.  
APPLICANT: Francis, Sharron H.  
APPLICANT: Kadlecsek, Ann  
APPLICANT: Loughney, Kate  
APPLICANT: McAllister-Lucas, Linda M.  
APPLICANT: Sonnenburg, William K.  
APPLICANT: Thomas, Melissa K.

TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific  
TITLE OF INVENTION: Phosphodiesterase Materials and Methods  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,949A  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/068,051  
FILING DATE: 27-MAY-1993

ATTORNEY/AGENT INFORMATION:  
NAME: No. 595583and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32706  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-463-949A-18

Query Match 1.8%; Score 11; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTC 327  
Db 15 TGAGGATCTTC 5

## RESULT 237

US-08-928-692-41  
Sequence 41, Application US/08928692  
Patent No. 5958727  
GENERAL INFORMATION:

APPLICANT: Brody, Howard  
APPLICANT: Yaver, Deborah S.  
APPLICANT: Lamsa, Michael  
APPLICANT: Hansen, Kim  
TITLE OF INVENTION: Methods for Modifying the Production of  
TITLE OF INVENTION: a Polypeptide  
NUMBER OF SEQUENCES: 80  
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.  
STREET: 405 Lexington Avenue  
CITY: New York  
STATE: NY

COUNTRY: USA  
ZIP: 10174

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,692

FILING DATE: 12-SEPT-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 4944.200-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-928-692-41

Query Match 1.8%; Score 11; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 GGATCTTCACC 330  
Db 1 GGATCTTCACC 11

## RESULT 238

US-09-156-979-44/c

Sequence 44, Application US/09156979

Patent No. 5962672

GENERAL INFORMATION:

APPLICANT: Cowsett, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF RHOB EXPRESSION

FILE REFERENCE: RTS-0013

CURRENT APPLICATION NUMBER: US/09/156,979

CURRENT FILING DATE: 1998-09-18

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 44

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-156-979-44

## Query Match

1.8%; Score 11; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGCTGC 165  
Db 14 AGAACGGCTGC 4

## RESULT 239

US-09-156-979-45/c

Sequence 45, Application US/09156979

Patent No. 5962672

GENERAL INFORMATION:

APPLICANT: Cowsett, Lex M.

TITLE OF INVENTION: ANTISENSE MODULATION OF RHOB EXPRESSION

FILE REFERENCE: RTS-0013

CURRENT APPLICATION NUMBER: US/09/156,979

CURRENT FILING DATE: 1998-09-18

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 45

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide

US-09-156-979-45

## Query Match

1.8%; Score 11; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 4e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGAACGGCTGC 165  
Db 17 AGAACGGCTGC 7

## RESULT 240

US-09-256-496-15

Sequence 15, Application US/09256496

Patent No. 5998206

GENERAL INFORMATION:

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF G-APLHA-12 EXPRESSION

FILE REFERENCE: RTS-0056

CURRENT APPLICATION NUMBER: US/09/256,496

CURRENT FILING DATE: 1999-02-23

NUMBER OF SEQ ID NOS: 86

SEQ ID NO 15

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-256-496-15

Query Match          1.8%; Score 11; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCAC 329
      |||||
Db 8 AGGATCTTCAC 18

RESULT 241
US-09-255-893-40/c
; Sequence 40, Application US/09255893A
; Patent No. 6008344
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2 GROUP IV EXPRESSION
; FILE REFERENCE: RTS-0055
; CURRENT APPLICATION NUMBER: US/09/255,893A
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-893-40

Query Match          1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 GGAAGGGCTG 495
      |||||
Db 17 GGAAGGGCTG 7

RESULT 242
US-09-358-381-16
; Sequence 16, Application US/09358381
; Patent No. 6020199
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
; FILE REFERENCE: RTS-0079
; CURRENT APPLICATION NUMBER: US/09/358,381
; CURRENT FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-358-381-16

Query Match          1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GAACGGCTGCC 166
      |||||
Db 6 GAACGGCTGCC 16
```

```
RESULT 243
US-08-464-410A-18/c
; Sequence 18, Application US/08464410A
; Patent No. 6037119
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Corbin, Jackie D.
; APPLICANT: Ferguson, Kenneth M.
; APPLICANT: Francis, Sharron H.
; APPLICANT: Kadlecik, Ann
; APPLICANT: Loughney, Kate
; APPLICANT: McAllister-Lucas, Linda M.
; APPLICANT: Sonnenburg, William K.
; APPLICANT: Thomas, Melissa K.
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,410A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037119and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32705
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-464-410A-18

Query Match          1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGGATCTTC 327
      |||||
Db 15 TGAGGATCTTC 5

RESULT 244
US-09-255-912-9
; Sequence 9, Application US/09255912
; Patent No. 6037142
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTS-0044
; CURRENT APPLICATION NUMBER: US/09/255,912
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 9
```

```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-912-9

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 ACAGCCTCTTG 15
        |||||
Db       3 ACAGCCTCTTG 13

RESULT 245
US-08-180-470-44
; Sequence 44, Application US/08180470
; Patent No. 6045994
; GENERAL INFORMATION:
; APPLICANT: ZABEAU, Marc
; APPLICANT: VOS, Pieter
; TITLE OF INVENTION: SELECTIVE RESTRICTION FRAGMENT
; TITLE OF INVENTION: AMPLIFICATION: A GENERAL METHOD FOR DNA
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swacker & Mathis
; STREET: The George Mason Bldg., Washington & Prince
; STREET: Sts.
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/180,470
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/950,011
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-180-470-44

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      36 TTACCAATTC 46
        |||||
Db       6 TTACCAATTC 16

RESULT 246
US-09-143-212-9

; Sequence 9, Application US/09143212B
; Patent No. 6077672
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia and Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRADD EXPRESSION
; FILE REFERENCE: RFS-0005
; CURRENT APPLICATION NUMBER: US/09/143,212B
; CURRENT FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-143-212-9

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      242 TCACCTCCTGG 252
        |||||
Db       2 TCACCTCCTGG 12

RESULT 247
US-09-289-466-72/c
; Sequence 72, Application US/09289466A
; Patent No. 6124272
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PDK-1 EXPRESSION
; FILE REFERENCE: RFS-0060
; CURRENT APPLICATION NUMBER: US/09/289,466A
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 72
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-289-466-72

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      451 TTTGTAGAAAA 461
        |||||
Db       12 TTTGTAGAAAA 2

RESULT 248
US-09-213-719-87
; Sequence 87, Application US/09213719B
; Patent No. 6150162
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF CD44 EXPRESSION
; FILE REFERENCE: RFS-0006
; CURRENT APPLICATION NUMBER: US/09/213,719B
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 87
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

US-09-213-719-87

Query Match 1.8%; Score 11; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 CCACCTCAGT 315  
DB 1 CCACCTCAGT 11

RESULT 249

US-09-156-856-7  
Sequence 7, Application US/09156856A  
Patent No. 6221591

GENERAL INFORMATION:  
APPLICANT: Aerts, Johannes M.

TITLE OF INVENTION: Determination of a genetic risk factor for infection  
TITLE OF INVENTION: and other diseases, and detection of activated  
TITLE OF INVENTION: phagocytes  
FILE REFERENCE: Sequence 1-20  
Patent No. 6221591

CURRENT APPLICATION NUMBER: US/09/156,856A  
CURRENT FILING DATE: 1998-09-18  
NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7

LENGTH: 18  
TYPE: DNA

ORGANISM: Homo sapiens

US-09-156-856-7

Query Match 1.8%; Score 11; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GCAAGCTGAG 366  
DB 5 GCAAGCTGAG 15

RESULT 250

US-09-038-637-141  
Sequence 141, Application US/09038637  
Patent No. 6235470

GENERAL INFORMATION:  
APPLICANT: Sidransky, David

TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA  
NUMBER OF SEQUENCES: 195  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/038,637

FILING DATE: 10-MAR-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/579,233

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/152,313

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/146001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 141:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

US-09-038-637-141

Query Match 1.8%; Score 11; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CGCTGGGCTAA 65  
DB 2 CGCTGGGCTAA 12

RESULT 251

US-09-338-907-414/c

Sequence 414, Application US/09338907

Patent No. 6265546

GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel

APPLICANT: Blumenfeld, Marta

APPLICANT: Ilya, Chumakov

APPLICANT: Bougueret, Lydie

TITLE OF INVENTION: PROSTATE CANCER GENE

FILE REFERENCE: GENSET.18CF1CP

CURRENT APPLICATION NUMBER: US/09/338,907

CURRENT FILING DATE: 1999-06-23

EARLIER APPLICATION NUMBER: 08/996,306

EARLIER FILING DATE: 1997-12-22

EARLIER APPLICATION NUMBER: 60/099,658

EARLIER FILING DATE: 1998-09-09

EARLIER APPLICATION NUMBER: 09/218,207

EARLIER FILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 578

SOFTWARE: Patent.pm

SEQ ID NO 414

LENGTH: 18

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: 1..18

OTHER INFORMATION: downstream amplification primer for SEQ 250, SEQ 327

US-09-338-907-414

Query Match 1.8%; Score 11; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GTTTCCTTACC 40  
DB 18 GTTTCCTTACC 8

RESULT 252

US-09-630-706-33/c

Sequence 33, Application US/09630706

Patent No. 6277640

GENERAL INFORMATION:  
APPLICANT: C. Frank Bennett

APPLICANT: Lex M. Cowsett

TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION

FILE REFERENCE: RTS-0053

CURRENT APPLICATION NUMBER: US/09/630,706

CURRENT FILING DATE: 2000-08-01

NUMBER OF SEQ ID NOS: 94

```
; SEQ ID NO 33
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-630-706-33

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACAGCCTCTTG 15
Db 17 ACAGCCTCTTG 7

RESULT 253
US-09-577-902-16
; Sequence 16, Application US/09577902
; Patent No. 6284538
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowseert
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
; FILE REFERENCE: ISPH-0463
; CURRENT APPLICATION NUMBER: US/09/577,902
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/358,381
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US99/29594,
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-577-902-16

Query Match      1.8%; Score 11; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GAACGCTGCC 166
Db 6 GAACGCTGCC 16

RESULT 254
US-09-339-972-41
; Sequence 41, Application US/09339972
; Patent No. 6323002
; GENERAL INFORMATION:
; APPLICANT: Brody, Howard
; APPLICANT: Brody, Deborah S.
; APPLICANT: Yaver, Michael
; APPLICANT: Lamsa, Michael
; APPLICANT: Hansen, Kim
; TITLE OF INVENTION: Methods for Modifying the Production of
; TITLE OF INVENTION: a Polypeptide
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6323002disk of No. 6323002th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
```

```
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,972
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/928,692
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4944.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-339-972-41

Query Match      1.8%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 320 GGATCTTACC 330
Db 1 GGATCTTACC 11

RESULT 255
US-09-218-207-414/c
; Sequence 414, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CP1
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 414
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer for SEQ 250, SEQ 327
US-09-218-207-414

Query Match      1.8%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GTTCTTTACC 40
Db 18 GTTCTTTACC 8

RESULT 256
US-08-584-040-8335
```

; Sequence 8335, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TITLE OF INVENTION: TREATMENT OF DISEASES OR  
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,040  
; FILING DATE: January 11, 1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/005,974  
; FILING DATE: October 26, 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 218/064  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 8335:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-584-040-8335

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 90.9%; Pred. No. 4e+04;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 156 GACGGCTGCC 166  
Db 3 GACGGCTGCC 13

RESULT 257  
US-08-679-645-1167/c  
; Sequence 1167, Application US/08679645  
; Patent No. 6350934  
; GENERAL INFORMATION:  
; APPLICANT: Zwick, Michael G.  
; APPLICANT: Edington, Brent E.  
; APPLICANT: McSwiggen, James A.  
; APPLICANT: Merlo, Patricia Ann Owens  
; APPLICANT: Guo, Lining  
; APPLICANT: Skokut, Thomas A.  
; APPLICANT: Young, Scott A.  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Merlo, Donald J.

; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1263  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/679,645  
; FILING DATE: July 12, 1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/001,135  
; FILING DATE: July 13, 1995  
; APPLICATION NUMBER: 08/300,726  
; FILING DATE: September 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 219/247  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1167:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-679-645-1167

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 375 GCTGCGCGGC 385  
Db 18 GCTGCGCGGC 8

RESULT 258  
US-08-679-645-1169/c  
; Sequence 1169, Application US/08679645  
; Patent No. 6350934  
; GENERAL INFORMATION:  
; APPLICANT: Zwick, Michael G.  
; APPLICANT: Edington, Brent E.  
; APPLICANT: McSwiggen, James A.  
; APPLICANT: Merlo, Patricia Ann Owens  
; APPLICANT: Guo, Lining  
; APPLICANT: Skokut, Thomas A.  
; APPLICANT: Young, Scott A.  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Merlo, Donald J.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION  
; TITLE OF INVENTION: IN PLANTS  
; NUMBER OF SEQUENCES: 1263  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street



STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/679,645  
FILING DATE: July 12, 1996  
CLASSIFICATION: 80C  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/001,135  
FILING DATE: July 13, 1995  
APPLICATION NUMBER: 08/300,726  
FILING DATE: September 2, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 219/247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1169:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-679-645-1169

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 375 GCTGCGCGCGC 385  
DB 15 GCTGCGCGCGC 5

RESULT 259  
US-09-167-109-145/c  
; Sequence 145, Application US/09167109  
; Patent No. 6399297  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: Cowsett, Lex M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Xu, Xiaoming S.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION  
; FILE REFERENCE: ISPH-0321  
; CURRENT APPLICATION NUMBER: US/09/167,109  
; CURRENT FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 228  
; SEQ ID NO 145  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-167-109-145

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 CTTTGGTTATC 145  
DB 135 CTTTGGTTATC 145

DB 11 CTTTGGTTATC 1

RESULT 260  
US-09-167-109-163  
; Sequence 163, Application US/09167109  
; Patent No. 6399297  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: Cowsett, Lex M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Xu, Xiaoming S.  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION  
; FILE REFERENCE: ISPH-0321  
; CURRENT APPLICATION NUMBER: US/09/167,109  
; CURRENT FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 228  
; SEQ ID NO 163  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
US-09-167-109-163

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AAGTTTCTTTA 38  
DB 7 AAGTTTCTTTA 17

RESULT 261  
US-09-387-341-105/c  
; Sequence 105, Application US/09387341  
; Patent No. 6410323  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, M. Luisa  
; APPLICANT: Cowsett, Lex M.  
; TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene  
; FILE REFERENCE: ISPH-0404  
; CURRENT APPLICATION NUMBER: US/09/387,341  
; CURRENT FILING DATE: 1999-08-31  
; EARLIER APPLICATION NUMBER: 09/156,424  
; EARLIER FILING DATE: 1998-09-18  
; EARLIER APPLICATION NUMBER: 09/156,979  
; EARLIER FILING DATE: 1998-09-18  
; EARLIER APPLICATION NUMBER: 09/156,807  
; EARLIER FILING DATE: 1998-09-18  
; EARLIER APPLICATION NUMBER: 09/161,015  
; EARLIER FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 233  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 105  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-387-341-105

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGACGGCTGC 165  
DB 14 AGACGGCTGC 4

## RESULT 262

US-09-387-341-106/c  
; Sequence 106, Application US/09387341  
; Patent No. 6410323  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, M. Luisa  
; APPLICANT: Cowbert, Lex M.  
; TITLE OF INVENTION: Antisense Modulation of Human Rho Family Gene  
; FILE REFERENCE: Expression  
; CURRENT FILING DATE: 1998-09-18  
; EARLIER APPLICATION NUMBER: US/09/387,341  
; CURRENT FILING DATE: 1999-08-31  
; EARLIER APPLICATION NUMBER: 09/156,424  
; EARLIER FILING DATE: 1998-09-18  
; EARLIER APPLICATION NUMBER: 09/156,979  
; EARLIER FILING DATE: 1998-09-18  
; EARLIER APPLICATION NUMBER: 09/156,807  
; EARLIER FILING DATE: 1998-09-18  
; EARLIER APPLICATION NUMBER: 09/161,015  
; EARLIER FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 233  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 106  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-387-341-106

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 155 AGACGGCTGC 165

Db 17 AGACGGCTGC 7

## RESULT 263

US-09-394-455-16/c  
; Sequence 16, Application US/09394455  
; Patent No. 6531305  
; GENERAL INFORMATION:  
; APPLICANT: Witman, George F.  
; APPLICANT: San Agustin, Jovenal  
; APPLICANT: Leszyk, John D.  
; TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING  
; FILE REFERENCE: NUCLEIC ACIDS, AND METHODS OF USE  
; CURRENT FILING DATE: 1999-09-10  
; EARLIER APPLICATION NUMBER: US/09/394,455  
; PRIOR FILING DATE: 1999-09-10  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Ovine  
US-09-394-455-16

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAACT 311

Db 14 AACCCCAACT 4

## RESULT 264

US-09-422-978-8311/c

; Sequence 8311, Application US/09422978  
; Patent No. 6537751  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT FILING DATE: 1999-10-20  
; EARLIER APPLICATION NUMBER: US/09/422,978  
; EARLIER FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 09/298,850  
; EARLIER FILING DATE: 1998-11-23  
; EARLIER APPLICATION NUMBER: US 60/109,732  
; EARLIER FILING DATE: 1998-04-21  
; EARLIER APPLICATION NUMBER: US 60/082,614  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 8311  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..18  
; OTHER INFORMATION: downstream amplification primer 99-1480 for SEQ 446, in complen  
US-09-422-978-8311

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GTTCTTTACC 40

Db 18 GTTCTTTACC 8

## RESULT 265

US-09-371-772B-3991  
; Sequence 3991, Application US/09371772B  
; Patent No. 6566127  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyne Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions  
; FILE REFERENCE: Levels of Vascular Endothelial Growth Factor Receptor  
; CURRENT FILING DATE: 1999-08-10  
; EARLIER APPLICATION NUMBER: US/09/371,772B  
; PRIOR FILING DATE: 1999-08-10  
; EARLIER APPLICATION NUMBER: US 60/005,974  
; PRIOR FILING DATE: 1995-10-26  
; PRIOR APPLICATION NUMBER: US 08/584,040  
; NUMBER OF SEQ ID NOS: 14225  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3991  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Mus sp.  
US-09-371-772B-3991

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 90.9%; Pred. No. 4e+04;  
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 156 GAACGGCTGC 166

Db 3 GAACGGCTGC 13

## RESULT 266

US-08-179-656A-9/c  
; Sequence 9, Application US/08179656A  
; Patent No. 6673893  
; GENERAL INFORMATION:  
; APPLICANT: Grotendorst, Gary R.  
; APPLICANT: Iida, Naoka  
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/179,656A  
; FILING DATE: 07-JAN-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/001,177  
; FILING DATE: 07-JAN-1993  
; APPLICATION NUMBER: 07/472,377  
; FILING DATE: 01-FEB-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: GZI-003C2  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-179-656A-9

Query Match 1.8%; Score 11; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TGAAGAAGACTT 475  
Db 15 TGAAGAAGACTT 5

RESULT 267  
PCT-US94-00300-9/c  
; Sequence 9, Application PC/TUS9400300  
; GENERAL INFORMATION:  
; APPLICANT: Grotendorst, Gary R.  
; APPLICANT: Iida, Naoka  
; TITLE OF INVENTION: LEUKOCYTE DERIVED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/00300  
; FILING DATE: 07-JAN-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/001,177  
; FILING DATE: 07-JAN-1993  
; APPLICATION NUMBER: 07/472,377  
; FILING DATE: 01-FEB-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: GZI-003C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
PCT-US94-00300-9

Query Match 1.8%; Score 11; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04; Indels 0; Gaps 0;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TGAAGAAGACTT 475  
Db 15 TGAAGAAGACTT 5

RESULT 268  
PCT-US94-06066-18/c  
; Sequence 18, Application PC/TUS9406066  
; GENERAL INFORMATION:  
; APPLICANT: The Board of Regents of the University of Washington  
; TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific  
; TITLE OF INVENTION: Phosphodiesterase Materials and Methods  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/06066  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/068,051  
; FILING DATE: 27-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Noland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32083  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 474-6300  
; TELEFAX: (312) 474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
PCT-US94-06066-18

Query Match 1.8%; Score 11; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TCAGGATCTTC 327  
DB 15 TCAGGATCTTC 5

## RESULT 269

US-08-271-942A-89  
; Sequence 89, Application US/08271942A  
; Patent No. 5550020  
; GENERAL INFORMATION:  
; APPLICANT: Gallie, Brenda L.  
; APPLICANT: Dunn, James M.  
; APPLICANT: Stevens, John K.  
; TITLE OF INVENTION: Method, reagents and kit for diagnosis  
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma  
; NUMBER OF SEQUENCES: 123  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Oppedahl & Larson  
; STREET: 1992 Commerce Street, Suite 309  
; CITY: Yorktown Heights  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10598-4412

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS 5.0  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/271,942A  
FILING DATE: 08-JUL-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Marina T. Larson  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN.P-003-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (914) 245-3252  
TELEFAX: (914) 962-4330  
TELEX:

## INFORMATION FOR SEQ ID NO: 89:

SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: human  
FEATURE:  
NAME/KEY: primer for exon 8 of human Rb1 gene

US-08-271-942A-89

Query Match 1.8%; Score 11; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AGATTATTTT 435  
DB 9 AGATTATTTT 19

## RESULT 270

US-08-474-177-6  
; Sequence 6, Application US/08474177  
; Patent No. 5624819  
; GENERAL INFORMATION:  
; APPLICANT: Skolnick, Mark H.  
; APPLICANT: Cannon-Albright, Lisa A.  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,177  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03537  
FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

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APPLICATION NUMBER: US 08/251,938

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APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938

Qy 20 ACCGAGGAG 30  
 Db 5 ACCGAGGAG 15

RESULT 271  
 US-08-487-033-6  
 ; Sequence 6, Application US/08487033  
 ; Patent No. 5739027  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kamb, Alexander  
 ; TITLE OF INVENTION: MTS1-Beta GENE  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
 ; STREET: 1201 New York Avenue, Suite 1000  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/487,033  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/03316  
 ; FILING DATE: 17-MAR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/251,938  
 ; FILING DATE: 01-JUN-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/215,087  
 ; FILING DATE: 18-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/215,086  
 ; FILING DATE: 18-MAR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/227,369  
 ; FILING DATE: 14-APR-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/214,582  
 ; FILING DATE: 18-MAR-1994  
 ; NAME: Innen, Jeffrey L.  
 ; ATTORNEY/AGENT INFORMATION:  
 ; REGISTRATION NUMBER: 28,957  
 ; REFERENCE/DOCKET NUMBER: 24884-109348-C  
 ; TELEPHONE: 202-962-4810  
 ; TELEFAX: 202-962-8300  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 19 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; US-08-487-033-6

Query Match 1.8%; Score 11; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ACCGAGGAG 30

Db 5 ACCGAGGAG 15

RESULT 272  
 US-08-431-896B-6  
 ; Sequence 6, Application US/08431896B  
 ; Patent No. 5773244  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ares, Manuel, Jr.  
 ; APPLICANT: Ford, Ethan E.  
 ; TITLE OF INVENTION: RNA Cyclase Ribozymes  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/431,896B  
 ; FILING DATE: 01-MAY-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/063,857  
 ; FILING DATE: 19-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Weber, Kenneth A.  
 ; REGISTRATION NUMBER: 31,677  
 ; REFERENCE/DOCKET NUMBER: 02307E-070000US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 576-0200  
 ; TELEFAX: (415) 576-0300  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 19 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-431-896B-6

Query Match 1.8%; Score 11; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 4e+04;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 403 CAAATAGCCAT 413  
 Db 6 CAAATAGCCAT 16

RESULT 273  
 US-08-480-810-6  
 ; Sequence 6, Application US/08480810  
 ; Patent No. 580236  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kamb, Alexander  
 ; TITLE OF INVENTION: MTS1 GENE  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
 ; STREET: 1201 New York Avenue, Suite 1000  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:



APPLICATION NUMBER: 08/246,985  
FILING DATE: 20-MAY-1994  
APPLICATION NUMBER: US 025,396  
FILING DATE: 24-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/922,493  
FILING DATE: 30-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Fabian, Gary R.  
REGISTRATION NUMBER: 33,875  
REFERENCE/DOCKET NUMBER: 4600-0201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: Primer 11F (JF)  
US-08-611-757-34

Query Match 1.8%; Score 11; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CTCCTGGAGCC 256  
Db 9 CTCCTGGAGCC 19

RESULT 276  
US-08-848-251-6  
Sequence 6, Application US/08848251  
Patent No. 5989815  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Cannon-Albright, Lisa A.  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND  
METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS  
TITLE OF INVENTION: GENE  
TITLE OF INVENTION: 36  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/848,251  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/474,083  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: PCI/US95/03537  
FILING DATE: 17-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/251,938  
FILING DATE: 01-JUN-1994  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/215,086  
FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348-G  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-848-251-6

Query Match 1.8%; Score 11; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ACCGGAGGAAG 30  
Db 5 ACCGGAGGAAG 15

RESULT 277  
US-08-874-186-3/c  
Sequence 3, Application US/08874186  
Patent No. 5989885  
GENERAL INFORMATION:  
APPLICANT: Teng, David H-F.  
APPLICANT: Tavtigian, Sean V.  
APPLICANT: Perry III, William L.  
APPLICANT: Skolnick, Mark H.  
TITLE OF INVENTION: SPECIFIC MUTATIONS OF MAP KINASE KINASE  
IN HUMAN TUMOR CELL LINES IDENTIFY IT AS A TUMOR  
SUPPRESSOR IN VARIOUS TYPES OF CANCER  
TITLE OF INVENTION: 4 (MKK4)  
TITLE OF INVENTION: SUPPRESSOR  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/874,186  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/782,482  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:

NAME: Saxe, Stephen A.  
REGISTRATION NUMBER: 38,609  
REFERENCE/DOCKET NUMBER: 24884-121392-01  
TELEPHONE: 202-962-4848  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "Primer for STS."  
US-08-874-186-3

Query Match 1.8%; Score 11; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 TTGCAATAAG 156  
DB 12 TTGCAATAAG 2

RESULT 278  
US-08-538-711A-18/c  
Sequence 18, Application US/08538711A  
Patent No. 5994062  
GENERAL INFORMATION:  
APPLICANT: MULSHINE, JAMES, L.  
TITLE OF INVENTION: AN EPITHELIAL PROTEIN AND  
TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154

COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/538,711A  
FILING DATE: 02-OCT-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KATHRYN M. BROWN

REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4201  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19  
TYPE: nucleic acid  
STRANDEDNESS: Unknown  
TOPOLOGY: Linear  
MOLECULE TYPE: other nucleic acid  
US-08-538-711A-18

Query Match 1.8%; Score 11; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 552 TGAGTTTGATG 562  
DB 17 TGAGTTTGATG 7

## RESULT 279

US-08-743-637B-85/c  
Sequence 85, Application US/08743637B  
Patent No. 5994066  
GENERAL INFORMATION:  
APPLICANT: BERGERON, Michel G.  
APPLICANT: PICARD, Francois J.  
APPLICANT: OUELLETTE, Marc  
APPLICANT: ROY, Paul H.  
TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA  
TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND  
TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED  
TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: QUARLES & BRADY  
STREET: 411 EAST WISCONSIN AVENUE  
CITY: MILWAUKEE  
STATE: WISCONSIN  
COUNTRY: USA  
ZIP: 53202-4497

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/743,637B  
FILING DATE: 04-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/526,840  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BAKER, Jean C.

REGISTRATION NUMBER: 35,433  
REFERENCE/DOCKET NUMBER: 850586.90012  
TELEPHONE: (414) 277-5000  
TELEFAX: (414) 277-5591  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Pseudomonas aeruginosa

US-08-743-637B-85  
Query Match 1.8%; Score 11; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCTTGATGAAC 21  
DB 16 TCTTGATGAAC 6

## RESULT 280

US-08-486-047-6  
Sequence 6, Application US/08486047  
Patent No. 5994095  
GENERAL INFORMATION:  
APPLICANT: Kamb, Alexander  
TITLE OF INVENTION: MTS2 GENE  
NUMBER OF SEQUENCES: 36



```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
; US-08-486-047-6

```

```

Query Match 1.8%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 20 ACCGGAGGAG 30
Db 5 ACCGGAGGAG 15

```

```

RESULT 281
US-08-526-840B-85/c
; Sequence 85, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; ADDRESSEE: OUELLETTE, Marc
; APPLICATION NUMBER: ROY, Paul H.
; FILING DATE:
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY

```

```

;
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OUELLETTE, Marc
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
;
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Pseudomonas aeruginosa
;
; US-08-526-840B-85

```

```

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 11 TCTTGATGAAC 21
Db 16 TCTTGATGAAC 6

```

```

RESULT 282
US-09-120-130-6
; Sequence 6, Application US/09120130
; Patent No. 6037462
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,130
; FILING DATE:
; CLASSIFICATION:

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,810
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Homo sapiens
;
US-09-120-130-6

```

```

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 20 ACCGGAGGAAG 30
   |||||
Db 5 ACCGGAGGAAG 15

```

```

RESULT 283
US-09-115-252-6
; Sequence 6, Application US/09115252
; Patent No. 6060301
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/115,252
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,810

```

```

; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Homo sapiens
;
US-09-115-252-6

```

```

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 20 ACCGGAGGAAG 30
   |||||
Db 5 ACCGGAGGAAG 15

```

```

RESULT 284
US-08-779-916A-89
; Sequence 89, Application US/08779916A
; Patent No. 6063567
; GENERAL INFORMATION:
; APPLICANT: Gallie, Brenda L.
; APPLICANT: Dunn, James M.
; APPLICANT: Stevens, John K.
; APPLICANT: Hui, May
; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
; TITLE OF INVENTION: and Targeted Screening for Retinoblastoma
; NUMBER OF SEQUENCES: 123
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street, Suite 309
; CITY: Yorktown Heights
; STATE: NY
; COUNTRY: USA
; ZIP: 10598-4412
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,916A

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FILING DATE: 18-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/227,369  
FILING DATE: 14-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/214,582  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109348  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-986-515-6

Query Match 1.8%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels

QY 20 ACCGAGGAGAG 30  
DB 5 ACCGAGGAGAG 15  
|||||||  
|||||||

RESULT 286  
US-08-388-029A-3/c  
Sequence 3, Application US/08388029A  
Patent No. 6110665  
GENERAL INFORMATION:  
APPLICANT: FENGER, CLARA K.  
APPLICANT: GRANSTROM, DAVID R.  
APPLICANT: GAJADHAR, SARV A.  
TITLE OF INVENTION: SARCOCYTIS NEURONA DIAGNOSTIC PRIMER  
NUMBER OF SEQUENCES: 97  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER  
STREET: 99 CANAL CENTER PLAZA, SUITE 300  
CITY: ALEXANDRIA  
STATE: VIRGINIA  
COUNTRY: US  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,029A  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PRICE, ROBERT L.  
REGISTRATION NUMBER: 22,685  
REFERENCE/DOCKET NUMBER: 434-046  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-684-1111  
TELEFAX: 703-684-1124  
TELEX: AMERPAT  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs

;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; US-08-388-029A-3

Query Match 1.8%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAAGCTGA 365  
DB 14 CGCAAGCTGA 4

## RESULT 287

US-09-120-128-6  
; Sequence 6, Application US/09120128  
; Patent No. 6140473

## GENERAL INFORMATION:

;; APPLICANT: Kamb, Alexander  
;; TITLE OF INVENTION: MTS2 GENE  
;; NUMBER OF SEQUENCES: 36  
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
;; STREET: 1201 New York Avenue, Suite 1000  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA

;; ZIP: 20005

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/120,128  
;; FILING DATE:

## CLASSIFICATION:

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/486,047  
;; FILING DATE: 07-JUN-1995  
;; APPLICATION NUMBER: PCT/US95/03316  
;; FILING DATE: 17-MAR-1995

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/251,938  
;; FILING DATE: 01-JUN-1994

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/215,087  
;; FILING DATE: 18-MAR-1994

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/215,086  
;; FILING DATE: 18-MAR-1994

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/227,369  
;; FILING DATE: 14-APR-1994

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/214,582  
;; FILING DATE: 18-MAR-1994

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Innen, Jeffrey L.

;; REGISTRATION NUMBER: 28,957

;; REFERENCE/DOCKET NUMBER: 24884-109349-B

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 202-962-4810

;; TELEFAX: 202-962-8300

;; INFORMATION FOR SEQ ID NO: 6:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 19 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Homo sapiens  
;; US-09-120-128-6

Query Match 1.8%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCGAGGAG 30  
DB 5 ACCGAGGAG 15

## RESULT 288

US-08-974-549A-404/C  
; Sequence 404, Application US/08974549A  
; Patent No. 6166178

## GENERAL INFORMATION:

;; APPLICANT: Cech, Thomas R.  
;; APPLICANT: Lingner, Joachim  
;; APPLICANT: Nakamura, Toru  
;; APPLICANT: Chapman, Karen B.  
;; APPLICANT: Morin, Gregg B.  
;; APPLICANT: Harley, Calvin B.  
;; APPLICANT: Andrews, William H.

;; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

;; NUMBER OF SEQUENCES: 727

## CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, Eighth Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-3834

## COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/974,549A  
;; FILING DATE: 19-NOV-1997

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/724,643  
;; FILING DATE: 01-OCT-1996

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/844,419  
;; FILING DATE: 18-APR-1997

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/846,017  
;; FILING DATE: 25-APR-1997

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/851,843  
;; FILING DATE: 06-MAY-1997

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/854,050  
;; FILING DATE: 09-MAY-1997

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/911,312  
;; FILING DATE: 14-AUG-1997

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/912,951  
;; FILING DATE: 14-AUG-1997

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/915,503  
;; FILING DATE: 14-AUG-1997

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/US97/17618

```
;
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 404:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..19
; OTHER INFORMATION: /note= "TCP1.30 primer"
US-08-974-549A-404

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 CTGGTTCACCT 247
DB 19 CTGGTTCACCT 9

RESULT 289
US-08-938-669A-22/c
; Sequence 22, Application US/08938669A
; Patent No. 6171788
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
; TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
; TITLE OF INVENTION: RELATED DISEASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,669A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/791,154
; FILING DATE: 28-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mendelson, Elliot
; REGISTRATION NUMBER: P-42,878
; REFERENCE/DOCKET NUMBER: 07425-0034
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-6857
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

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;
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-938-669A-22

Query Match 1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GCAAGGCTGAG 366
DB 15 GCAAGGCTGAG 5

RESULT 290
US-09-120-129-6
; Sequence 6, Application US/09120129
; Patent No. 6180776
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,129
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

```
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-120-129-6

Query Match      1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      20 ACCGGAGGAAG 30
Db      5 ACCGGAGGAAG 15

RESULT 291
US-09-201-139-6
; Sequence 6, Application US/09201139
; Patent No. 6210949
; GENERAL INFORMATION:
; APPLICANT: Stone, Steven
; APPLICANT: Jiang, Ping
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,139
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/508,735
; FILING DATE:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER:
; FILING DATE: 18-MAR-1994
; NAME: Ihnen, Jeffrey L.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-201-139-6

Query Match      1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      20 ACCGGAGGAAG 30
Db      5 ACCGGAGGAAG 15

RESULT 292
US-09-120-131-6
; Sequence 6, Application US/09120131
; Patent No. 6218146
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,131
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,047
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER:
; FILING DATE: 18-MAR-1994
; NAME: Ihnen, Jeffrey L.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-120-131-6

Query Match      1.8%; Score 11; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      20 ACCGGAGGAAG 30
Db      5 ACCGGAGGAAG 15
```

Db 5 ACCGGAGGAG 15

## RESULT 293

US-08-725-027-18/c  
; Sequence 18, Application US/08725027  
; Patent No. 6251586  
; GENERAL INFORMATION:  
; APPLICANT: MUSHINE, JAMES, L.  
; APPLICANT: TUCKMAN, MELVIN, S.  
; TITLE OF INVENTION: AN EPITHELIAL PROTEIN AND  
; TITLE OF INVENTION: DNA THEREOF FOR USE IN EARLY CANCER DETECTION  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/725.027  
; FILING DATE: 02-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US08/538,711  
; FILING DATE: 02-OCT-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATHRYN M. BROWN  
; REGISTRATION NUMBER: 34,556  
; REFERENCE/DOCKET NUMBER: 2026-4201US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19  
; TYPE: nucleic acid  
; STRANDEDNESS: Unknown  
; TOPOLOGY: Linear  
; MOLECULE TYPE: other nucleic acid  
US-08-725-027-18

Query Match 1.8%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 552 TGAGGTTGATG 562

Db 17 TGAGGTTGATG 7

## RESULT 294

US-09-338-907-507/c  
; Sequence 507, Application US/09338907  
; Patent No. 6265546  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Ilyva, Chumakov  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: PROSTATE CANCER GENE  
; FILE REFERENCE: GENSET.18CF1CP  
; CURRENT APPLICATION NUMBER: US/09/338.907  
; CURRENT FILING DATE: 1999-06-23  
; EARLIER APPLICATION NUMBER: 08/996.306  
; EARLIER FILING DATE: 1997-12-22  
; EARLIER APPLICATION NUMBER: 60/099.658  
; EARLIER FILING DATE: 1998-09-09

; EARLIER APPLICATION NUMBER: 09/218.207  
; EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 578  
; SOFTWARE: Patent.pm  
; SEQ ID NO 507  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1..19  
; OTHER INFORMATION: potential microsequencing oligo for 4-22-174.mis2  
US-09-338-907-507

Query Match 1.8%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTCAAAAATGT 53

Db 17 TTCAAAAATGT 7

## RESULT 295

US-09-338-907-508/c  
; Sequence 508, Application US/09338907  
; Patent No. 6265546  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Ilyva, Chumakov  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: PROSTATE CANCER GENE  
; FILE REFERENCE: GENSET.18CF1CP  
; CURRENT APPLICATION NUMBER: US/09/338.907  
; CURRENT FILING DATE: 1999-06-23  
; EARLIER APPLICATION NUMBER: 08/996.306  
; EARLIER FILING DATE: 1997-12-22  
; EARLIER APPLICATION NUMBER: 60/099.658  
; EARLIER FILING DATE: 1998-09-09  
; EARLIER APPLICATION NUMBER: 09/218.207  
; EARLIER FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 578  
; SOFTWARE: Patent.pm  
; SEQ ID NO 508  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1..19  
; OTHER INFORMATION: potential microsequencing oligo for 4-22-176.mis2  
US-09-338-907-508

Query Match 1.8%; Score 11; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 TTCAAAAATGT 53

Db 19 TTCAAAAATGT 9

## RESULT 296

US-09-218-307-507/c  
; Sequence 507, Application US/09218207  
; Patent No. 6346381  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Ilyva, Chumakov  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Prostate cancer gene

FILE REFERENCE: GENSET.018CP1  
CURRENT APPLICATION NUMBER: US/09/218,207  
CURRENT FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 08/996,306  
EARLIER FILING DATE: 1997-12-22  
EARLIER APPLICATION NUMBER: 60/099,658  
EARLIER FILING DATE: 1998-09-09  
NUMBER OF SEQ ID NOS: 578  
SOFTWARE: Patent.pm  
SEQ ID NO 507  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..19  
OTHER INFORMATION: potential microsequencing oligo for 4-22-174.mis2  
US-09-218-207-507

Query Match 1.8%; Score 11; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 TTCAAAAATGT 53  
Db 17 TTCAAAAATGT 7

RESULT 297  
US-09-218-207-508/c  
Sequence 508, Application US/09218207  
Patent No. 6346381  
GENERAL INFORMATION:  
APPLICANT: Cohen, Daniel  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Ilyia, Chumakov  
APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: Prostate cancer gene  
FILE REFERENCE: GENSET.018CP1  
CURRENT APPLICATION NUMBER: US/09/218,207  
CURRENT FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 08/996,306  
EARLIER FILING DATE: 1997-12-22  
EARLIER APPLICATION NUMBER: 60/099,658  
EARLIER FILING DATE: 1998-09-09  
NUMBER OF SEQ ID NOS: 578  
SOFTWARE: Patent.pm  
SEQ ID NO 508  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1..19  
OTHER INFORMATION: potential microsequencing oligo for 4-22-176.mis2  
US-09-218-207-508

Query Match 1.8%; Score 11; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 TTCAAAAATGT 53  
Db 19 TTCAAAAATGT 9

RESULT 298  
US-09-306-828-22/c  
Sequence 22, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.

APPLICANT: Chen, Pu  
APPLICANT: Chen, Hua  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis ;  
CURRENT APPLICATION NUMBER: US/09/306,828  
CURRENT FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 09/227,881  
EARLIER FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 22  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-22

Query Match 1.8%; Score 11; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4e+04;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 356 GCAAGGCTGAG 366  
Db 15 GCAAGGCTGAG 5

RESULT 299  
US-08-912-951-171/c  
Sequence 171, Application US/08912951  
Patent No. 6475789  
GENERAL INFORMATION:  
APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND  
NUMBER OF SEQUENCES: 335  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,951  
FILING DATE: 14-AUG-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643



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; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-912-951-171

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Query Match 1.8%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 237 CTGGTTCACCT 247
DB 19 CTGGTTCACCT 9

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RESULT 300
US-09-336-946B-69
; Sequence 69, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A Pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 69
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-09-336-946B-69

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Query Match 1.8%; Score 11; DB 4; Length 19;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 166 CACGTGGAATT 176
DB 1 CACGTGGAATT 11

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Search completed: March 4, 2004, 23:34:15
Job time : 83 secs

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